(K138N (N166D (A137G (A137G

```
gene
gene
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-FEB-1990.
08-AUG-1988; 010706.
08-AUG-1988; FR-010706.
(GEOR\) Georges M.
Georges M. Vassart G, Christophe D, Dumont J, Young M;
WPI; 90-093373/13.
Determn. of sex of ruminant embryos-by hybridisation assay using specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       District 19 19 37pp; French.

This sequence is used as a probe and is contained in plasmid pSP64.2 5EI. This sequence is used as a probe and is contained in plasmid pSP64.2 5EI. It is homologous to the sequence of a 2.5 kb fragment of the Per gene of Drosophila. The motifs ACNGGN and/or TCAGGC (N=T, U, G, A, or C) or their complementary sequences are repeated in the probe. It is used in a hypridistation assay to determine the sex of ruminant embryos. Either (i) Southern or (ii) Dot-blot techniques can be utilised and Y-chromosome shows up as intense signal either obscuring most of the hybridisation track in (i) or surrounding the dots in (ii). Significant results can be obtd. using samples of less than 50 ng weight.
protease g
protease g
protease g
protease g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X20561;
05-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
enzyme production; ds.
Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 99-081273/07.
New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis
Mutant B
Mutant B
Mutant B
Mutant B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 ArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAs 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 19
Gaps: 0
Percent Identity: 52.632
   6675
6675
6675
6675
1.1e+03
1.1e+03
1.1e+03
1.1e+03
                                                                                                                                                                                                                                                        Q03665; standard; DNA; 2465 BP.
Q03665; 07-AUG-1989 (first entry)
Sequence homologous to Drosophila Per gene
                                                                                                                                                                                                                                                                                                                                                                                            Sex determination; ruminant embryos; ss. FR2635116-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1 to: 2465
   95.22
95.22
95.22
95.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X20561 standard; DNA; 4354 BP
X20561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44.00
2.933
78.947
                                                                                                                                                              seq_name: N_Geneseq_36:003665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:X20561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1998,
23-JUN-1998, U13041.
24-JUN-1997; US-050667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: Q03665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-31 x Q03665
                                                                                                                                                                                                                   seq_documentation_block:

DE Q03665 standard; DNA AC 003665 standard; DNA AUG-1989 (first DE Sequence homologous NA SEGS5116-A.

PD 09-FEB-1990 (PF 08-AUG-1988; 010706.

PR 08-AUG-1988; 010706.

CC 11 sequence is use of it is homologous to complementary sequence complementa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1960 GCACAGG 1966
N_Geneseq_36:Q10414
N_Geneseq_36:Q10415
N_Geneseq_36:Q10411
N_Geneseq_36:Q10412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 nGluArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCKSH3 domain-combining proteil Bacillus circulans CTTase Comples Trons 268209.31 from CDNA EST locus ze82009.31 from CDNA EST locus yy23e03.31 from CDNA EST locus yy23e03.31 from CDNA EST locus yy23e03.31 from CDNA EST locus yf1le03.31 from CDNA H. pylori GHPO 718 gene. New 1 Human immunophilin Clone hmil-Homo saplens P-TEN timnus supplement of IMAGE clone 264611. Nu IDNal specificity phosphatase P PFP 140 gene and regulatory relational tumnur suppressor TS1092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polynucleotide sequence from the pab-CWV19. O-glycosylated alph pab-CWV10 expression vector. C pab-CWV1 contg. a Tumour Necrol pab-CWV1 o-glycosylated alpha pab-CWV1 expression vector. O-sequence of circular plasmid programmer of circular plasmid prolynucleotide sequence from the polynucleotide sequence of circular plasmid prolynucleotide sequence from the page of circular plasmid prolynucleotide sequence from the page of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 -4aa IL-6 SSSS mutein. New cyst Human interleukin-6 (Ahal), Se Conding sequence for -4aa SSCC matibiotic resistance gene blaz Human caalcium signal-modulatin Enterococous faecalis genome clocksH3 domain-combining protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterococcus faecalis genome d
Mutant protease gene (deltal37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus aureus contig S
Mycobacterlophage genomic DS6A
NheI-D fragment of DS6A genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacteriophage DS6A Nhel fr
Mycobacteriophage DS6A Nhel-D
Human secreted protein cDNA fr
Cellulomonas fimi endoglucanas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence homologous to Drosoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRP 378 gene and regulatory re
                                                                                                                                                                                                                                                     -MODEL-frame-f_D2D.model -DEV-x1p
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/cgn1_1/USPTO_spool/US08653294/runat_0402000_16000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -QGAPEXT=0.000 -XGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cd1 -LIST=45 -DOCALIGN=200 -THK_SCORE-pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=Pfs -NORM-ext -MINLEN=0
-MAXLEN=1000000 -USER-US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
      out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.86
1290.22
2283.39
2283.39
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33
303.33

   N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.026
1113.30276
1104.94
1004.94
1004.94
1004.94
1004.94
1004.94
1004.94
1004.94
1120.83
1120.83
1124.45
1124.45
1124.45
1123.96
1123.96
1123.96
1124.45
1124.45
1124.45
1124.45
1124.45
1125.83
1124.45
1124.45
1124.45
1124.45
1125.83
1126.83
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127.43
1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000
OM of: US-08-653-294-31 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
Query: US-08-653-294-31
Query length: 20
                                                                                                                                                                                                                          Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:T93342
N_Geneseq_36:T93352
N_Geneseq_36:T93344
N_Geneseq_36:X14180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_36:020732
N_Geneseq_36:006283
N_Geneseq_36:020766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:043360
N_Geneseq_36:043361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:V37110
N_Geneseq_36:T07329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:T18796
N_Geneseq_36:V45137
N_Geneseq_36:T93354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_36:x07339
N_Geneseq_36:Q13865
N_Geneseq_36:Q14235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:X13111
N_Geneseq_36:Q10416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:X20561
N_Geneseq_36:Q20765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:020733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:089359
N_Geneseq_36:T39892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:X13498
N_Geneseq_36:X40398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36:T93335
N_Geneseq_36:T93353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:V74765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:T51223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:T70491
N_Geneseq_36:X37535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_36:Q34545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:Q88185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_36:V46392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:Q13864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:T09311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:X20551
                                                               Date: Feb 8, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:T7171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
```

```
'label- DHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                     misc_feature
                                                                                                                                     misc_feature
                                                                                                                                                              misc_feature
                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                          DE4021917-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                            rep_origin
                                                                                 3'utr
                                                exon
                                                                                                                                                                                        cds
   MER G
Claim 1; Page 528-530; 1150pp; English.
X20500-21243 represent polynuclectide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrella infections in animals, and for the production of biosynthetic products such as enzymes. Sequence 4354 BP; 1148 A; 1183 C; 1064 G; 931 T;
                                                                                                                                                                                                                                                                                                                                                                                                                  41. .805
*tag. e
note= "from human beta-globin (Splice acceptor)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= j
/note= "promoter and 5' non-coding region from
namster DHFR gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              non-coding region from
                                                                                                                                                                                                                                                                                                       1. .21

1. 4499 a

7.00te "binding site for oligonucleotide

EBI-2133 (022519)"

7.tag b

7.tag D

7.tote "CMV enhancer and promoter"
                                                                                                                                                                                                                                                                            Interferon; O-glycosylation; beta-globin; IFNalpha 2C;
                                                                                                 Length: 14
Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                               ...590
/*tag= c
/note= "CMV enhancer and promoter"
                                                                                                                                                                             5 IleargLeuAsnGluArgTyrArgLeuAlaIleArgLeuAsn 18 :::|||||||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= d
/note= "from CMV (Splice donor)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= g
/label= multi-cloning_site
923. .1055
/*tag= h
//note= from SV40"
                                                                                                                                                             to: 4354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag= i
note= "promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                            836. .853
/*tag= f
/label= T7_promoter
                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       namster DHFR gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "exon 1"
040. .2333
                                                                                                                                                             Align seg 1/1 to: X20561 from: 1
                                                                                                                                                                                                                                seq_documentation_block:
ID Q20765 standard; DNA; 6062 BP.
AC Q20765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= k
/label= DHFR
                                                                                                                                                                                                                                                        21-APR-1992 (first entry) pAD-CMV19.
                                                                                                                                                                                                                                                                                                                                                                                           .740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62. .922
                                                                                                 44.00
3.385
92.857
                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q20765
                                                                                                                                             US-08-653-294-31 x X20561
                                                                                                Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                      cytomegalovirus;
                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polya_signal
                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter
                                                                                                                                                                                                                                                                                                                                         promoter
                                                                                                                                                                                                                                                                                                                                                                   enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                 promoter
                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
```

```
contg. a sultable expression plasmid
Disclosure; Fig 7(A-D); 24pp; German
Disclosure; Fig 7(A-D); 24pp; German
Disclosure; Fig 7(A-D); 24pp; German
DAD-CANT9 includes CAW promoter, modified DHFR gene, splice donor and acceptor sites, Sv40 early adenylating signal, Sv40 origin, and multicloning site. The 5'-non-coding region of human IFNalpha 2C-encoding CDNA was replaced with the non-coding region of human beta-globin mRNA using PCR. A PCR product of 0.64kb resulting from HindIII and XbaI restriction enzyme digests was isolated and ligated into appropriate restriction enzyme sites of plasmid pAD-CMV19. E.coli HB101 were transformed with the ligation prods. and an expression plasmid pAD-BAD19-IFN secreting O-glycosylated human IFN-alpha 2C was identified. See also Q20764-66 and Q22517-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-JAN-1992.
10-JUL-1999; DE-021917.
10-JUL-1999; DE-021917.
10-BOEH ) BOEHRINGER INGELHEI.
Himmler A, Adolf G;
WPI: 92-025485/04.
0-91ycosylated alpha interferon, used as medicament - isolated following secretion into conditioned medium of mammalian cells
                                                  /*tag= m
/note= "binding site for EBI-1857 (Q22522)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "binding site for EBI-2134 (022518)"
                                                                                                                                                                                                                                                                                                                                                                                   3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                    q
"pBluescript portion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q20765 from: 1 to: 6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= s
/label= beta-lactamase
6038. .6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3-MX-1992 (first entry)
pAD-CMV19 expression vector.
Interferon; IFN; O-glycosylation; ss.
                                                                                                                                                                     /note= "exons 2-6"
2822. .3474
/note= "intron
2151. .2168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                  /*tag= o
/label= DHFR
3475. .3812
/*tag= p
/label= SV40
                                                                                                                                                                                                                                           DHFR
                                                                                                                                                                                                                                                                                                                  SV40
                                                                                                                        /*tag= n
/label= DHFR
                                                                                                                                                                                                                                                                                                                                           3813. .6055
/*tag= q
                                                                                               2344. .2821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q20732 standard; DNA; 6062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:020732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-31 x Q20765
```

ო

```
Tumour treatment and to understand mechanisms to rused in tumour treatment and to understand mechanisms to INF action blast style (1-4); Slpp; German.

Tumour treatment and to understand mechanisms to INF action blast style (1-4); Slpp; German.

Disclosure; Fig 6(1-4); Slpp; German.

In produce INF-BPIS (16282) is one of 30 positives clones in a screened cDNA library from induced INF-induced fibrosarcoma cells. A INF-BP had been isolated from the unithe of patients with uraemia and probes/primers were constructed from the determined amino acid sequence.

To produce a vector expressing a soluble form of TNF-binding constitution in this plasmid was cut with Xmm1, amplified by PCR and the amplified DNA cut with BamHI and EcoRI.

The resulting 0.75 kb DNA fragment was inserted into pT7/T3 alpha-19 (BRL) cut with the same enzymes to recover pINF-BP. This was cut with BamHI and EcoRI, and the recovered fragment inserted into pab-CMV1 to give the required plasmid paprNF-BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 29-7AN-1991 (first entry)

E pAD-CMV1 contg. a Tumour Necrosis Factor-Binding Protein insert.

W Tumour necrosis factor binding protein; TNF-BP; TNF-receptor;

N PAD-CMV1; SS.

N PE-393438-A.

N EP-393438-A.

Z 4-0CT-1990;

R 21-APR-1999; DE-913101.

R 21-APR-1999; DE-913101.

R 21-APR-1999; DE-913101.

R 21-APR-1999; DE-913101.

R (BOBH) BOEHRNESE 108ELHEIMINT.

I HAUDTMANN R, Himmler A, Maurer-Fogy I, Stratowa C;

R PVI; 90-312987/43.
Adolf G, Himmler A, Ahorn HJ, Kalsner I, Maurer-Fogy I; 92-056870/07.
0-glycosylated alpha-interferon - used for treatment of viral of tumour diseases
Disclosure; Fig 7 (A-D); 104pp; English.
A DNA sequence encoding IFN-alpha may be inserted into pAD-CMV19 and the recombinant prod. used to transform cells of a multicellular organism, pref. a vertebrate. The cell supernatant is harvested and the O-glycosylated prod. recovered by known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ë
                                                                                                                                                                                                                           1448 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1174 CIGGCCATICACGIAAACAGAAGAITCCGCCICAAGTICCGGTIA 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1554 G;
                                                                                                                                                                                                                           1528 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                       Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                         1506 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1565 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: Q20732 from: 1 to: 6062
                                                                                                                                                                                                    See also Q20731-43 and Q20523-26.
Sequence 6062 BP; 1580 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1679 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID Q06283 standard; DNA; 6414 BP.
                                                                                                                                                                                                                                                                                                       44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:Q06283
                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-31 x Q20732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-31_x Q06283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6414 BP;
                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seguence
                                                                                                                                                                                     methods
```

to: 6414

from: 1

to: Q06283

Align seg 1/1

```
alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                         DE4021917-A
rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             enhancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                   cds
                                                                                                                                                                                                                                                                                                                                                                                                      . ,
                                                                                                                                                                                         /*tag= a
label= EBI-1733(022529)
//octe= "start of CMV enhancer_promoter (from CDM8)"
                                                                                                                                                                                                                                           /*tag= b
/label= EBI-1733(022529)
529. "start of CMV enhancer-promoter (from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag- n
/note= "end of DHFR gene (from pSV2gptDHFR20)"
3832. 4169
/*tag- o
/label- SV40_or1
/note= "from SV2gptDHFR20"
                                                                                                                                                                                                                                                                                                                                                                                                                             /14. .1412
/*tag= f
//note= "SV40 intron and poly-adenylation site
(from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                       **tag= e
note= "SV40 intron and poly-adenylation site
from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /+tag- g
/note= "5' non-coding region and promoter of
hamster DHFR gene (from pSV2gptDHFR20)"
| 1413. 2310
| +tag- h
/note= "5' non-coding region and promoter of
hamster DHFR gene (from pSV2gptDHFR20)"
                                                                                                                                                                                                                                                                                                                             /*tag- d
/label- multi-cloning_site
/note- "HindIII-XbaI from EBI-1823,EBI-1829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= 'deletion between BglII and BamHI
'' non-coding region"
         *tag= 1
/label= mutation
/note= "A->G, disturbing EcoRI site"
(272. .3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= j
/label= mutation
/note= "A-7", disturbes PstI site"
2701. 3178
/*tag= k
/label= DHFR
/note= "exons 2-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2311. .2396
/*tag= i
/label= DHFR
/note= "hamster DHFR: exon
                                                                                                                                                                                                                                                                                             /*tag= c
/label=_T7_promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= deletion
                                                                                    seq_documentation_block:
ID Q20766 standard; DNA; 6414 BP.
                                                                                                                         |-APR-1992 (first entry)
                                                                                                                                                                                                                                                                                                                         558. .713
                                                            seq_name: N_Geneseq_36:Q20766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_difference
                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                              polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rep_origin
                                                                                                                                         pAD-CMV1.
                                                                                                                                                                               promoter
                                                                                                                                                                                                                                  enhancer
                                                                                                                                                                                                                                                                                    promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_rna
                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
```

```
O-glycosylated alpha-interferon, used as medicament - isolated following secretion into conditioned medium of mammalian cells contq. a suitable expression plasmid oblisclosure; Fig 11(A-D): 24pp; German. Plasmid pAD-CMV1 is formed from pCDM8, psv2gptDHFR20 and pBluescript SK+. The multi-cloning site is useful for the insertion of heterologous DNA, e.g. IFN. The plasmid is replicable in E.coli. See also 020764-66 and 025177-29. Sequence 6414 BP; 1677 A; 1563 C; 1557 G; 1617 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
//rate= "binding region of EBI-1733 (Q20525), start
of CMV enhancer-promoter (from CDM8)"
632. .649

    .21
    4tag a
    /note="binding region of EBI-1733 (Q20525), start of CMV enhancer-promoter (from CDM8)"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= e
/label- multi_cloning_site
/note= "HindIII-Xbal from EBI-1823, EBI-1829"
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag- b
/note- "binding region of EBI-1733 (Q20525),
of CMV enhancer-promoter (from CDM8)"
                                                                                                                                                                                           /label= EBI-1729(Q22528)
/note= "end of pBluescript vector sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 15
Gaps: 0
Percent Identity: 60.000
*tag= p
/label= M13_ori
/note= "from pBluescript SK+"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 6414
                                                                                                    /*tag= q
/label=_beta_lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O-glycosylation; ss
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= d
/label= T7_promoter
658. .713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q20766 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:

ID Q20733 standard; DNA; 6414 BP
AC Q20733;
DT 19-MAY-1992 (first entry)
DE pAD-CMV1 expression vector.

KW Interferon; IFN; O-glycosylat.
FH Key Location/Qual.
FT misc_feature 1. .21

/*tag= a
                                                                                                                                                                                                                                                                                                       10-JUL-1990; DE-021917.
(BOEH ) BOEHRINGER INGELHEI.
Himmler A, Adolf G;
WPI; 92-025485/04.
                                                                                                                                             6395. .6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.00
3.143
93.333
                                                                                                                                                                        /*tag= r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:Q20733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-31 x Q20766
                                                                                                                                                                                                                                                            16-JAN-1992.
10-JUL-1990; 021917
```

1616 T;

1558 G;

```
10-JUN-1993.
25-NOV-1992; E02718.
25-NOV-1991; DE-138621.
(BOEH ) BOEHRIGER INBELHEIM INT GMBH.
CZETTILOFSKY AP, HIMMLER A, Stratowa C, Weyer U;
Lamche H, Schaefer R;
WPI; 93-197073/24.
Screening substances that modulate receptor-dependent signal transmission path - using test cells transformed with reporter gene and regulatory sequence sensitive to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Hygromycin B phosphotransferase gene
1913. .4161
                                                                                                                                                                                                                                                                                 3 LeuAlalleArgLeuAsnGluArgTyrArgLeuAlalleArgLeu 17
                                                                                          Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag- g
/label- HSV Thymidine kinase
/note- "with polya signal"
2857. .3912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- HSV Thymidine Kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag- b
//abel- T7
//abel- T7
/*tag- c
/*tag- c
/*tag- d
/*tag- d
/*tag- d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= e
/label= Hamster DHFR gene
1737. .2261
                     1562 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label- Sv40 t intro
/note- "and polyA signal"
1553. .1736
                                                                                                                                                                                                                       to: Q20733 from: 1 to: 6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= k
/label= linker sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         13-SEP-1993 (first entry)
Sequence of circular plasmid pAHygCMV1
PCR, primer; oligonucleotide.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label = EBV or1 P
2262. .2856
                 1678 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label- pBR322
                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q43360 standard; DNA; 6623 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= cmv
68. .785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6532. .6623
                                                                                        44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:Q43360
                                                                                                                                                                   alignment_block:
US-08-653-294-31 x Q20733
                     6414 BP;
                                                                                                               Ratio:
Percent Similarity:
                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09311257-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_recomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_recomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rep_origin
                                                                                                                                                                                                                         Align seg 1/1
                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5'utr
                     g
                                                                                                                                                                                                                                                                                                                                                                                           Disclosure: Fig 11 (A-E): 104pp; English.

This expression plasmid contains an intron sequence between the multi-cloning sequence and the poly(A) site. Variations may be multi-cloning sequence and the poly(A) site. Variations may be made from pAD-CWVI, according to the amt. and position of introns w.r.t. the multi-cloning site. For example, pAD-CWVI9 (020732) comprises only one intron between the CWV promoter and the multi-cloning site. A DNA sequence encoding IFN-alpha may be then be inserted into pAD-CWVI9 and the recombinant prod. used to transform cells of a multicellular organism, pref: a vertebrate. The cell supernatant is harvested and the 0-glycosylated prod. recovered by
note= "SV40 intron and poly(A) site (from CDM8)"
                                                           *tag= g
note= "SV40 intron and poly(A) site (from CDM8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= o
note= "end of DHFR gene (from pSV2gptDHFR20)"
832. 4169
                                                                                                                                                                 413. 2310

**tag= i

note= "promoter and 5' non-coding region of

namster DHFR gene (from pSV2gptDHFR20)"
                                                                                                                             note= "promoter and 5' non-coding region of master DHFR gene (from pSV2gptDHFR20)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= s
/*tag= "binding region of EBI-1729 (Q20524),
end of pBluescript vector"
                                                                                                                                                                                                                                                                                                                           /*tag= k
/label= mutation
/note= "A -> T, disturbing the PstI site of
DHFK intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= m
label= mutation
note= "A -> G, disturbing the EcoRI site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= n
note= "deletion between BglII and BamHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09201055-A. 23-JAN-1992. 23-JAN-1992. 20-JAN-1990. DE-021917. 10-JUL-1991; DE-021917. 12-NOV-1990; DE-035877. 12-NOV-1990; DE-035877. 14-JADOL G, HIMINGER INGELHEIM. MADLÍ G, HIMINGER A, Ahorn HJ, Kalsner I, Maurer-Fogy I; WPI; 92-056870/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O-glycosylated alpha-interferon - used for treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "from pBluescript SK+". 5640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= p
/label= SV40_ori
^.^^e= "from pSV2gptDHFR20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HFR 3' non-coding region
                                                                                                             *tag= h
note= "promoter and 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= r
label= beta-lactamase
                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= 1
label= DHFR
note= "exons 2-6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also Q20731-43 and Q20523-26.
                                                                                                                                                                                                                                                                                        'note= "exon 1"
516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= q
label= M13_ori
                                                                                                                                                                                                                                        2311. .2396
/*tag= j
/label= DHFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .3273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5395. .6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
780. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   known methods
                                                                                                                                                                                                                                                                                                              misc_feature
                                      polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rep_origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rep_origin
                                                                                            promoter
                                                                                                                                                                   5'utr
                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                         THE STATE OF THE S
```

```
seq_name: N_Geneseq_36:x20551
                                                                                                                                                                                                                                        DAC DACE DATE OF THE STATE OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ID ACCEPTAGE OF THE STANDACCE FOR STANDACCE ST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmission path - using test cells transformed with reporter gene and requiatorry sequence sensitive to gene and requiatorry sequence sensitive to gene and requiatorry sequence sensitive to gene and respective to prostice 1.14,5-tripeptide and disacylgylycerine(s)

Example; Pages 107-112; 170 pp; German.

Example; Pages 107-112; 170 pp; German.

Franside for the expression of genes or cDNA under the franscription control of genes or cDNA under the for hygromycin B resistance were constructed from expression plasmids pah-CMV1 and pah-CMV2 (EPA sigh sigh) and path-CMV1 and pah-CMV2 (EPA sigh sigh) and pathore cet al 1985). Plasmid pahlygCMV1 contains the many features, given in FT. Plasmid pahlygCMV2 differs from pahlygCMV1 only in respect of the polycloning site. 'N' in quality associated in the patent application was illegible.

Sequence printed in the patent application was illegible.

Sequence 6630 BP; 1655 A; 1704 C; 1628 G; 1643 T;
inositol-1,4,5-tri:peptide and di:acyl:glycerine(s)
Example: Pages 102-107: 170 pp. German.
Plasmids for the expression of genes or cDNA under the
transcription control of CMV promoters/enhancer and selectable
for hygromycin B resistance were constructed from expression
plasmids pAD-CMV1 and pAD-CMV2 (EPA 393 438) and pHEBO (Sugden
et al 1985). Plasmid pAHyGCMV2 contains the many features,
given in FT. Plasmid pAHyGCMV2 differs from pAHyGCMV1 only in
respect of the polycloning site. 'N' in q43360 denotes where the
sequence printed in the patent application is illegible.
Sequence 6623 BP; 1651 A; 1701 C; 1626 G; 1640 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1671 CTGGCCATTCACGTAAACAGAAGATTCCGCCTCAAGTTCCGGTTA 1715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1678 CTGGCCATTCACGTAAACAGAAGATTCCGCCTCAAGTTCCGGTTA 1722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-NOV-1992; E02718.
25-NOV-1991; DE-138621.
(BOEH ) BOEHRINGER INGELHEIM INT GMBH.
Czernilofsky AP, Himmler A, Stratowa C, Weyer U;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 15
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LeuAlalleArgLeuAsnGluArgTyrArgLeuAlalleArgLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: Q43360 from: 1 to: 6623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: Q43361 from: 1 to: 6630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-58P-1993 (first entry)
Sequence of circular plasmid pAHygCMV2
PCR; primer; oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seg_documentation_block:
ID Q43361 standard; DNA; 6630 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44.00
3.143
93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:Q43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-31 x Q43360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lamche H, Schaefer R;
WPI; 93-197073/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-31 x Q43361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1993
```

```
detecting
                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Treponema pallidum nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of T. pallidum infections, particularly syphilis (laim 1; Page 483-487; ll50pp; English. X20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, diagnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detection diseases related to Borrella infections in animals, and for the production of blosynthetic products such as enzymes. Sequence 6993 BP; 1914 A; 2019 C; 1404 G; 1647 T;
                                                                           DS-MX1-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal;
enzyme production; ds.
Treponema pallidum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers

1. .543
/*tag= a /*tag= /
/product= IL-6_mutein
/note= "first 4 N-terminal amino acids are deleted
and Cys residues at positions 45, 51, 74
and 84 of wild-type IL-6 are substd. by
ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-1991; US-724698.

(IMCL-) IMCLONE SYSTEMS INC.

(UNC-) UNIV NORTH CAROLINA.

FOWIKES DM, SKelly SM, Snouwaert JN, Tackney CT;

WPI: 93-045433/05.

WPI: 93-045433/05.

New cysteine-depleted interleukin-6 mutein - for promoting cell

differentiation (e.g. of B-cells), as antiinflammatory agents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1993 (first entry)
-4aa IL-6 SSSS mutein.
Interleukin-6; mutant protein; pBgal/EK/cfIL-6; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 14
Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 IleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAsn 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: X20551 from: 1 to: 6993
                                                                                                                                                                                                                                                    30-DEC-1998.
23-JUN-1998.
24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  멾
                          X20551 standard; DNA; 6993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID Q34545 standard; DNA; 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.00
3.385
92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:034545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-31 x x20551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JAN-1993.
02-JUL-1992; U05612.
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 99-081273/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                          WO9859034-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9301212-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                  Fraser CM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                034545;
```

```
Example 1; Fig 2; 118pp; Endlish.

Plasmid pBgal/EK/cfiL-6 contains a DNA sequence which encodes a cusion protein comprising beta-galactosidase, followed by an enterokinase cleavage site, which is, in turn, followed by an enterokinase cleavage site, which is, in turn, followed by an enterokinase cleavage site, which is, in turn, followed by a synthetic IL-6 peptide sequence. The IL-6 mutein sequence is that the four cysteine residues, which occur at positions 45, 51, 74 and 84 of the mature full-length IL-6 molecule are replaced by serine residues. A truncated 0.58kb cysteine-free IL-6 sequence lacking the first 4 N-terminal most can be isolated by EcoRII-HindIII digestion. The fragment was used in the preparation of various IL-6 muteins, either full-length con N-terminally truncated. It was found that restoring the last two cys residues (at positions 74 and 84) resulted in a mutein which retained IL-6 activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                089359;
07-JUL-1995 (first entry)
Human interleukin-6 -(Alal), Ser45, Ser51, Ser74, Ser84 DNA.
Human interleukin-6; IL-6; -(Alal), Ser45, Ser51, Ser74, Ser84; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R 02-UUL-1991; 124698.

R 02-UUL-1991; US-724698.

R 02-UUL-1991; US-724698.

A (IMCL-) IMCLONE SYSTEMS INC.

INCWN-) UNIV NORTH CAROLINA.

R WPI; 94-341061/42.

R P-PSDB; R72211.

I.L-6 Mutehns in which the first two cysteine residues are replaced by scrine residues - have good activity comparable to that of native IL-6

S Example 1; F19 2; 37pp; English.

C 089359 encodes R72211 the human interleukin-6 (IL-6) mutein - (Ala1), Ser 45, Ser 51, Ser 74, Ser 84; where the native IL-6 cysteine residues in posistions 45, 51, 74 and 84 have been replaced by scrine residues, and the Ala residue in Sequence 589 BP; 193 A; 145 C; 134 G; 117 T;
                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LeuAlalleArgLeuAsnGluArgTyrArgLeuAlalleArg 16
                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                              Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: Q34545 from: 1 to: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
for treating thrombocytopenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
Q89359 standard; DNA; 589 BP.
                                                                                                                                                                                                                                                                                                                                                    43.00
3.909
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43.00
3.909
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seg_name: N_Geneseg_36:Q89359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .543
                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-31 x Q34545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-31 x Q89359
                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5359034-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5-0CT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sed
```

```
Prepare worsels worsels with two cys residues replaced and opt. N-terminal deletion, can be produced in high yield and are more active than native protein, useful e.g. as immuno-therapeutic or anti-inflammatcry agents

Frample 2; Column 31-34; 41pp; English.

Correspond to the invention. IL-6 is also known under numerous synonyms, including interferon-beta-2 (IFN-B2), B-cell stimulation factor (BSF-2), and hepatocyte stimulating factor (HSF). The mutein of the invention.

Correctin, and hepatocyte stimulating factor (HSF). The mutein IL-6 protein, and hepatocyte stimulating cells, to stimulate proliferation and differentiation of B or T cells, megakaryocytes or multipotent correcting the progenitor cells. The muteins can also induce acute phase proteins in liver cell. The proteins can be used as immunotherapeutic conferent patients undergoing chemotherapy or bone marrow transplantation. Correcting and anti-inflammatory agents, in the treatment of thrombocytopaenia, and to treat patients undergoing chemotherapy or bone marrow transplantation. By eliminating 2 of the Cys residues, purification and isolation of IL-6 is simplified, as only one Cys-Cys disulphide bond can form during comparison to wild type IL-6. By removing the hydrophobic N-terminus, the yield can be further improved. The mutein sof the invention correction which have 22 N-terminal residues deleted have activity 250-400 times that the protein and some control of the comparison of the protein and activity 250-400 times that the comparison of the protein and the control of the c
                                                                                                                                                                                       seq_documentation_block:

ID T3982

ID T0-DEC 1996 (first entry)

IN Interleukin-6. In-6; mutuchin, proliferation; differentiation; therapy;

KW T cell; megakaryocyte; multipotent haematopoletic progenitor cell; BSF-2;

KW anti-inflammatory agent; thrombocytopaenia; bone marrow transplantation;

KW interferon-beta-2; B-cell stimulation factor-2; 26 kDa protein; IFN-B2;

KW B-cell hybridoma/plasmacytoma growth factor; HPGF; HGF; HSF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ĥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Snouwaert JN, Tackney CT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 14
Gaps: 0
Percent Identity: 57.143
                                             -4 aa interleukin-6 SSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
/note= "optionally deleted"
to: 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .546
  Align seg 1/1 to: 089359 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the wild type IL-6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .340
/*tag= a
/product= .
1. .72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-JUL-1991; US-724698.
02-JUL-1992; US-907710.
10-MAR-1994; US-209122.
(UYPR-) UNIV PRINCETON.
FOWLKES DM, SKelly SM, 9
WPI; 96-383669/38.
                                                                                                                                              seq_name: N_Geneseq_36:T39892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.909
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-31 x T39892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         724698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
   Quality:
   Ratio:
   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; W05586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   that of
```

37. .927 /\*tag= a

```
P-PSDB; R87038.

Talcium signal-modulating cyclophilin, and DNA encoding it - useful for diagnostic purposes, and for identifying agents for modulating the calcium-induced activation pathway.

The calcium-induced activation pathway.

Claim 1; Page 20-21; 33pp; English.

Claim 1; Page 20-21; 33pp; English.

Claim 1; Page 20-21; 33pp; English.

This sequence encodes human calcium signal-modulating cyclophilin ligand (CAML). It may be used as a probe to identify CAML genes in effect on CAML expression, to provide antisense sequences to hosts other than human, in diagnosis, to screen agents, to produce investigate cellular responses to external agents, to produce recombinant capacity. Any also be used to express a fragment of the CAML protein, and to express a fragment of the CAML may also be used to screen putative modulators of the calcium-activated pathway for their effects on expression of one or more genes under regulatory control of the pathway. Host cells for expression of recombinant CAML include Escherichia coli, capacitate the role of CAML are usually mammalian cells used to investigate the role of CAML are usually mammalian cells.

Claim-activated pathway for their are usually mammalian cells used to investigate the role of CAML are usually mammalian cells.

Claim-activated pathway for the pathway can include the role of CAML are usually mammalian cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutic contraception, infertility, learning and memory disorders and the like.
                                                                                              28-DEC-1995.
16-JUN-1995; U07752.
17-JUN-1994; US-261662.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bram RJ, Crabtree GR;
WPI; 96-058511/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-31 x T07329/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
   Will 99 - 20 follogonucleotide primers and probes - for detection, dentification and quantification of bacteria, fungi and bacterial dentification and quantification of bacteria, fungi and bacterial antification and quantification of bacteria, fungi and bacterial claim 19; Page 108; 167pp; English.

The present sequence represents an antibiotic resistance gene blaz (resistant to beta-lactams), and was used to design PCR primers (resistant to beta-lactams), and was used to probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and amount of nucleic acids from a bacterial antibiotic resistance gene and specific bacterial and fungal species in any sample suspected of containing the bacterial or fungal nucleic acids, where each of the nucleic acid or variant or part comprises a selected target region hybridisable with the probes or primers and detecting the presence of hybridised probes or amplified products as an indication of the presence of the specific bacterial or fungal species and bacterial antibiotic resistance genes. The methods and products can be used to detect and identify the bacterial and fungal species and genera and determine the bacterial resistance to antibiotics.

Sequence 846 BP; 356 A; 99 C; 135 G; 256 T;
                                                                                                                                                                                                                                                                                                                                                                                       Antibiotic resistance gene blaz for beta-lactams.
Detection; bacterial antibiotic resistance gene; bacteria;
fungal species; identification; beta-lactam; ds.
                                                                                                  16
                                                            3 LeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1998.
04-NOV-1997; CA0829.
(IDII-) IDI INFECTIO DIAGNOSTIC INC.
Bergeron MG, Ouellette M, Picard FJ, Roy PH;
WPI; 98-286967/25.
Align seg 1/1 to: T39892 from: 1 to: 589
                                                                                                                                                                                                                                                             seq_documentation_block:
ID     V37110 standard; DNA; 846 BP.
                                                                                                                                                                                                                                                                                                                                                     04-SEP-1998 (first entry)
                                                                                                                                                                                             seq_name: N_Geneseq_36:V37110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
```

```
1194 AAGTTAGAGGAAAGGTACAGAATAGGAATTCTGATTAACAAGAAA 1150
                                                                                  6 ArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAsnGluArg 20
Align seg 1/1 to reverse of: T07329 from: 1 to: 1391
```

Length: 12 Gaps: 0 Percent Identity: 58.333

Align seg 1/1 to reverse of: V37110 from: 1 to: 846

alignment\_block: US-08-653-294-31 x V37110/rev

Ratio: 3.583 Percent Similarity: 100.000

43.00

Quality:

8 AsnGluArgTyrArgLeuAlaIleArgLeuAsnGlu 19

seq\_documentation\_block:
ID T07329 standard; cDNA; 1391 BP.

seq\_name: N\_Geneseq\_36:T07329

05-JUL-1996 (first entry)

Human calcium signal-modulating cyclophilin ligand coding sequence. Human calcium signal-modulating cyclophilin ligand; DNA probe; calcium-activated pathway modulator drug screening; diagnosis; treatment; contraception; infertility; learning disorder; memory disorder; Escherichia coli; Saccharomyces cerevislae; CHO; COS; Jurkat; Chinese hamster ovary; H9C2(2-1); ds. Homo sapiens.

Location/Qualifiers

362 T;

332 G;

280 C;

417 A;

Percent Identity: 46.667

43.00 3.071 93.333

Length:

us-08-653-294-31.rst

```
qv02b02.x1 NCI_CGAP
SRN035KS Winter flo
qm21e02.x1 NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                        ELVATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 427)

1 (Dases 1 to 427)

1 NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

1 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

1 Tumor Gene Index

1 Unpublished (1997)

1 On May 18, 1998 this sequence version replaced gi:3138601.

2 Contact: Robert Strausberg, Ph.D.

2 Tel: (301) 496-1550

2 Email: Robert Strausbergenih.gov

2 Oligo-dr track not found, Not I site shown in beginning of sequence is likely internal to the message. CDNA Library Preparation: M.B.

3 Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

3 Www-bb.linl.gov/bbpp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /u. ac. /
/ L. ac. /
/
                                                                                                                                                                   seq_documentation_block:
LOCUS AW015295 427 bp mRNA EST 10-SEP-1999
DEFINITION UI-H-BIO-aap-d-02-0-UI.sl NCI_CGAP_Subl Homo sapiens CDNA clone
IMAGE:2709939 3', mRNA sequence.
   AI287354 AW013132 SAI279828
99.07
103.52
125.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .427
   134.58
134.24
132.77
                                                                                                                                                                                                                                                                                           AW015295
AW015295.1 GI:5864052
                                                                                                                     seq_name: gb_est37:AW015295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLYA-NO.
                                                                                                                                                                                                                                                                                                                                                                                   human.
   gb_est25:AI287354
gb_est37:AW013132
gb_est25:AI279828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AM49243 ti27g11.x1 NCT_CGAP_KI
AI762057 w153a10.x1 NCT_CGAP_KI
AI443378 ED30004.x1 Zebrafish W
AI447227 da16c03.x1 normalized
AW47713 da16c03.x1 normalized
AW47713 da16c03.y1 normalized
AV074366 Mus musculus
AI070642 UI-R-CZ-mv-q-10-0-01.s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A157818 and A177818 and A1778986 and A1778988 and A177878 and A17787878 and A177878 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1328939 a8a03ne.fl Neurospora
A0514060 HS_5184_A1_E05_SP6E RH
A0500194 V3377 mTn=3xHA/lac2
AV266473 AV266473 RIKEN full-le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AI649944 486099E09.x1 486 - lea
AG008494 Homo sapiens genomic D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ! AQ892181 HS_5339_B1_F08_SP6 RF
! C95817 C95817 Marchantia polymo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL051558 Drosophila melanogaste
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  yy29d12.s1 Soares meland
                                                                                                                                                                                           Command line parameters:
-MODEL-frame+_p2n.model -DEV-xlp
-Q-fcgnll_I/USPTO_spool/VS08653294/runat_04022000_160700_15770/app_query.fasta.2
-Q-fcgnll_I/USPTO_spool/VS08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB-EST -QFWT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -PGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YARAP-1 -MATHIX-blosum62 -TRANS-human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE-PCT -ALIGN=15 -MODE-LOCAL
-UST=45 -NORM-ext -MINLEN-0 -MAXLEN-1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EScore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1123.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.0000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.0000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.0000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.0000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.0000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.000
1140.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.41
76.11
56.64
72.67
94.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                785036
1158.16
1158.16
1158.16
1159.16
1150.16
1147.32
1147.32
1147.33
1147.09
1137.00
1134.96
1137.00
1131.34
1130.33
1131.34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134.99
1334.79
133.67
132.81
131.35
130.00
130.00
129.96
129.86
      ESI: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 7600.090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.2.00
25.2.00
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
25.2.000
   OM Of: US-08-653-294-31 to:
                                                            6:23 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query: US-08-653-294-31
Query length: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence

9b_est37:AW015295

9b_est23:AI7492423

9b_est27:AI437378

9b_est27:AI437378

9b_est27:AI437277

9b_est27:AI47713

9b_est40:AW147773

9b_est33:AV074366

9b_est23:AI070642

9b_est27:AI997515

9b_est26:AI328939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss15:AQ593550
gb_est32:AI757858
gb_est32:AI757463
gb_est32:AI755661
gb_gss11:AQ305795
gb_gss14:AQ579370
gb_gss5:AQ579370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_gss15:A0591361
gb_est34:AV139866
gb_est1:D15447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss14:AQ514060
gb_gss13:AQ500194
gb_est41:AV266473
gb_est37:AI998122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est5:N32286
gb_est30:A164994
gb_gss1:AC008494
gb_gss1:CNS008B1
gb_gss6:AQ892181
gb_est30:C95817
                                                         Date: Feb 8, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est39:AV209827
gb_est19:AA773968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gssll:AQ334845
gb_est32:AI738375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_est19.AA263821
gb_est28.AI512344
gb_est28.AI543580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est14:AA454364
gb_est24:AI103506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss10:AQ215334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_gss4:AQ691068
```

```
3.714
                                                                                                                                                               52.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est32:AI762057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS A1762057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sednence.
                                                                                                                                                                  Quality:
                                                                                                                                                                                                   Percent Similarity:
                                                            97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                         18 nGlu 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 CGAG 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumor Gene Index Tile Index Contest States From France Index (1997)
On May 7, 1998 this sequence version replaced g1:3121386.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nlh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CLOR distribution: No. CRAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINE at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NoT_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI492423 523 bp mRNA EST 30-WAR-1999
ti27g11.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2131748 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo Sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 523)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                        to: 427
                                                                                                                                                             Length: 18
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .523
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ImAGE:2131748"
/clone_lib="NCI_CGAP_Kid11"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ww-bio.lln1.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AW015295 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert Length: 731 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 453. Location/Qualifiers
                                                              57
TAG_LIB=NCI_CGAP_Pr22
TAG_TISSUE=prostate
TAG_SEQ=AAGIG"
                                                            161 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI492423.1 GI:4393426
                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-31 x AW015295/rev
                                                                148 c
                                                                                                                                                                                  3.714
                                                                                                                                                                  52.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est28:A1492423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
AI492423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                  Quality:
                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                    Ratio:
                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                         18 nGlu 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 CGAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                 ORIGIN
```

```
/note-"Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_CO10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.D., Ph.D. CDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. CDNA Elbrary Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wi59a10.x1 NCI_CGAP_co16 Homo sapiens cDNA clone IMAGE:2393946 3' similar to contains TAR1.tl MER22 MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Matazoa, Chordata, Craniata, Vertebrata, Mammalia, Butherla, Primates, Catarrhini, Hominidae, Homo.

Butherla, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 524)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Carmor Gene Index.

Unpublished (1997)

On Jun 5, 1996 this sequence version replaced gi:3187034.

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov

Tissue_Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
(cloneIDs 1322376-1323911, 1456007-1456775, and 1500522-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAs 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 18
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:239346"
/clone_lib="NCI_CGAP_Co16"
/tissue_type="colon tumor, RER+"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::
2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnI.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AI492423 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469.
                                                                                                   152 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -40UP from Gibco
High quality sequence stop: 4
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AI762057.1 GI:5177724
                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-31 x AI492423/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 bp
```

```
/tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est27:A1416006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     zebrafish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 G 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 u 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESM Danio rerio

Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Actinopterygli; Reopterygli; Teleostel; Euteleostel; Ostariophysi; Cypriniformes; Cyprinoidea; Cyprinidea; Rasborinae; Danio.

I (bases 1 to 525)

Cyprinoson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R., and Wilson,R., Waterston,R., and Wilson,R., Washu Zebrafish EST Project 1998

Nu Unpublished (1998)

On May 18, 1998 this sequence version replaced gi:3138276.

Contact: Stephen L., Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A1437378 525 bp mRNA EST 09-MAR-1999 fb30h04.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA 3' similar to SW:PTEN_HUMAN 000633 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Zbrafish@watson.wustl.edu
CDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
from a pool of 5,000 clones made from the same library (cloneins 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
193 c 190 g 78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Possible reversed clone: similarity on wrong strand
                                                                                                                                                                                                                                                                                                                                                                                          1. .525
/organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                 to: 524
                                                                                                                                                                                  Length: 18
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: T7 ET from Amersham
High quality sequence stop: 426
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AI762057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
A1437378
A1437378.1 GI:4285423
                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-31 x AI762057/rev
                                                                                                                                                                             52.00
3.714
77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est27:A1437378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS A1437378
                                                                     ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zebrafish
                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
                                                                     63
                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 nGlu 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :|||
14 CGAG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
```

```
**Label Computer State S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Exaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopteryg11; Buckaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopteryg11; Releoste1; Buteleoste1; Ostariophys1; Cypriniformes; Cyprinoidea; Cyprinidae; Rasborinae; Danio.

I (bases 1 to 531)

SS Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Ferson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998

AL Unpublished (1998)

On May 7, 1998 this sequence version replaced gi:3119070.
Contact: Stephen L., Johnson

Washington University School of Medicine

4444 Forest Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS A1416006 531 bp mRNA EST 09-FEB-1999
DEFINITION 12 26brafish WashU MPING EST Danio rerio CDNA 5' similar to SW:PTEN_HUMAN 000633 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE PTEN ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrargleualaileargleuasnGluargTyrargleualaileargle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 17
Gaps: 0
Percent Identity: 52.941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
AI416006
AI416006.1 GI:4259510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.00
3.188
94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: AI437378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-31 x AI437378
```

```
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                    TITLE
JOURNAL
                   REFERENCE
                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: InfoGenomesystems.com) and Research Genetics, Huttsville, Alabama (web address: www.resgen.com) (amail contact: infoGenomesystems.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS AW14727 235 bp mRNA EST 30-NOY-1999
DEFINITION dal6c03.x1 normalized Xenopus laevis gastrula Xenopus laevis cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;
                                                                                                                                                                                                                                                                                            /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone XENOPUS_SOURCE_ID:Xlnga001n05 3', mRNA sequence.
AW147227
AW147227.1 GI:6195123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 17
Gaps: 0
Percent Identity: 52.941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AI416006 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 t
                                                                                                                                                                                                                                                                                                              stage embryos"
/lab_host="XL1-blue MRF"
zbrafish@watson.wustl.edu
                                                                                                                                                                                                                        /organism-"Danio rerio"
                                                                                                                                   www.rzpd.de)
Seg primer: T3 ET from Amersham
High quality sequence stop: 485.
Location/Qualifiers
1. 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 g
                                                                                                                                                                                                                                                                            /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-31 x AI416006/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.00
3.188
94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est40:AW147227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357 G 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 u 17
                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
```

```
1 (bases 1 to 235)
Johnson, S.L., Blumberg, B., Song, J., Clifton, S., Hillier, L.,
Pape, D., Martin, J., Wylie, T., Underwood, K., Theising, B., Bowers, Y.,
Person, B., Gibbons, M., Harvey, N., Ritter, E., Jackson, Y., McCann, R.,
Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
Library constructed by Bruce Blumberg
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
Hos library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AW147713 246 bp mRNA EST 30-NOV-1999
DEFINITION dailoc03.yl normalized Xenopus laevis gastrula Xenopus laevis cDNA clone XENOPUS_SOURCE_ID:xlnga001n05 5', mRNA sequence.
ACCESSION AW147713 GI:6195609
                                                                                                                                                               On Dec 20, 1995 this sequence version replaced gi:1135577.
Other ESTs: daisc03.y1
Contact: Stephen L. Johnson/WashU Xenopus EST project, 1999
WashU Xenopus EST project, 1999
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="normalized Xenopus laevis gastrula"
/tissue_type="gastrula (stages 10.5, 11.5 mixed)"
/lab_host="Top-10 F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .235
/organtsm="xenopus laevis"
/db_xref="taxon:8355"
/clone="xENOPUS_SOURCE_ID:xinga001n05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AW147227 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blumberg, unpublished).
                                                                                                                 WashU Xenopus EST project, 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-31 x AW147227/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 4.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est40:AW147713
```

TITLE JOURNAL COMMENT

FEATURES

REFERENCE AUTHORS

KEYWORDS

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Manmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinee; Mus.

2E 1 (bases 1 to 287)

3S Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K., Akahira, S., Akiyama, J.; Fukuda, S., Fukunishi, Y., Funayama, T., Akahira, S., Akiyama, J.; Fukuda, S., Fukuchi, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Gwai, J., Kikuchi, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Gwai, J., Sayahara, Y., Shizaki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y., Tominaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T., Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.

Unpublished (1999)

On Dec 20, 1995 this sequence version replaced gi:1134354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 81-298-36-9145

Fax: 81-298-36-9098

Email: genome-researc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length CDNA (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))

Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))

Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
AV074366 287 bp mRNA EST 24-JUN-1999
AV074366 Mus musculus stomach C57BL/6J adult Mus musculus CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS A1070642 345 bp mRNA EST 05-JUL-1999
DEFINITION UI-R-C2-mv-g-10-0-UI.sl UI-R-C2 Rattus norvegicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Mus musculus stomach C57BL/6J adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ArgleualalleargleuasnGluargTyrargleualalleargleuas 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koyadai, Isukuba, Ibaraki 305-0074, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 19
Gaps: 0
Percent Identity: 57.895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism-"Mus musculus"
                                                                          clone 2210008P05, mRNA sequence.
AV074366
AV074366.1 GI:5194194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2210008P05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="stomach"
/dev_stage="adult"
76 c 63 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Socation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AV074366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Science Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-31 x AV074366/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.00
3.000
84.211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est22:AI070642
                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                  house mouse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 nGluArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 GCTCAGG 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
       LOCUS
                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                     ACCESSION
                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                               Xenopus.

'Se (bases 1 to 246)

'S Johnson,S.L., Blumberg,B., Song,J., Clifton,S., Hillier,L.,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Pape,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Waterston,R. and Wilson,R., Hirvey,N., Ritter,E., Jackson,Y., McCann,R.,
Washu Xenopus EST project, 1999

'M. Unpublished (1999)

On May 1, 1997 this sequence version replaced gi:2059622.

Other_ESTs: dal6c03.x1

Washington University School of Medicine

#444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810

Email: est@watson.wustl.edu

Library constructed by Bruce Blumberg

Library constructed by Jihwan Song

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Asnopus clone distribution information for

this library can be found through Research Genetics, visit their

web page at: http://www.resgen.com/
Seq primer: -don/Oniminifica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualiflers

Location/Gualiflers

/clone="XENOPUS_SOURCE_ID:xInga001n05"

/clone="XENOPUS_SOURCE_ID:xInga001n05"

/clone="Incompose the constant of the color o
                                                                                                                 Amphibia;
Xenopodinae;
                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blumberg, unpublished)." 52 c 59 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AW147713 from: 1 to: 246
                                          African clawed frog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 48.00
Ratio: 4.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-31 x AW147713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est33:AV074366
                                                                                     Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                              ORGANISM
```

BASE COUNT

```
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AI997515.1 GI:5844420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.00
3.429
73.684
                                                         to: AI070642
     US-08-653-294-31 x AI070642
                                                                                                                                                                                                                                                                                                                          seq_name: gb_est37:A1997515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                         Align seg 1/1
                                                                                                                                                                                                                                                                           338 G 338
                                                                                                                                                                                                                      19 u 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
                                                                                                                                                                                                                                                                                                                                                                                              Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 315 8256
Email: msoares@blue.weeg.ulowa.edu
Fax: 319 335 9565
Email: msoares@blue.weeg.ulowa.edu
The sequence tag present in the cDNA between the NotI site and the
Oligo-dr track served to identify it as a clone from the normalized
adult 12-Day-Embryo library. CDNA Library Preparation: M. Fatima
Bonaldo, Ph.D. Clone distribution: clones will be available through
Research Genetics This clone is also available through the
I.M.A.G.E. Consortium at LLNL (info@image.llnl.gov). IMAGE
Del?AeNo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev. stage="adult" R-C2"
//dev. stage="adult" R-C2"
//dev. stage="adult" R-C2"
//dev. stage="adult" R-C2"
//lab_host="vector: pT73D-Pac (Pharmacia) with a modified
//lab_host="vector: pT73D-Pac (Pharmacia) with a modified
polylinker: Site_1: Not I; Site_2: Eco RI; The UI-R-C2
library; which is a subtracted library derived from the
UI-R-C0 library. The UI-R-C0 library consisted of a
mixture of individually tagged normalized libraries
constructed from rat placenta, adult lung, brain, liver,
kidney, heart, spleen, ovary, muscle, 8, 12 and 18-day
embryo. The tag is a string of 3-5 nucleotides present
between the Not I site and the oligo-dT track which allows
identification of the library of origin of a clone within
the mixture. The subtracted library (UI-R-C2) was
constructed as follows: PCR amplified cDNA inserts from
UI-R-C1 clones from within 3' Sirgh abeen derived was
used as a driver in a hybridization with the UI-R-C1
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DHIOB bacteria (Life Technologies) to generate the
UI-R-C2 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-805, 1996,
                                                                                                                                                                                                                 1 (bases 1 to 345)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                    Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                              On Sep 12, 1996 this sequence version replaced gi:1404937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 58.824
UI-R-C2-mv-g-10-0-UI 3', mRNA sequence.
AI070642

    .345
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="UI-R-C2-mv-g-10-0-UI"
/clone_lib="UI-R-C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                    Genome Rés. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 g
                                                       AI070642.1 GI:3396893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48.00
                                                                                                                Norway rat
                                                                                                                                                                                                                                                                                                      discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                 ACCESSION
                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                     MEDLINE
                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
```

DEFINITION

18

ACCESSION

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

```
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
7e1: (206) 616-3887
Fax: (206) 616-3887
Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pleteréde-jong.med-buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 760 row: I column: 9
                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                    AQ514060 507 bp DNA GSS 05-MAY-1999 HS_5184_A1_E05_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=760 Col=9 Row=I, genomic survey sequence. AQ514060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
119 c 107 g 143 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence-tagged connectors: A sequence approach to mappin scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=760 Col=9 Row=I"
/clone_llb="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAs 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 19
Gaps: 0
Percent Identity: 47.368
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AQ514060 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 507.
Location/Qualifiers
1. 507
                                                                                                                                 AQ514060.1 GI:4746351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-31 x AQ514060/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.00
2.765
89.474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_gss13:AQ500194
                       seq_documentation_block:
LOCUS AQ514060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             388 AGAAAGA 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 nGluArg 20
                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                             a8a03ne.fl Neurospora crassa evening cDNA library Neurospora crassa cDNA clone a8a03ne 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"vector: pBlueScript SK-; Site_1: XbaI; Site_2:
ECORI; See: Bell-Perdersen,D., et al. PNAS 93:13096,1996.
5' end of cDNA cloned into XbaI site of pBluescript; 3'
end of cDNA cloned into ECORI site of pBluescript"
16 c 9 c 9 Il8 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: broe@ou.edu
We anticipate the future release of the cDNA clones to the Fungal
Genetics Stock Center
Seq primer: Universal Forward Primer
High quality sequence stop: 343.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Neurospora crassa evening cDNA library" /tissue_type="tissue harvested following 22hr growth in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 484).
Zhu, H., Lal, H., Kupfer, D., Dunlap, J.C. and Roe, B.A.
Two Neurospora crasa EST Databases
Unpublished (1998)
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Fax: 405 325 4912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neurospora crassa.
Neurospora crassa
Eukaryota; Fungi; Ascomycota; Pyrenomycetes; Sordariales;
                                                                                                                                 2 ArgLeuAlaIleArgLeuAsnGluArgTyrArgLeuAlaIleArgLeuAs
                                                                   to: 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to reverse of: AI328939 from: 1 to: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 68.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. 484
/organism="Neurospora crassa"
/strain="Strain 30-7 (bd; A)"
/db_xref="taxon:5141"
                                                                   to reverse of: A1997515 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="a8a03ne"
                                                                                                                                                                                                                                                                                                                                                                                                                                                AI328939.1 GI:4065498
alignment_block:
US-08-653-294-31 x AI997515/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-31 x AI328939/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47.00
3.615
81.250
                                                                                                                                                                                                                                                                                          seq_name: gb_est26:AI328939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_gss14:AQ514060
                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
Locus AI328939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                              295 CTATCGA 289
                                                                                                                                                                                                    nGluArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
```

to: 507

BASE COUNT ORIGIN

```
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.

1 (bases 1 to 533)

1 (bases 1 to 533)

1 (bases 1 to 503)

2 (bases 1 to 503)

2 (bases 1 to 503)

2 (bases 1 to 503)

3 (bases 1 to 503)

4 (bases 1 to 503)

4 (bases 1 to 503)

5 (bases 1 to 503)

5 (bases 1 to 503)

6 (bases 1 to 503)

6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pHSS6-Sal; A yeast genomic DNA library leakth.pdf. leakthg mitochondrial DNA) was prepared in pHSS6-Sal; genomic DNA was size-fractionated (DNA of roughly 2-3 kb in length) prior to cloning. This library was ubsequently mutagenized with a min-3xHA/Lacz minitransposon containing lacz, URA3, and tet resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.

Mus musculus.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia: Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 271)

Ronno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,

Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,

Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV266473 271 bp mRNA EST 05-NOV-1999 AV266473 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 4930518A01 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Distriction and 1955 of the read conduct of interposed regards on Peb 19, 1999 this sequence version replaced gi:4143976. On Peb 19, 1999 this sequence version replaced gi:4143976. Contact: Kumar A Michael Snyder, Dept. of Mol. Cell. and Dev. Biology vale University P.O. Box 208103, New Haven, CT 06520-8103, USA Tel: 203 432 9949 Fra: 203 432 9161 Email: anul kumareyale.edu te of mrn-3xHA/lacz insertion. Seq primer: GGCCTTCTTTGTGAAGTAC Class: transposon-tagged. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .533
/organism="Saccharomyces cerevisiae"
/db_xxef="kaxon:4932"
/clone_lib="mTn-3xRA/lac2 Insertion Library"
/lab_host="E. col1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 14
Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AQ500194 from: 1
                                                                                                                                                       Saccharomyces cerevisiae
                                    AQ500194.1 GI:4705016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV266473.1 GI:6254510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47.00
3.615
92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-31 x AQ500194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est41:AV266473
                                                                                                                       baker's yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AV266473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AV266473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                    VERSION
KEYWORDS
SOURCE
ACCESSION
                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

```
RAIL C. ACRAHLA. Y. KINCHA, N. Y. Ojima, Y. W. Orda, H. Ohrazhi, Y. Ohalestowan T. WHILE H. M. C. M. C. Shiber N. Shiber N. Salo, H. Sazok, Sazo, M. Sazok, Shiber N. Shiber N.
```

```
18 nGluArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/cultivar="Columbia Col-0"
/cultivar="Columbia Col-0"
/cultivar="Columbia Col-0"
/clone="701672303"
/clone="701672303"
/clone="1016720303"
/clone="1016720303"
/clone="1016720303"
/clone="1016720303"
/clone="1016720303"
/clone="1016720303"
/clone="1016720303"
/clone="101672030"
/clone="101672030"
/clone="1016720"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen, J., Momiyama, M., Chan, E., Mooney, M., Carroon, B., Gilliland, D., Wang, X., Hillman, J., Guegler, K., Kim, C., Doyle, M., Brzoska, P., Gorgone, G., Burns, D., Griffin, J., Mouanoutoua, M., Nguyen, D., Tan, R., Rose, M., Warren, B., Too, B., Kastury, K., Borillo, C., Carpio, T., Policky, J., Suzuki, G., Argentine, C., Shah, S., Nobriga, A., Murry, L., Turner, C., Krikorian, S., Elder, L. and Hanson, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                           A1998I22 330 bp mRNA EST 08-SEP-1999 7016/2303 A. thaliana, COlumbia Col.0, rosette-1 Arabidopsis thaliana cDNA clone 701672303, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189440.
Contact: David Smoller, Ph.D.
Genome Systems, Inc., a wholly owned subsidiary of Incyte Pharmaceuticals, Inc.
4633 World Parkway Circle, St. Louis, MO 63134, USA
Fax: 314-427-273
Email: service@genomesystems.com.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana Gene Expression MicroArray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 19
Gaps: 0
Percent Identity: 52.632
                                                                                                                                                                                                                   169 GCTGTAAGAGTAAATGCTAGGTATCGAGTTGCTGTCACCCTC 210
                                                                                                                                                                    4 AlaileArgLeuAsnGluArgTyrArgLeuAlaileArgLeu 17
                                                                                  to: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the pSPORT vector.
                                                                                  to: AV266473 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI998122.1 GI:5844957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis.
1 (bases 1 to 330)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.00
2.875
84.211
US-08-653-294-31 x AV266473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-31 x AI998122
                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est37:AI998122
                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               thale cress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
```

to: 330

from: 1

Align seg 1/1 to: A1998122

```
||||||||:::::||||||:::
150 AGGCTCANGCTCAGGCTCAGGCTCAGGCTCAGGCTCAGGCTCAG 199
2 ArgleuAlalleArgleuAsnGluArgTyrArgleuAlalleArgleuAs 18
```

200 GCTCAGG 206

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 4.434 Million cell updates/sec Run on:

US-08-653-294-32

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 Total number of hits satisfying chosen parameters:

188963 seqs, 23686106 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	1de	3270	2	Peptide B2702.60-8	Peptide fragment o	HLA-B2702 CTL modu	HLA-B2705.60-84. C	Sequence of the hu	Sequence encoded b	CTL modulating pep	Human HLA-B27 alph	fragme	CIL	_:	60-84	of o	eq ID No	e of HLA	HLA-Bw53 exon. HLA	Ø	. 7	Peptide B2702.70-8	Human HLA-B27 alph	Peptide fragment o	HLA-Bw62 CTL modul	HLA-Bw62.60-84. Co	Peptide fragment o	HLA-Bw46 CTL modul	-09:	ď	c exon Cb-1	št C	Peptide fragment w	335
SUMMAKIES	DI DI		R83090	R95416	W33794	R41221	R83091	R95417	P70590	P70155	R83071	W58992	R48286	R83093	R95422	R95431	R03142	Y06801	R03144	R12463	P80911	R92912	W33795	W58993	R41207	m	n	R41206	m	n	$\overline{}$	$\sim$	^	R41203	$\sim$
	DB	- 7	ᆏ	Н	П	Н	7	Н	П	٦	H	1	П	1	1	П	П	Н		Н	-		П	-	П	-	-	Н	-	-	7		-	Н	Н
	Length	. 7	25	25	25	25	25	S	337	9	56	21	25	25	25	25	9	œ	362	9	_	15	15	13	25	25	25	25	25	22	45	366	9	12	362
	Query		•		•																													51.1	
04-			Н	-	-																														
	Score	13	133	133	133	118	118	118	118	118	112	109	106	106	106	104	101	95	95	95	88	74	74	73	72	72	72	70	70	70	70	70	2	9	99
	Result No.		7	m	4	S	9	7	80	ģ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

HLA-C exon Cb-2. H Human HLA-B27-(62- Human MHC 1 alpha Probe F10-encoded HLA B27 hypervaria MHC Class I-derive MHC I peptide Dk-( Human MHC 1 alpha Peptide fragment o HLA-B2702/05 CTL m HLA-B2702/05 CTL m
R12466 R71442 R71435 P81149 P81149 R50266 R20116 R69619 R41213 R81076 R95424
нанананана
366 177 177 3454 165 100 100 100 100
4444444444 8777888444 94499111444
00000000000000000000000000000000000000

## ALIGNMENTS

AC R41205 standa AC R41205; DT 15-MAR-1994 DE PEPTIDE fragm Human leukocy KW Parasitic dis Os Synthetic. PN W09317699-A. PD 16-EEP-1993. PR (STRD) UNIV PI (STRD) CIANDE FREE CONTRACTOR CONTR	(first entry) ent of Class I HLA peptide. teantiges; HLA; peptide; transguase; cytotoxic T lymphocyte; m U01758. U01758. Krensky AM; A/38. Crensky AM; A/38.
	(first entry) ent of Class I HLA peptide.  te antigen; HLA; peptide; transplant ease; cytotoxic T lymphocyte; modula U01758. US-844716. US-844716. US-84716. US-84716. US-854716. US-8519P; English: US-851 51PP; English: US-852 51PP; English: US-854 51PP; English: US-854 10 amino entry US-855 61PP; English: U
	(inter entry) te antigen; HLA, peptide, transplant tease; cytotoxic T lymphocyte; modula ease; cytotoxic T lymphocyte; modula 101758. US-644716. LELAND STANFORD JUNIOR. KRENSKY AM; A38. Dased on Class I HLA antigen domai totoxic T-lymphocyte activity towarc 5.55; Glpp; English. entry English. minus to a sequence other than that sed to modulate cytotoxic T-lymphocy ised to modulate cytotoxic T-lymphocy ised to modulate cytotoxic T-lymphocy ishtinon or stimulation. It can be u toxicity in transplantations, for
	case; cytotoxic T lymphocyte; modula case; cytotoxic T lymphocyte; modula colors.  US-844716.  LELAND STANFORD JUNIOR.  "Krensky AM; 4/38 do no class I HLA antigen domaitoxic T-lymphocyte activity toward totoxic T-lymphocyte activity toward so a fragment of at least 10 amino aminus to a sequence other than that seed to modulate cytotoxic T-lymphocyte activity in that seed to modulate cytotoxic T-lymphocyte is to modulate cytotoxic T-lymphocyte is to modulate cytotoxic T-lymphocyte is to modulate cytotoxic T-lymphocyte to modulate cytoxic T-lymphocyte to modulate cy
	Gase; cytotoxic T lymphocyte; modula 101758. US-844716. LELAND STANFORD JUNIOR. LELAND STANFORD JUNIOR ACTIVITY COWATCH STANFORD ACTIVITY LOWATCH STANFORD ACTIVITY LAMPHOCY ACTIVITY LAMPHOCY ACTIVITY LAMPHOCY ACTIVITY LAMPHOCY ACTIVITY ACTI
	US-844716. US-844716. LELAND STANFORD JUNIOR.  KRENSKY AM; 4/38.  14/38.  15 Si 51pp; English:  15 Si 51pp; English:  15 Si 51pp; English:  minus to a sequence other than that sed to modulate cytotoxic T-lymphocyte is the sequence other than that sed to modulate cytotoxic T-lymphocyte is the sequence other than that sed to modulate cytotoxic T-lymphocyte in transplantation. It can be ut toxicity in transplantations, for the sequence of the sequence other than that sequence of modulate cytotoxic T-lymphocyte in transplantations, for the sequence of the
	U01758.  LELAND STANFORD JUNIOR.  KRENSKY AM; 4/38.  1/38.  Totoxic T-lymphocyte activity toward; 5/3 f flpp; English.  minus to a sequence other than that sed to modulate cytotoxic T-lymphocyte ised to modulate cytotoxic T-lymphocyte ised to modulate cytotoxic T-lymphocyte ised to modulate cytotoxic T-lymphocyte iblition or stimulation. It can be ut toxicity in transplantations, for
	US-84716.  US-844716.  VELAND STANFORD JUNIOR.  LATAN EARLY AM:  4/38.  1) based on Class I HLA antigen domaintotoxic T-lymphocyte activity toward and ragment of at least 10 amino on a fragment of at least 10 amino on a sequence other than that used to modulate cytotoxic T-lymphocytibition or stimulation. It can be ut toxicity in transplantations, for
	US-844716. LELAND STARFORD JUNIOR.  "Rensky AM; "A rensky AM; "Dased on Class I HLA antigen domaitorized T-1ymphocyte activity towarcifoloxic T-1ymphocyte activity towarcised for a fragment of at least 10 amino eminus to a sequence other than that sied to modulate cytotoxic T-1ymphocytichtion or stimulation. It can be un toxicity in transplantations, for
	Krensky AM;  Krensky AM;  Jased on Class I HLA antigen domai (138);  Siglp; English.  Totoxic T-lymphocyte activity toward (159);  Siglp; English.  Minus to a sequence other than that sed to modulate cytotoxic T-lymphocyte idbition or stimulation. It can be in toxicity in transplantations, for it toxicity in transplantations, for
	r CA, Krensky AM; 03134/38.  60154/38.  gets based on class I HLA antigen domains - used for g cytotoxic T-lymphocyte activity towards targets  Rage 5; 61pp; English.  Rage 6 or a fragment of at least 10 amino acids, joined at at terminus to a sequence other than that of wild type HLA is used to modulate cytotoxic T-lymphocyte (CTL) activity, inhibition or stimulation. It can be used for g cTL toxicity in transplantations, for inducing CTL
	00134/38.  de(s) based on Class I HLA antigen domains - used for geytotoxic T-lymphocyte activity towards targets  Page 53; 61pp; English.  de (or a fragment of at least 10 amino acids, joined at at terminus to a sequence other than that of wild type HLA is used to modulate cytotoxic T-lymphocyte (CTL) activity, inhibition or stimulation. It can be used for the intancity in transplantations, for inducing CTL
	de(s) based on Class I HLA antigen domains - used for g cytotoxic T-lymphocyte activity towards targets bage 53; 61pp; English.  de (or a fragment of at least 10 amino acids, joined at at terminus to a sequence other than that of wild type HLA is used to modulate cytotoxic T-lymphocyte (CIL) activity, inhibition or stimulation. It can be used for g CIL toxicity in transplantations, for inducing CIL
	g cytotoxic T-lymphocyte activity towards targets Page 53; 61pp; English.  de (or a fragment of at least 10 amino acids, joined at at terminus to a sequence other than that of wild type HLA 1s used to modulate cytotoxic T-lymphocyte (CIL) activity, inhibition or stimulation. It can be used for 9 CTL toxicity in transplantations, for inducing CTL
	Adde or a fragment of at least 10 amino acids, joined at at terminus to a fragmence other than that of wild type HLA is used to modulate cytofoxic T-lymphocyte (CTL) activity, inhibition or stimulation. It can be used for grintly in transplantations, for inducing CTL
	de (or a Indyment of at least 10 amain actus, joined at at terminus to a sequence other than that of wild type HLA is used to modulate cytotoxic T-lymphocyte (CTL) activity, inhibition or stimulation. It can be used for g CTL toxicity in transplantations, for inducing CTL
	is used to modulate cytotoxic T-lymphocyte (CTL) activity, inhibition or stimulation. It can be used for g CTL toxicity in transplantations, for inducing CTL
	inhibition or stimulation. It can be used for grut toxicity in transplantations, for inducing CTL
	for
	and
	. The peptide can also be used for identifying CTLs which
CC bind to it	and removing subsets of CTLs from
ednence čs	23 AA;
Query Match Best Local Sin Matches 25;	Match 100.0%; Score 133; DB 1; Length 25; Local Similarity 100.0%; Pred. No. 4 le-14; hes 25; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 1 WDRE	WDRETQICKAKAQTDRENLRIALRY 25
Db 1 WDRE	WDRETQICKAKAQTDRENLRIALRY 25
RESULT 2	
808	
	R83090 standard; peptide; 25 AA.
DT 16-MAY-1996	96 (first entry) Cmr modulation mentide (m0700 60-84)
	Control of Tumphocyte: CTL: major histocompatibility complex: MHC:
	pressant; graft versus host disorder; transplantation; therapy;
	•
7N WOSDZOS/V-AL.	.TWT.
	95: 1104349
05-APE	(-1994; US-222851.
(STRD	NIV LELAND STANFORD JUNIOR.
Claybe	r C, Krensky AM, Parham P;
DR WPI; 95-3	
PT Extension of	of acceptance period of transplants from MHC unmatched

ö

```
This is a second to the factor of the factor
                                               Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1996 (first entry)
HIA-187702.60-84
HIA-1874: alphal-helix; human-leucocyte-associated antigen; inhibitor;
HIA: p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
- using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 133; DB 1;
Pred. No. 4.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 133; DB 1;
ilarity 100.0%; Pred. No. 4.1e-14;
Conservative 0; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI: 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R95416 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 100.0%;
1 Similarity 100.0%;
25; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 25; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                          25 AA;
                                                                                                                                                                                                                                                                                                                                                                            of the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R95416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ٣
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              원
```

Gaps

ö

Indels

Best Local Similarity Matches 25; Conserv

Query Match

Length 25;

```
Treating autofimmure diseases

Example 1: Page 19: 41pp; English.

Peptides Wi3784-98 and Wi3778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or creminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (C-terminal amidated compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa80 = E or V; aa77 = C, S or N; aa79 = R or G; aa80 = I or N; aa76 = E or V; aa77 = C, T or C, aa70 = R or L; aa83 = G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HIA-B alphal domain (positions 79-84). They can be used to inhibit cyctoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or I new form also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to an II-C33. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, consulting the products can also be consulted to the products can also be consulted to the consultation of transplants or proteins of treating autoimmune and the products can also be
                                                                                                                                                                                                                                                                                                                                             19-JUN-1998 (first entry)
Peptide B2702.60-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoAmmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41221;
15-WAR-1994 (first entry)
Peptide fragment of HiA-B2705 antigen.
Human leukocyte antigen; HiA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1997.
22-MAY-1995.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STRD ) 98-086530/08.
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 133; DB 1;
100.0%; Pred. No. 4.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1993; 001758.
25-PRB-1993; 001758.
02-PRR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used for detection and diagnosis
                                                                                                                                                                                                                                                                    W33794 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R41221 standard; peptide; 25 AA
1 WDRETQICKAKAQTDRENLRIALRY
                                        1 WDRETQICKAKAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WDRETQICKAKAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                     g
                                                                                                                                                                                                                                                                    PARMENT PARMEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
```

Sequence

9

ò

```
Example; page 9; 29pp; English.

Example: Page 9; 20pp; English.

Example: Page 10pp; Engl
                               HIA-B2705.60-84.
HIA-B2705.60-84.
HIA: p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Such DNA, antigen or antibody
Disclosure; Page 5: 5pp; German.
The DNA may be used as a hybridisation probe for detecting the HLA
B27 gene, eg for assessing susceptibility to rheumatic disorders
such as ankylosis spondylitis, or may be used to transform cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA coding for antigen HLA B27 - and diagnostic reagents contg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88.7%; Score 118; DB 1; Length 25;
88.0%; Pred. No. 8.1e-12;
tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1991 (first entry)
Sequence of the human histocompatibility antigen HLA B27
Rheumatic disorder; genetic screening; diagnosis;
ankylosing spondylltis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BEHW ) BEHRINGWERKE AG.
Riethmuller G, Meo T, Welss E, Szots H; WPJ: 97-157893/23.
N-PSDB; N70935.
                                                                                                                                                                                       cytolysis; antigen presenting cell. Synthetic. W09513288-A1.
                                                                                                                                                                                                                                                                                                         18-MAX-1995.
10-NOV-1994, U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WDRETQICKAKAQTDREDLRTLLRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P70590 standard; protein; 337 AA.
P70590;
       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-545576.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clayberger C, Kr. WPI; 95-194027/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
P70590
       HERE AND A COURT OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R93907-F92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-MAY-1996 (first entry)
HIA-B2702 CTL modulating peptide (B2702.60-84).
Cytotoxic T lymphocyte: CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
                                                                                                         modulating cytotoxic T-lymphocyte activity towards targets
Example 13; page 39; 61pp; English.
The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
activity, either by inhibition or stimulation. It can be used for
inhibiting CTL toxicity in transplantations, for inducing CTL
inhibiting CTL coxicity in transplantations, for inducing CTL
infection. The peptide can also be used for identifying CTLs which
bind to it and removing subsets of CTLs from T reell composition.
This peptide is derived from the HLA B2705 antigen and corresponds
to the amino acid positions 60-84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
New peptide(s) based on Class I HLA antigen domains - used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.7%; Score 118; DB 1; Length 25; 88.0%; Pred. No. 8.1e-12; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.7%; Score 118; DB 1; Length 25; 88.0%; Pred. No. 8.1e-12; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R83091 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R95417 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WDRETQICKAKAQTDREDLRTLLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.7
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
```

host

R95417;

a a

RESULT R95417

ò g

ö

Gaps

ö

```
26-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-1996 (first entry)
Cycl modulating peptide #5.
Cytotoxic T lymphocyte; #Ti. major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA coding for human histocompatibility antigen HIA-B 27 - useful for diagnosis and antigen and antibody prodn.

Disclosure: p6: 13pp; German.

THE DNA may be used to detect the HIA-B 27 gene (opt. mutated) in human genetic material. The HIA-B 27 may be used to detect anti-HIA-B 27 antibodies in human serum. The antibodies may be used to detect anti-HIA-B 27 antibodies in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in immunoassay. Sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   03-APR-1991 (first entry)
Sequence encoded by genomic DNA encoding human histocompatibility
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88.7%; Score 118; DB 1; Length 362;
88.0%; Pred. No. 1.6e-10;
tive 1; Mismatches 2; Indels
                                                                                                                           Length 337;
                                                                                                      Score 118; DB 1; Lengtn 5-
Pred. No. 1.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G; WPI: 87-171469/25.
N-PSDB; N70225.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ankylosing spondylitis; rheumatic disorder; diagnosis.
                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 WDRETQICKAKAQTDREDLRTLLRY 108
                                                                                                                                                                                                          1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                              60 WDRETQICKAKAQTDREDLRTLLRY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                   P70155 standard; protein; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label - Asn, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Ile, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Ala, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R83071 standard; peptide; 26 AA.
                                                                                                                           88.7%;
88.0%;
                                                                                                                     Query Match
Best Local Similarity 88.0°
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-JUN-1987.
21-NOV-1986; 116139.
01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERKE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_difference 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_difference 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen HLA-B 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09526979-A1.
12-OCT-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
EP-226069-A.
                                                                                                                                                                                                                                                                                                                                                                                              10-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       class I MHC
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R83071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
R83071
R83071
AC R83071.
DE TL-MAY.
DE TL-MAY.
DE CYCLOOK
KW ALMINIOS
KW ALMINIO
                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                               RESULT
P70155
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                          g
    22228
                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
```

```
Treatment and diagnosis of HLA-dependent autoimmune disease - using peptide(s) derived from HLA-B27 or human keratin VI, e.g. for intis, uveitis, rheumatic disease etc.

PT 1111s, uveitis, rheumatic disease etc.

PS Claim 2. Page 9; 57pp; German

CW 58992-W55001 are peptides isolated from the alpha-1 or alpha-2 domain with 9992-W55001 are peptides isolated from the alpha-1 or alpha-2 domain cof HLA-B27 or human keratin IV and are used in methods for diagnosis and/or treatment of HLA, (human leucocyte affigen)-dependent autoimmune diseases. Such as such as a conflor treatment of HLA-B27

CG class I and II-associated autoimmune diseases, especially non-HLA-B27

CG class I and II-associated autoimmune diseases, especially non-HLA-B27

CG class I and II-associated autoimmune diseases, such as arbitis, uveitis, psoriatic arthritis or juvenile rheumatic arthritis and arbitis, uveitis, psoriatic arthritis or juvenile rheumatoid arthritis and HLA-B27 diseases (iritis, uveitis, psoriatic arthritis or juvenile rheumatoid arthritis and tha-B27 diseases (orally, or as nasal or pulmonary spray). This method results in antigens that are more specific than complete protein antigens, so provide a more exact classification of disease, they also have better solubility. Compared with complete proteins, peptides are easier to propage of production, have better storage stability when dry, are less likely to cause allergy and have a regulatory effect on the immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                              Disclosure; Page 9; 80pp; English.
R83061-R83085, R83090-R83096 and R82907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUL-1998 (first entry)

Human HLA-B27 alpha-1 domain (aa. 60-80) peptide B27PA.

Human leucocyte antigen; HLA; alpha-1 domain; alpha-2 domain; HLA-B27;

Keratin VI; diagnosis; treatment; HLA-dependent autoimmune disease;

Class I-associated autoimmune disease; iritis; uveitis; psoriasis;

Class II-associated autoimmune disease; rheumatic disease; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                          Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%; Score 112; DB 1; Length 26; 84.0%; Pred. No. 7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ankylosing spondylitis; antigen; regulator.
                                                                           Krensky AM, Parham P;
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WDRETQICKARAQTDRNXLRXXLRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W58992 standard; peptide; 21 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 84.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-SEP-1997; E05124.
18-SEP-1996; DE-038108.
                                                                                         Clayberger C, Krer
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (WILD/) WILDNER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 98-217206/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapiens
```

```
1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WDRNTQICKTNTQTYRENLRIALRY
                                                                                        Query Match
Best Local Similarity 80.0
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                   R95422;
                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
888888888
                                                                                                                            ð
                                                                                                                                               윰
                                                                                                                                                                                            à
                         ö
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                             HLAB38 CTL modulating peptide (B38.6084).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLAB38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Page 32; 80pp; English. R83061.R83085, R83080-R83086 and R92907-R92913 represent fragments of R83061.R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                          Gaps
                                                                                                                                    Peptide fragment of HLA-B38 antigen.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                         ö
                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                   Score 106; DB 1; Length 25; Pred. No. 5.6e-10; Mismatches 5; Indels
       Length 21;
      Score 109; DB 1; I
Pred. No. 1.6e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                        1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                         1 WDRNTQICKTNTQTYRENLRIALRY 25
82.0%; Sco..
100.0%; Prf
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R83093 standard; peptide; 25 AA.
                                                                                                         R48286 standard; peptide; 25
R48286;
                                                   1 WDRETQICKAKAQTDRENLR 20
                                                                                                                                                                                                                                                                                                                                                                    79.7%;
80.0%;
                                                                                                                          15-MAR-1994 (first entry)
Peptide fragment of HLA-B38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                           1 WDRETQICKAKAQTDRENLR
                Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                      20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1995.
05-APR-1995; U04349
                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Kre
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MÕ9526979-A1.
                                                                                                                                                                        WO9317699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-MAY-1996
HLAB38 CTL m
                                                                                                                                                                                                                                                                                                                                to the am
Sequence
       Query Match
Best Local 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R83093;
                Best Loca
                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                 R48286
                                                                                                                                                                                                                                                                                                                                                                                                                                                             R83093
                                                            g
                                                                                                          å
                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                         g
```

```
While Cycloytic activity and differentiation of CTLS.

Tompsons. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 9: 29p; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLAB38.6084. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 lis a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSc70. P74 is found in a cells. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column colls. P74 can be isolated by lysis of a suitable cell with an amphoteric detergent, and HA-B2702 palindromic peptide.

CC ontaining a covalently bound HLA-B2702 palindromic peptide.

CC containing a covalently bound HLA-B2702 palindromic peptide.

CC compositions comprising the extracellular fragment of P74 combined with the extracellular portion of P74, and determining the amount of binding between the candidate compound and P74.

CC T-cells, by combining them with the extracellular portion of P74, and determining the amount of binding between the candidate compound and p74.

CC T-cells, by combining them with the extracellular portion of p74, in an amount sufficient to compete containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the containing T-cells and antigen presenting cells (APCS), by adding to the contain the binding of the P74, in an amount sufficient to compete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
HIAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLAB38.6084. HLAB38.6084. HLAB38.6084. HLAB38.6084. HLAB38.6084. HLAB38.70. HLAB38.6084. HLAB38.70. HLAB38.70. HLAB3.70. HLAB3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79.7%; Score 106; DB 1; Le
80.0%; Pred. No. 5.6e-10;
Y. W. W. W. W. S. S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.7%; Score 106; DB 1; L
80.0%; Pred. No. 5.6e-10;
ive 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(S-ND ) UNIV LELAND STANFORD JUNIOR.
(Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R95422 standard; peptide; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1996 (first entry)
```

us-08-653-294-32.rag

```
WILL'S JOURNEY LOUNCE AND STATEMENT OF THE NATION OF TAILS.

PART INDIDIT CYCOLYLIS.

FOR STANDARD FOR THE STANDARD OF THE STANDARD FOR THE ST
                                                                                                                                                                HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CIL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with p74 for the binding of the p74 ligand
                                                                                                                                                                                                                                                                                                                                                                                              10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRO) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI: 95-194027/25
R95431
ID R95431 standard; peptide; 25 AA.
                                                                                                   (first entry)
                                                                                                   12-NOV-1996
HLA-B7.60-84
```

ö 78.2%; Score 104; DB 1; Length 25; llarity 95.0%; Pred. No. 1.1e-09; Conservative 1; Mismatches 0; Indels Query Match Best Local Similarity Matches 19; Conserv

1 WDRETQICKAKAQTDRENLR 20

ŝ g

1 WDRETQICKAKAQTDRESLR 20

Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

 protein search, using sw model OM protein

February 7, 2000, 18:04:40; Search time 111.22 Seconds (without alignments) 10.603 Million cell updates/sec Run on:

US-08-653-294-32 133 1 WDRETQICKAKAQTDRENLRIALRY 25 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_62:\* Database :

piri:\* pir2:\* pir3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	class I histocompa	class I histocompa	MHC class I histoc		MHC class I histoc	oho	MHC class I histoc	-	class I histocompa	class I histocompa	class I histocompa	class I histocompa	н	class I histocompa	class I histocompa	MHC HLA-B38 chain	MHC class I histoc	н	class I histocompa	gene HLA B-1517 pr	alpha-chai	33	MHC class I histoc	MHC HLA-B44.2 chai	transmembrane glyc	I bi	class I	Η	clas	MHC HLA-B transmem
			I59308	180167	HLHU12	156116	нгнива	I37485	137515	I54289	JH0541	JH0539	JH0540	I80169	I80171	S07113	803537	I54463	B30345	S24434	180168	I62045	137516	S25415	A45850	161861	84	I54442	382	A45834	A30345	IS9633
		DB		7		7	Н	~	7	7	~	~	~	~	~	~	7	7	~	7	7	~	~	7	~	7	~	7	7	~	7	~
			354	354	359	338	362	362	362	362	362	362	362	355	355	363	363	274	362	362	354	362	355	362	362	362	362	362	273	362	362	362
dР	Query	Match	93.2	93.2	。	88.7	88.7	88.7	88.7	88.7	85.7	85.7	85.7	-: 0	80.5	。	80.5	o,				73.7	72.2	72.2	72.2	٠.	72.2	72.2	71.4		71.4	71.4
		Score	124	124	120	118	118	118	118	118	114	114	114	107	107	107	107	106	101	101	86	98	96	96	96	96	96	96	95	95	95	95
	Result	Q		7	m	4	2	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

MHC class I histoc MHC class I histoc HIA-AW24 profesin -	MHC class I histoc MHC class I histoc MHC class I histoc	class I histocompa MHC class I histoc MHC class I histoc lymphocyte antigen	HLA-Bw57.2 antigen MHC class I histoc MHC class I histoc	class I histocompa class I histocompa
137120 S77963 154416	154493 HLHU32 A35997	1801/4 HLHUB4 HLHUB8 184490	I37521 S42102 D35997	180165 JH0537
444	1010	2448	0 H 0	0.0
362 365 365	365 274 364	362 362 362	362 363 364	354 365
71.4	70.7	0000 0000 0000 0000	68 4.4.4.	67.7
യ യ യ സ സ സ	00000 00400	7444	9116	0 6 6
31 32 33	ው የነው የነ ያ ቀ የኒ ነው የ	78867 3887	4 4 4 1 2 6	44 5 5

#### ALIGNMENTS

RESULT 1 159308	class I histocompatibility antigen - pygmy chimpanzee (fragment) C;Species: Pan paniscus (pygmy chimpanzee, bonobo)	C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 23-Jul-1999 C;Accession: 159308	R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994	A.Title: A uniquely high level of recombination at the HLA-B locus. A.Reference uniber: 159308; MUID:94286544 A.Accession: 159308	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule 1-34a <pre>cpre&gt; A;Molecule type: mRNA A;Molecu</pre>	A;Cross-references: EMBL:U05575; NID:9454767; PIDN:AAA50178.1; PID:9454768 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology	Query Match 93.2%; Score 124; DB 2; Length 354; Best Local Similarity 92.0%; Pred. No. 9.4e-12; Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0
			ж. Е.;				;0

Wat

# 76 WDRNTQICKAQAQTDRENLRIALRY 100 1 WDRETQICKAKAQTDRENLRIALRY 25 ద ä

Cispecies: Pan paniscus (pygmy chimpanzee (fragment)
C;Species: Pan paniscus (pygmy chimpanzee, bonobo)
C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 23-Jul-1999
C;Accession: 180167
E;McAdam, S.N.; Boyson, J.E.; iilu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Mat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A.Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
A;Accession: 180167
A;Accession: 180167 ~

Query Match 93.2%; Score 124; DB 2; Length 35 Best Local Similarity 92.0%; Pred. No. 9.4e-12; Matches 23; Conservative 1; Mismatches 1; Indels ò

ö

Gaps

; 0

Length 354;

g

molecular appro

Genetics:

```
C; Date: 13-Aug-1986 #sequence_revision 28-Apr-1995 #text_change 22-Jun-1999
C; Accession: S07441; A25092; B25092; A94087; S34180; S44942; A90493; B24741; I55965;
R; Weiss, E.H.; Kuon, W.; Doerner, C.; Lang, M.; Riethmueller, G.
Immunobloology 170, 367-380, 1965
A; Title: Organization, sequence and expression of the HLA-B27 gene: a molecular appro
A; Reference number: S07441; MUID:86138405
A; Rolecule type: DNA
A; Residues: 1-362 <WEI>
A; Molecule type: DNA
A; Residues: 1-362 <WEI>
A; Note: the authors translated the codon GAC for residue 61 as Ala and the codon CAG
A; Note: this allele is designated B*27052 (formerly 27W)
R; Seemann, G.H.A.; Rein, R.S.; Brown, C.S.; Ploegh, H.L.
EMBO J. S, 547-552, 1986
A; Title: Gene conversion-like mechanisms may generate polymorphism in human class I g
A; Reference number: A91061; MUID:86220133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-139, 'H', 141-362 < CDAM>
A; Residues: 1-139, 'H', 141-362 < CDAM>
A; Cross-references: EMBL: 233453; NID: 9486652; PIDN: CDAR83876.1; PID: 9486653
B; Ezquerra, A.; Bragado, R.; Vega, M.A.; Strominger, J.L.; Woody, J.; Lopez de Castro
Biochemistry 24, 1733-1741, 1985
A; Title: Primary structure of papain-solubilized human histocompatibility antigen HLA
A; Reference number: A90493; MUID: 85226361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restriction analysis of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Aparicio, P.; Bragado, R.; Lopez de Castro, J.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-B27 genomic exon sequences isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Szoets, H.; Riethmueller, G.; Welss, E.; Meo, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 1428-1432, 1986
A;Title: Complete sequence of HLA-B27 cDNA identified through the characterization (A;Reference number: A94087; MUID:86149317
A;Accession: A94087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein

A; Molecule type: protein

R; Residues: 25-265, Fe', 267-295 <EZQ>

R; Wega, M.A.; Ezquerra, A.; Rojo, S.; Aparicio, P.; Bragado, R.; Lopez de Castro,

Proc. Natl. Acad. Sci. U.S.A. 82, 7394-7398, 1985

Proc. Natl. Acad. Sci. U.S.A. 82, 7394-7398, 1985

A; Title: Structural analysis of an HLA-B27 functional variant: identification of

A; Reference number: A94070; MUID:86042671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-362 <SEE>
A;Crosz-references: GB:X03665; NID:932250; PIDN:CAA27302.1; PID:g871297
A;Note: this allele is designated B*27051 (formerly 27W)
A;Accession: B25092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Residues: 1-100, NY, 102-103, IA', 106-362 <SE2>
A.Cross-references: GB:X03664; NID:g32236; PIDN:CAA27301.1; PID:g871296
A.Note: this allele is designated B*2702 (formerly 27K)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-100,'S',102-137,'D',139,'Y',141-175,'E',177-362 <VIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:X73578
A;Note: this allele is designated B*2706
R;D'Amato, M.; Sorrentina Insa Library, May 1994
A;Description: Identification of a novel HLA-B27 subtype by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
R; Residuas: 86-100, N'.102-103, 'IA', 106-107; 171-181 < VEG>
R; Coppin, H.I.; McDevitt, H.O.
J: Immunol. 137, 2168-2172, 1986
A; Title: Absence of polymorphism between HiA-B27 genomic of Reference number: 155965; MUID: 87009855
A; Recession: 155965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residuas: 25-205, 'v', 207-362 <S20>
A;Cross-references: GB:M12678
A;Note: this allele is designated B*27052 (formerly 27W)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reference number: S34180 ; Scatus: ... S34180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: S44942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nyliches, C.
Submitted to the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S44942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Map position: 6p21.3
A; Map position: 6p21.3
A; Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
A; Introns: 22/1; 112/1; 204/1; 296/1; 335/1; 346/1
C; Superfamily: class I histocompatibility antigen; Immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantati
F; 22-35/Product: class I histocompatibility antigen HLA alpha chain #status predicted < F; 22-304/Domain: extracellular #status predicted < EXT>
F; 22-311/Domain: alpha-1 < EXI>
                                                                                                                    hun
                                                                                                                                                                                                                                                                                                                                                                                                                           R;Choo, S.Y.; Fan, L.A.; Hansen, J.A.
J. Immunol. 147, 174-180, 1991
A. Title: A novel HLA-B27 allele maps B27 allospecificity to the region around position A;Reference number: 156116; MUID:91268545
                                                                                                                    (clone pHLA 12.4) -
                                                                                                                                                                                                                                                R;Malissen, M.; Malissen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A;Title: Exon/intron organization and complete nucleotide sequence of an HLA gene.
A;Reference number: A02189; MUID:82151002
A;Accession: A02189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    НІНИВ2
MHC class I histocompatibility antigen HLA-B27 alpha chain precursor - human
C:Species: Homo saplens (man)
                                                                                                             MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHL?
C;Species: Homo sapiens (man)
C;Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC HLA-B27-HS - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul_1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
Cross 1-38 < RES>
A;Cross references: GB:M62852; NID:g187760; PIDN:AAA59647.1; PID:g187761
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:305-329/Domain: transmembrane #status predicted <TMM>
F:335-359/Domain: intracellular #status predicted <INT>
F:375-359/Domain: intracellular #status predicted <INT>
F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:224-280/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 120; DB 1; Length 359;
Pred. No. 4e-11;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 118; DB 2;
Pred. No. 7.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :112-203/Domain: alpha-2 <5x2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 WDRNTQICKAQAQTERENLRIALRY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WDRETQICKAKAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 WDRETQICKAKAQTDREDLRTLLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88.7%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.2
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: I56116
A; Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Accession: I56116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
```

ò g

000025

ŏ

rest

Matches

RESULT

g ò

ö

```
C;Species: Homo sapiens (man)
C;Date: 02-041-1996 #sequence_revision 02-041-1996 #text_change 23-041-1999
C;Accession: 154289
R;Choo, S.Y.; St. John, T.; Orr, H.T.; Hansen, J.A.
Hum. Immunol. 21, 209-219, 1988
A;Title: Molecular analysis of the variant alloantigen HLA-B27d (HLA-B*2703) identifi A;Reference number: 154289; MUID:88227491
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comparison to huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - lowland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-Jul-1999
                                                                                                                                                                                     A;Cross-references: EMBL:X73578; NID:g975658; PIDN:CAA51980.1; PID:g975659 C;Genetics:
                                                                                                                                                                                                                                                                               A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3 Gp21.3
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
X;Residues: 1-362 <LAMP.
A;Cross-references: EMBL:X60254; NID:g22869; PIDN:CAA42806.1; PID:g22870
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M54883; NID:g187663; PIDN:AAA59616.1; PID:g187664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OH0541

class I histocompatibility antigen Gogo-B0103 heavy chain precursor class I histocompatibility antigen Gogo-B0103 heavy chain precursor C; Species: Gorilla gorilla gorilla (lowland gorilla)
C; Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-JuC; Accession: JH0541
R; Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A; Title: Gorilla class I major histocompatibility complex alleles: c
A; Reference number: JH0534; MUID: 92078860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Score 118; DB 2; L6
Pred. No. 8.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 88.7%; Score 118; DB 2; L
Best Local Similarity 88.0%; Pred. No. 8.2e-11;
Matches 22; Conservative 1; Mismatches 2;
A; Title: Nucleotide sequence of HLA-B*2706.
A; Reference number: 137515; MUID:94102824
A; Accession: 137515, translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 WDRETQICKAKAQTDRESLRTLLRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                          88.7%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-362 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHC HLA-B27d - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: JH0541
                                                                                                                                                           A; Residues: 1-362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: HLA-B
                                                                                                                                                                                                                                                         A; Gene: GDB: HLA-B
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                           A; Molecule type: DNA
A; Residues: 116-192 <BLA>
A; Cross-references: EMBL:X83737
C; Comment: This allele for HLA-B correlates with the development of ankylosing spondyllt
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                   A. Consolition: 6p21.3-6p21.3
A. Map position: 6p21.3-6p21.3
A. Map position: 6p21.3-6p21.3
A. Map position: 6p21.3-6p21.3
A. Introns. 25/1.1 114/1. 207/1; 299/1; 338/1; 349/1
A. Introns. 25/1. 114/1; 207/1; 299/1; 338/1; 349/1
C. Superfamily: class I histocompatiblity antigen: immunoglobulin homology
C. Keywords: ankylosing spondylitis; duplication; glycoprotein; heterodimer; transmembran F. 124/Domain: signal sequence #status predicted <SIG>
F: 25-36/Product: class I histocompatibility antigen HLA-B27 alpha chain #status predict F: 25-307/Domain: extracellular #status predicted <EXT>
F: 25-114/Domain: alpha-1 <EXIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restriction analysis of a cytotox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Del Porto, P.: D'Amato, M.; Fiorillo, M.T.; Tuosto, L.; Piccolella, E.; Sorrentino, J. Immunol. 153, 3093-3100, 1994
A:Title: Identification of a novel HLA-B27 subtype by restriction analysis of a cytoto A; Reference number: 137485; MUID:94375872
A; Accession: 137485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC class I histocompatibility antigen HLA-B*2706 alpha chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human lymphocyte antigen HLA-B27 - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-362 < RES>
A; Cross-references: EMBL:233453; NID:9486652; PIDN:CAA83876.1; PID:9486653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                A;Cross-references: GB:M14013; NID:g187743; PIDN:AAA59643.1; PID:g187744 R;Blasczyk, R.; Weber, M.; Salama, A. submitted to the EMBL Data Library, January 1995 A;Reference number: S52291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;210-285/Domain: immunoglobulin homology <IMM>
F;300-331/Domain: irransmembrane *status predicted <IMM>
F;323-362/Domain: intracellular *status predicted <INT>
F;110/Binding site: carbohydrate (Asn) (covalent) *status experimental
F;115-188,227-283/Disulfide bonds: *status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.7%; Score 118; DB 1; Length 362; Best Local Similarity 88.0%; Pred. No. 8.2e-11; Matches 22; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.7%; Score 118; DB 2; L
88.0%; Pred. No. 8.2e-11;
tive 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Vilches, C.; de Pablo, R.; Kreisler, M.
Immunogenetics 39, 219, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115-206/Domain: alpha-2 <EX2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
   A; Residues: 25-298 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: 137485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: 137515
R;Vilches, C.; de P
                                                                                                                                                                                                                                                                                                                                                A; Gene: GDB: HLA-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q
```

qorilla

ö

```
Class I histocompatibility antigen - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 18017]
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology C; Keywords: transmembrane protein F;1-24,Domain: signal sequence #status predicted <SIG>F;1-24,Domain: signal sequence #status predicted <SIG>F;25-362,Product: class I histocompatibility antigen heavy chain, Gogo-B0102 #status F;25-114,Domain: alpha-1 <ALI>F;115-206,Domain: alpha-2 <ALI>F;207-298/Domain: alpha-3 <ALI>F;207-298/Domain: alpha-3 <ALI>F;207-298/Domain: immunoglobulin homology <IMM>F;299-362/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Pan troglodytes (chimpanze)
C;Species: Pan troglodytes (chimpanze)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: I80169
E;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
A;Accession: I80169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-352 < RES>
A; Cross-references: EMBL:U05580; NID:9454777; PIDN:AAA50183.1; PID:9454778
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1355 <RES>
A;Cross-references: EMBL:U05582; NID:q454781; PIDN:AAA50185.1; PID:g454782
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   class I histocompatibility antigen - chimpanzee (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 107; DB 2; L6
Pred. No. 4.1e-09;
                                                                                                                                                                                                                                                                                                                                 Score 114; DB 2; 1
Pred. No. 3.5e-10;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 107; DB 2; I
Pred. No. 4.1e-09;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.5%;
84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.5%;
84.0%;
                                                                                                                                                                                                                                                                                                                                     Query Match 85.7%;
Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: I80171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Wolecule type: DNA
A.Residues: 1-362 <LAM>
A.Residues: 1-362 <LAM
A.Roross-references: EBM-transformed B cell
C.Genetics: 25/1; 115/1; 207/1; 209/1; 338/1; 349/1
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
C.Reywords: transmembrane protein
F.124/Domain: signal sequence *status predicted <SIG>
F.124/Domain: signal sequence *status predicted <SIG>
F.25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0101 *status pre
                                                                       pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      class I histocompatibility antigen Gogo-B0101 heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla gorilla (lowland gorilla) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999 R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P. J. Exp. Med. 174. 1491-1400
                                                             Gogo-B0103 #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to
A;Reference number: JH0534; MUID:92078860
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 class I histocompatibility antigen Gogo-B0102 heavy chain precursor - lowland class I histocompatibility antigen Gogo-B0102 heavy chain precursor - lowland class is decise; Gorilla gorilla (lowland gorilla)
C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Accession: JH0540
R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison the ference number: JH0540
A;Reference number: JH0540
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Gross-references: EMBL:X60693; NID:g22867; PIDN:CAA43101.1; PID:g22868
A;Cross-references: EBN-transformed B cell
C;Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
      C; Keywords: transmembrane protein
F:1-24/Domain: stynal sequence *status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen heavy chain,
F:25-114/Domain: alpha-1 <ALI>
                                                                                                                                                                                                                                                                                                      Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 114; DB 2; Length 36
Pred. No. 3.5e-10;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F)25-362/Product: class i histocompatibility antigen hea
F:25-114/Domain: alpha-1 <ALI>
F:115-206/Domain: alpha-2 <ALI>
F:207-298/Domain: limmunoglobulin homology <IMM>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-362/Domain: intracellular #status predicted <INT>
                                                                                                                  F;115-206/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
F;220-285/Domain: immunoglobulin homology <IMM>
F;299-362/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                  Score 114; DB 2; L
Pred. No. 3.5e-10;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                         85.7%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 85.7%;
Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 88.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JH0539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ð
```

Wat

ö

Gaps

ö

Indels

Length 355;

ö

Gaps

ö

Indels

Length 355;

ö

Gaps

ö

Indels

Length 362;

```
à
                                                                              q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession of the comparation of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.24/Domain: signal sequence #status predicted <SIG>
1.25-363/Product: class I histocompatibility antigen alpha chain #status predicted <MAT>
1.25-384/Domain: extracellular #status predicted <EXT>
1.20-285/Domain: immunoglobulin homology <IMM>
1.299-338/Domain: transmembrane #status predicted <TMM>
1.399-338/Domain: intracellular #status predicted <IMM>
1.339-363/Domain: intracellular #status predicted <IMM>
1.339-363/Domain: intracellular #status predicted <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Nuclectide sequences of chimpanzee MHC class I alleles: evidence for trans-spec
A;Reference number: S01171; MUID:89030641
A;Accession: S03537
                                                                                                                                                                                 NiAlternate names: MHC ChiA chain
C:Species: Pan troglodytes (chimpanzee)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 23-Jul-1999
C:Accession: S07113; I36957
R:Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
A;Tille: HLA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A;Reference number: S06424; MUID:88319000
A;Reference number: S064113
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        class I histocompatibility antigen ChLA-B1 alpha chain precursor - chimpanzee C; Species: Pan troglodytes (chimpanzee) C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Oct-1996

    chimpanzee

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 107; DB 2; Length 363;
Pred. No. 4.2e-09;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 107; DB 2; Length 363;
Pred. No. 4.2e-09;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R; Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer, EMBO J. 7, 2765-2774, 1988
                                                                                                                                             antigen Ch39 alpha chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-363 < LAW>
R; Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A; Title: Diversity and diversification of HLA-A,B,C alleles.
A; Reference number: 136956; MUID:89235215
A; Accession: 136957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 WDRETRNVKASAQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 80.5%;
Best Local Similarity 84.0%;
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: class I histocompa
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL:X13115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21; Conservative
                                                                                                                                             class I histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-363 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-363 <MAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: S03537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
```

Search completed: February 7, 2000, 18:04:41 Job time: 22207 sec

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

- protein search, using sw model OM protein Run on:

February 8, 2000, 01:26:01; Search time 68.63 Seconds

(without alignments)
10.879 Million cell updates/sec

US-08-653-294-32 Perfect score:

1 WDRETQICKAKAQTDRENLRIALRY 25 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 82229 seqs, 29864866 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Desci iperon	317 homo	33 hото sa	рошо	рошо	рошо	рошо	рошо		gorilla	gori	pan trog	homod	homod	рошо	рошо	рошо	homod	homo	homo		homo	homo	рошо	homo	homo	homo	homo	goril	рошо	homo	рошо	P30475 homo sapten	рошо	homo sa
SUMMARIES	1D	1B15_HUMAN		1B20_HUMAN	ᆌ	- 1	1B18_HUMAN	1B19_HUMAN	1B01_GORGO	1B02_GORGO	1B03_GORGO	1B01_PANTR	1B47_HUMAN	m	1B05_HUMAN		1B42_HUMAN	1B49_HUMAN	- 1	1B54_HUMAN	1A23_HUMAN	1A24_HUMAN	1A32_HUMAN	1A25_HUMAN		1B60_HUMAN	J	- 1		Z,		1B29_HUMAN	3	1B45_HUMAN	1B02_HUMAN
Y 1 1 1 1 1 1 1	rengen.	0 362 1	362	7 338	7 361	7 362	7 362	7 362	7 362	7 362	7 362	5 359	362	362	362	2 362	2 362	4 362	4 36	362	4 365	365	7 365	365	4 359	4 362	362	362	365	7 362	7 362	362	7 362	362	362
& Query	ו ע	133 100.	on I	œ	æ	œ	ထ	œ	œ	ထ	∞	œ	7	7	7	7	7	7		7	7	7	7	9	φ	9	9	68	. 99	64.	64.	64.	64.	64.	63.
Result		1	7	m	4	Ŋ	ø	7	<b>6</b> 0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

PFAM: PF00047; 19:1.
PFAM: PF00129; MHC\_I: 1.
PFAM: PF00129; MHC\_I: 1.
SIGNAL I: 2.4

P30480 homo sapten P30492 homo sapten P30493 homo sapten P30494 homo sapten	P30496 homo sapten P30476 homo sapten P01894 oryctolagus P06140 oryctolagus P16210 pan troglod P13751 pan troglod
1839_HUMAN 1855_HUMAN 1856_HUMAN 1857_HUMAN	1B59_HUMAN 1B32_HUMAN HA1A_RABIT HA1B_RABIT 1A02_PANTR
-	нанана
22222 28622 3862 386	3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
000000000000000000000000000000000000000	660 600 600 600 600 600 600 600 600 600
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	881 79 76 76
88888 8888 8888	4 4 4 4 4 0 1 2 8 4 8

#### ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE: 86042671.

VEGA M.A., EZQUERRA A., ROJO S., APARICIO P., BRAGADO R.,

LOPEZ DE CASTRO J.A.;

Structural analysis of an HLA-B27 functional variant: identification
of residues that contribute to the specificity of recognition by
of residues that contribute to the specificity of recognition by
cytolytic T lymphocytes.";

Proc. Natl. Acad. Sci. U.S.A. 82:7394-7398(1985).

-: FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-: SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                             MEDLINE; 86220133.
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOECH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human class I genes.";
EMBO J. 5:547-552(1986).
                                                   01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALPHA CHAIN
PRECENSOR (B-27K) (827.2).
                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                    SECUTION N.A.
PARHAM P., ARNETT K.L., ADAMS E.J.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                    362 AA.
                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X03664; CAA27301.1; -.
EMBL; X03667; CAA27301.1; JOINED.
EMBL; L38504; AAA69724.1; -.
PIR; B25092; HLHUBK.
HSSP; P03989; 1HSA.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 86-107 AND 171-181.
                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICROGLOBULIN).
                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 86220133.
                                                                                                                                                    HLA-B OR HLAB.
1815_HUMAN
ID 1815_HUMAN
AC P10317;
```

Length 362;

~

```
Score 120; DB 1;
Pred. No. 4.8e-11;
 BY SIMILARITY.
BY SIMILARITY.
5E610F63 CRC32;
                                                                                                                  2; Mismatches
                                                                                                                                                                25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                 1 WDRETQICKAKAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WDRETQICKAKAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDRETQICKAKAQTDREDLRTLLRY
                                40850 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ž.
                                                                                  90.2%;
88.0%;
                                                                       Query Match
Best Local Similarity 88.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1182
224
2284
3308
338
1164
259
 110
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
183
275
285
309
86
101
203
38 A
                                                                                                                                                                                                                               RESULT 3
1B20_HUMAN
ID 1B20_HUMAN
 CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                               P30467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
     SEES
                                                                                                                                                  ð
                                                                                                                                                                                g
                                                                                                                                                                                                                                                                   STATE THE TERM SOLD OF THE TERM SERVICE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                   Gaps
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2702 ALFHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 82151002.
MALISSEN M., MALISSEN B., JORDAN B.R.;
"Exon/intron organization and complete nucleotide sequence of an
                                                                                                                                                                                                                                                                                                                                                                                                               HIAH_HUMAN STANDARD; PRI; 362 AA.
P01893;
21-JUL-1986 (Rel. 01, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
-!- THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                 100.0%; Score 133; DB 1; 100.0%; Pred. No. 5.1e-13;
                                                                                  CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE
                                                                                                                  CYTOPLASMIC TAIL.
                                                                                                                                                                                   9798FOBB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC TAIL.
                                                                                                                                   SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HI
ALPHA CHAIN H.
                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J00191; AAA36218.1; ALT_INIT.
PIR; A02189; HLHU12.
                                                                                                                                                                                                                                                                                                                     84 WDRETQICKAKAQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                     BY
                                                                                                                                                                  ΒY
                                                                                                                                                                                   MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A02189; HLHU12.
HSSP; P03989; 1HSA.
MIM; 142800; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                40397
                                                                                                                                                                                                                                                                   25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; G1
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1114
206
208
308
362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HLA-AR) (HLA-12.4).
HLA-H OR HLAH.
                              25
115
207
209
339
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICROGLOBULIN).
                                                                                                                                                                                                                                               Best_Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
1115
207
209
333
                                                                                                                                                 DISULFID
DISULFID
SEQUENCE
                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                   Query Match
                                DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  RESULT 2
HLAH_HUMAN
     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
   ô
                                                                                                                                                                                                                                                                                                                                 g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINES, 91268545.
CHOO Y.S., FAN L.A., HANSEN J.A.;
CHOO Y.S., FAN L.A., HANSEN J.A.;
A novel HLA-B27 allele maps B27 allospecificity to the region around position 70 in the alpha 1 domain.";
J. Immunol. 147:174-180(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2707 ALPHA CHAIN
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIA-B OR HLAB.
HOMO Saplens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M62852; AAA59647.1; -. HSSP; P03989; 1HSA.
MIM; 142830; -. PROSITE; PS00290; IG_MHC; 1. PFAM; PF00047; 1g; 1. PFAM; PF00129; MHC_I; 1. DOMAIN 1 90 EXTRACELLULAR ALPHA-1. DOMAIN 91 182 EXTRACELLULAR ALPHA-2. DOMAIN 183 274 EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.;
33FB8134 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88.7%; Score 118; DB 1;
88.0%; Pred. No. 9e-11;
11ve 1; Mismatches
                                                                                                                                                                                                                                                                        338 AA.
```

m

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           and
                                                  23-0CT-1986 (Rel. 02, Created)
13-MUG-1987 (Rel. 05, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOPEZ DE CASTRO J.A.; Primary structure of papain-solubilized human histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
MEDLINE; 92405152.
MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;
"The three-dimensional structure of HLA-B27 at 2.1-A resolution suggests a general mechanism for tight peptide binding to MHC."; cell 70:1035-1048(1992).
                                                                                                                                                                                                                                                                                                                                    MEDLINE; 86149317.
SZOGTS H., RIETHMUELLER G., WEISS E., MEO T.;
SCORTS H., RIETHMUELLER G., WEISS E., MEO T.;
Complete Sequence of HLA-B27 cDNA identified through the
characterization of structural markers unique to the HLA-A, -B,
C allelic series.'
Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-295.
MEDILINE: 85256361.
EZQUENRA A: BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
LOPEZ DE CASTRO J.A.;
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 86138405.
WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.;
"Organization, sequence and expression of the HLA-B27 gene: a molecular approach to analyze HLA and disease associations.";
Immunobiology 170:367-380(1985).
                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROCLOBULIN).
-:- DISEBASE: THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF ANKYLOSING SPONDYLITIS.
                        361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL: X03945; CAA27578.1; ALT_TERM. PRR. AS21528; HLHUB2. PIR: S07441; S07441. PDB: 1HSA; 15-OCT-92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen HLA-B27.";
Biochemistry 24:1733-1741(1985).
                                                                                                                                                                                                                                                                                                          [2]
SEQUENCE OF 25-361 FROM N.A.
                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE IMMUNE SYSTEM.
                      1B14_HUMAN
P03989;
```

PROSITE; PS00290; IG\_MHC; 1. PFAM; PF00047; ig; 1.

MIM; 142830;

```
ö
                                                                                                                                                                                                                                                                     Gaps
           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                            Length 361;
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                            Score 118; DB 1; Length 36
Pred. No. 9.6e-11;
1; Mismatches 2; Indels
                                                          3).
                                                                                                                                                                                                                                               802130D5 CRC32;
                                         CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                           Ą.
                                                                                                                                                                                                                                                                                                           362
                                                          NIC
                                                          > \( \)
                                                                                                                                                                                                                                                                                 25
                                                          4 O
                                                                                                                                                                                                                                                                             1 WDRETQICKAKAQTDRENLRIALRY
                                                                                                                                                                                                                                               40464 MW;
                                                                                                                                                                                                                                                            88.7%;
88.0%;
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
                    1B16_HUMAN
ID 1B16_HUMAN
                            DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                           STRAND
SEQUENCE
                                                 DISULFID
                                                          CONFLICT
                                              CARBOHYD
                    DOMAIN
                                                                              TURN
STRAND
TURN
STRAND
HELIX
TURN
HELIX
TURN
                                                                                                                   STRAND
TURN
STRAND
TURN
                                                                      TURN
                                                                                                                                                                                                  TURN
STRAND
HELIX
STRAND
STRAND
                                                                                                                                                HELIX
HELIX
TURN
HELIX
TURN
HELIX
TURN
STRAND
                                                                                                                                                                                                                              HELIX
STRAND
TURN
                                                                                                                                        TURN
                                                                                                                                                                                          STRAND
                                                                                                                                                                                                                       STRAND
        SIGNAL
                                                                  STRAND
                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                  RESULT
```

```
SEEMANN G.H.A., REIN R.S., BROWN C.S., PLOEGH H.L.;
"Gene conversion-like mechanisms may generate polymorphism in human
class I genes.";
EMBO J. 5:547-552(1986).
                                                                                                                            WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.: "Organization, sequence and expression of the HLA-B27 gene: a molecular approach to analyze HLA and disease associations."; Immunobiology 170:367-380(1985).
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                              [3]
3D-STRUCTURE MODELING OF 115-206.
                                                                                                        SEQUENCE FROM N.A. MEDLINE; 86138405.
                       SEQUENCE FROM N.A.
                                  86220133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S:
Matches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 88227491.
CHOO S.Y., ST JOHN T., ORR H.T., HANSEN J.A.;
"Molecular analysis of the variant alloantigen HLA-B27d (HLA-B*2703) identifies a unique single amino acid substitution.";
Hum. Immunol. 21:209-219(1988).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASS I HISTOCOMPATIBILITY ANTIGEN,
            ol-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2703 ALPHA CHAIN
PRECISSOR (B-27D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2705 ALPHA CHAIN
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
                                                                                                                                                                                                             THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118; DB 1; Length 362;
Pred. No. 9.6e-11;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               B*2703 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATI
B-27 B*2703 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7261C3AB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE: PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 WDRETQICKAKAQTDRENLRIALRY 25
         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last seq
01-FEB-1995 (Rel. 31, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.7%;
                                                                                                                                                                                                                                                                                                                                                    EMBL; M54883; AAA59616.1; -. HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                     MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
1115
207
209
309
333
110
1125
227
                                                                    HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1B18_HUMAN
P10318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1818_HUMAN
1D 1818_H
AC P1018
DT 01.WAR
DT 01.WAR
DT 01.WAR
DE HA CL
DE PRECUR
GN HAA-B
GN HAA-B
OS HAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
ò
```

```
This.SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
MEDLINE; 95148615.
ROGNNN D., SCAPOZZA L., FOLKERS G., DASER A.;
"Rational design of nonnatural peptides as high-affinity ligands for the HLA-B*2705 human leukcyte antigen.";
Proc. Natl. Acad. Sci. U.S.A. 92:753-757(1995).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-27 B*2705 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                       THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR ALPHA-2 EXTRACELLULAR ALPHA-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 118; DB 1; Le
Pred. No. 9.6e-11;
...-matches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNECTING PEPTÍDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

73243566 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                         EMBL; X03665; CAA27302.1; -.
EMBL; X03666; CAA27302.1; JOINED.
EMBL; MI2967; AAA36221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88.7%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDB; 1ROH; 30-SEP-94.
PDB; 1ROI; 30-SEP-94.
PDB; 1ROJ; 30-SEP-94.
PDB; 1ROK; 30-SEP-94.
PDB; 1ROL; 30-SEP-94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1ROG; 30-SEP-94
1ROH; 30-SEP-94
                                                                                                                                                               MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
115
207
299
309
313
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A25092; HLHUBW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
```

362 AA.

```
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GGGO-B0101 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (LOWLand gorilla)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1802_GORGO
ID 1802_GORGO
AC P30380;
                    1B01_GORGO
P30379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
1801_GORGO
AC DISONGO
AC DISONGO
AC DISONGO
BUT ON APR
BE CLASS
OC BUT ON APR
RAT GONI
RT GONI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B-27 B*2706 ALPHA CHAIN.

EXTRACELLULAR ALPHA-1 (BY SIMILARITY).

EXTRACELLULAR ALPHA-2 (BY SIMILARITY).

CONNECTING PEPTIDE (BY SIMILARITY).

BY SIMILARITY.

CYTOPLASMIC TAIL (BY SIMILARITY).

POTENTIAL.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 96134006.
RUDMALEIT M., BOWNESS P., WORDSWORTH P.;
RUDMALEIT M., BOWNESS P., WORDSWORTH P.;
RUDMALEIT M., BOWNESS P., WORDSWORTH P.;
Substitution in exon 4 which is also present in HLA-B*2706.";
Immunogenetics 43:160-162(1996).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-:- SUBUNIT: DIERR OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2706 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 118; DB 1; Length 362;
Pred. No. 9.6e-11;
; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> G (IN REF. 1).
0D402027 CRC32;
                                                         362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94102824.
VILCHES C., DE PABLO, R., KREISLER M.;
"Nucleotide sequence of HLA-B*2706.";
Immunogenetics 39:219-219(1994).
                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40456 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X73578; CAA51980.1; -.
EMBL; U35734; AAC50447.1; -.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1114
206
208
308
332
332
362
1110
1188
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHC I; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
115
207
209
309
333
110
125
227
235
362 AA;
                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1
25
                                                                                                                                                                                                HLA-B OR HLAB.
                                                                                             01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Simi
Matches 22;
                                                         1B19_HUMAN
Q08136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                      1B19_HUMAN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
SEQUENCE FROM N.A.
MEDILINE; 92078860.
LAWLOR D.A., WARRENE E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanate class I.";
To human and chimpanate class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
Gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-BOLO ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                     THE IMMUNE SYSTEM.

1- SUBBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.7%; Score 114; DB 1; Length 36
88.0%; Pred. No. 3.9e-10;
.ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
7; 2E33E2B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSILE, .....

PFAM; PF00149; MG_I; 1.

MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WDRETQICKAKAQIDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40170 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, JH0539, JH0539.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X60255; CAA42807.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 88.0
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114
206
208
308
332
362
362
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25
200
200
300
333
227
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCOOPING
```

84 WDRETQICKAKAQTDRESLRILLRY 108 WDRETQICKAKAQTDRENLRIALRY 25

~

ò g œ

RESULT

us-08-653-294-32.rsp

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                            LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison
to human and chimpenzee class I.";
to human and chimpenzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-BO102 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                              -:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 85.7%; Score 114; DB 1; Length 362; Best Local Similarity 88.0%; Pred. No. 3.9e-10; Matches 22; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
3CF119AD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
MHC MHC MHC MHC_II SIGNILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₩.
                                                                                                                                                                                                                                                                                                         EMBL; X60693; CAA43101.1; -. PIR; JH0540; JH0540.
                                                                                                                                                                                                                                                                                                                                                          PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40204
                                                                                                               THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                         HSSP; P03989; 1HSA
PROSITE; PS00290;
SEQUENCE FROM N.A.
               MEDLINE; 92078860
                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
```

g ò

```
MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLAS. I HISTOCOMPATIBILITY ANTIGEN; GOGO-B0103 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (LOW-HORD GOTILLA)
ELNATYOTA: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarihin; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                             -! - FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                             362 AA
                              PRT;
                              STANDARD;
                                                                                                                                                                                                                                                                                                              IMMUNE SYSTEM
                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
            1B03_GORGO
ID 1B03_GORGO
                                          P30381;
RESULT
```

5 F

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch). ö mourties reactions or send an email to cor send an email to correct the correct send and correct send an email to correct send and correct send an email to correct send and correct send Gaps ö Length 362; 2; Indels Score 114; DB 1; Pred. No. 3.9e-10; 1; Mismatches 2; CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; FEA6A941 CRC32; 1 WDRETQICKAKAQTDRENLRIALRY 25 MW. 85.7%; 88.0%; 40248 Conservative 1114 2006 2008 3008 332 332 1188 1188 1100 25 115 207 209 339 125 227 110 362 AA; Query Match Best Local Similarity Matches 22; Conserv DISULFID CARBOHYD SEQUENCE à

01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-AR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR 359 AA PRT; troglodytes (Chimpanzee). STANDARD; 1801\_PANTR P13750; FRAGMENT 셤

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution."; EMBO J. 7:2765-2774(1988). Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan. MEDLINE; 89030641. MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G., MICROGLOBULIN). SEQUENCE FROM N.A. REVISIONS. MAYER W.; KLEIN

```
Query Match
Best Local Similarity 80.0%;
Matches 20; Conservative
                             EMBL; M24037; AAA02950.1; -.
                                                                                                                                                                                                                         40581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA59645.1;
                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                  188
283
                                                                                                                               1114
2206
3309
3333
110
                                                                                                                              25
115
207
310
334
110
125
327
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M22795;
M22796;
                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                 1B53_HUMAN
P30490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Immunol
                                                                                                                                                                                                                                                                                                                                                                                                                                PRECURSOR.
                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                   DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                  DOMAIN
CARBOHYD
                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                         1853_HUMAN
ID 1853_H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
EMBL;
                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                     ö
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                              01-FER-1993 (Rel. 25, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-49(B-21) B*4901 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 93056529.
HILDEBRAND W.H., MADRIGAL J.A., BELICH M.P., ZEMMOUR J., WARD F.E., WILLIAMS R.C., PARHAM P.;
"Serologic cross-reactivities poorly reflect allelic relationships in the HLA-B12 and HLA-B21 groups. Dominant epitopes of the alpha 2
                                                                                                                    CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-1 ALPHA CHAIN.
STRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 149:3563-3568(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               Score 107; DB 1; Length 359;
Pred. No. 4.5e-09;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDIINE: 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                       CONNECTING PEPTIDE
                                                                                                                                                                                          CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                   Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
5395FFC9 CRC32;
                          EMBL; X13115; CAA31507.1; -.
PIR; S03537, S03537.
HSSP; P03989; LHSA.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
NON_TER 1
SIGNL < 2
CHIA CLASS I HIS;
                                                                                                                                                                                                                                                                                                                                                                             362 AA.
                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                  90 WDRETRNMKASAQTDRENLRIALRY 104
                                                                                                                                                                                                                                                                                                        WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                   40173 MW;
                                                                                                                                                                                                                                                               80.5%;
                                                                                                                                                                                                                                                              Query Match 80.59
Best Local Similarity 84.07
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MICROGLOBULIN).
                                                                                                                                                                                                                                    ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                 1B47_HUMAN
ID 1B47_HUMAN
AC P30487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
REVISION TO
                                                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
DISULFID
                                                                                                                                                                                                               DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            helix.";
                                                                                                                                                  DOMAIN
                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                        _
 ò
                                                                                                                                                                                                                                                                                                                           g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 89080265.
HAYARHI H., ENNIS P.D., ARIGA H., SALTER R.D., PARHAM P., KANO K., TAKIGUCHI M.;
TAKIGUCHI M.;
"HLA-B51 and HLA-Bw52 differ by only two amino acids which are in the helical region of the alpha 1 domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-52(B-5) B*5201 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ဥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunol 142:306-311(1989).
FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 101; DB 1; Length 362;
Pred. No. 3.7e-08;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                 B-49(B-21) B*4901 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i, E996F82F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 AA.
                                                                                                                   HSSF; P30491; IAIM.
MIM; 142830; -.
PPROSTIE; PS00290; IG_MHC; 1.
PFAM; PF00047; 4g; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M22799; AAA59645.1; ALT_SEQ.
EMBL; M22793; AAA59645.1; JOINED.
EMBL; M22794; AAA59645.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
```

```
40474
                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                             PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; G1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBUNIT: DIMER C
MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                  362 AA;
    MICROGLOBULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1B41_HUMAN
P30481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Immunol
                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                            DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                     MHC I;
SIGNAL
                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 15
1B41_HUMAN
                                                                                                                                                                                                         CHAIN
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                               Gaps
                                                                                                              CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                 01.APR-11933 (Rel. 25, Last sequence update)
15-3701-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-13 B*1301 ALPHA CHAIN
PRECURSOR (B13.1).
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 96053518.
LIN L., TOKUNAGA K., NAKAJIMA F., ISHIKAWA Y., KASHIWASE K.,
TANARA H., KUNAGA K., SIDELTSEVA E., AKAZA T., TADOKORO K.,
SHIBATA Y., CHANDANAYINGYONG D., JUJI T.;
"Both HAL-B*1301 and B*1302 exist in Asian populations and are
associated with different haplotypes.";
Hum. Immunol. 43:51-56(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZEMMOUR J., ENNIS P.D., PARHAM P., DUPONT B.; "Comparison of the structure of HLA Bw47 to HLA-B13 and its relationship to 21-hydroxylase deficiency."; immunogenetics 27:281-287(1988).
                                                                                                              HLA CLASS I HISTOCOMPATIBILITY
BW-52(B-5) B*5201 ALPHA CHAIN.
EXTRACELULAR ALPHA-2.
EXTRACELULAR ALPHA-3.
                                                                                                                                                                                                                                                          Length 362;
                                                                                                                                                                                                                                                        Score 101; DB 1; Length 36
Pred. No. 3.7e-08;
0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE: 89235215.
PARHAM P., LAWLON D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                 CONNECTING PEPTIDE
                                                                                                                                                                                             NY SIMILARITY.

SY SIMILARITY.

SY SIMILARITY.

3B436FE8 CRC32;
                                                                                                                                                                                   CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
EMBL; M22797; AAA59645.1; JOINED.
EMBL; M22798; AAA59645.1; JOINED.
PIR; B30345; B30345.
PIR; B30548; B30348.
HSSP, P30491; IAIM.
MIM; 142830.
PROSTEZ; P500290; IG_MHC; 1.
PROSTEZ; P500290; 10; 1.
PRAM; PF00129; MHC_I; 1.
MC I: Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                    362 AA.
                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                            1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, Created)
                                                                                                                                                                                                                                                       75.9%;
                                                                                                                                                                                                                            40521
                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                 227
362 AA;
                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 88152906.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                         1805_HUMAN
ID 1805_HUMAN
AC P30461;
                                                                                                                                                                                                       DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                           TRANSMEM
                                                                                                                                   DOMAIN
                                                                                                                                             DOMAIN
                                                                                                                                                        DOMAIN
                                                                                                                                                                 DOMAIN
                                                                                                                CHAIN
    ð
                                                                                                                                                                                                                                                                                                                  ద
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 ALPHA CHAIN
PRECURSOR (B44.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-13 B*1301 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. 142:3937-3950(1989).
FUNCIYON: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO STUBINE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDINE; 89235215.
PARIARM P., LAWLON D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 96; DB 1; Lengran No. 2.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
28B67875 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WDRETQISKTNTQTYRENLRTALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY
BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.2%;
76.0%;
                                                                                                                                                                                                                                       EMBL; M24041; AAA59660.1; -.
EMBL; M19757; AAA52657.1; -.
EMBL; D50291; BAA08822.1; -.
HSSP; P30491; IAIM.
                                                                                                                                                                                                                                                                                                                                                             MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
```

Search completed: February 8, 2000, 01:26:01 Job time: 1561 sec

ô

Gaps

ö

Query Match 72.2%; Score 96; DB 1; Length 362; Best Local Similarity 76.0%; Pred. No. 2.1e-07; Matches 19; Conservative 0; Mismatches 6; Indels

oy D THIS PAGE BLANK (USPTO)

troglod sapien

Omor

029936 029936 029932 002932 0029961 0029961 019779 019625 0779935

homo saplen homo saplen

095528 029941 031602 019607

saplen

homo homo homo

OM protein

Run on:

Searched:

Database

Result No.

```
O19189;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      095524 PRELIMINARY; PRT; 354 AA.
095524;
01-FEB-1997 (TYEMBLTEL: 02, Created)
01-FEB-1997 (TYEMBLTEL: 02, Last sequence update)
01-NOV-1999 (TYEMBLTEL: 12, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
100.0%; Score 133; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15491 MW; 3A3BC802 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AA.
                                                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
030988
029936
095362
095362
02961
062922
029667
019625
029637
097393
097393
097393
097393
097393
097393
                                                                                                                                                                                                                                                                  029941
031602
019607
019608
019609
019610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                           133 AA;
MHC I.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              019189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
019189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
Q95524
 STAN TRANCOCCON TO THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        019189 homo sapien
Q95524 pan paniscu
Q95527 pan paniscu
Q46697 gorilla gor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homo sapien
pan troglod
pan troglod
pan troglod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pan paniscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pan troglod
                                                                                                                     (without alignments)
9.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hylobates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     porilla
                                                                                                    February 8, 2000, 19:16:17; Search time 176.54 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  019688
019193
078142
019692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             029934
029693
029846
P79612
078189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 046696
019354
095412
095529
                                                                                                                                                                                                                                                                                               225878
               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                         133
1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                  225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                     summaries
                                                                        - protein search, using sw model
                                                                                                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0095524
0095527
0196689
019193
019193
019193
029693
029693
029693
07918189
078189
078189
0786693
076693
076693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sp_invertebrate:*
sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_organelle:*
sp_phage:*
sp_plant:*
sp_trodent:*
sp_virus:*
sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                               sp_archea:*
sp_bacteria:*
sp_fung1:*
                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                            US-08-653-294-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ВВ
                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_human:*
                                                                                                                                                                                                                                                                                                                                                                                                                   SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1224
1120
1118
1118
1118
1118
1118
1118
1117
                                                                                                                                                                                                                      Scoring table:
```

ö

Gaps

ö

```
Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%; Score 120; DB 7; Length 90; 88.0%; Pred. No. 1.5e-11; tive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 118; DB 7; Length 39
Pred. No. 1.3e-11;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                  GRIMSLEY C., MATHER R.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF022172; AAC99794.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
BLASCIK R., WEBER M., SALAWA A.;
SUBMILTED (JAN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; X83127; CAA58689.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              019193 PRELIMINARY; PRT; 90 AA. 019193; 01-17AN-1998 (TTEMBLrel. 05, Created) 01-17AN-1998 (TTEMBLrel. 05, Last sequence update) 01-17AN-1998 (TTEMBLrel. 08, Last annotation update) HISTOCOMPATIBILITY ANTIGEN ALPHA 1 DOMAIN (FRAGMENT). HOMO Sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
                              01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HIA-H ORTHOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-B27 VARIANT EXON 2 (ALPHA1 DOMAIN) (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 1
90 90
90 AA; 10689 MW; 5E5F2495 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6F714D4C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 WDRETQICKAKAQTDREDLRTLLRY 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.7%;
Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1
39 39
39 AA; 4748 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               STRAIN-SHAMBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
019193
ID 01197
AC 011
DT 011
DT 011
DE HIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT NO SET OF SET OF
         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ő
                                                                                                                                                                         STRAIN-LOREL;
MEDLINE; 94286544.
MCDLINE; 94286544.
MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
EMBL: U05575; AAAS0178.1;
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00290; IG_MHC; 1.
PPAM: PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BOSONDJO;
MEDLINE; 9428644.
MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
"A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).
EMBL; UD5578; AAA50181.1; --
PROSTE; PS00209: IG_MHC; 1.
HLA-B.
Pan paniscus (Pygmy chimpanzee) (Bonobo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Pan.
Primates; Catarrhin1; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan paniscus (Pygmy chimpanzee) (Bonobo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.2%; Score 124; DB 7; Length 354; Best Local Similarity 92.0%; Pred. No. 1.4e-11; Matches 23; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.2%; Score 124; DB 7; Length 354; Best Local Similarity 92.0%; Pred. No. 1.4e-11; Matches 23; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1 SEQUENCE 354 AA; 39227 MW; 5D75939D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER 1 1 SEQUENCE 354 AA; 39401 MW; 6E38CFFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76 WDRNTQICKAQAQTDRENLRIALRY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095527
095527;
```

m

RESULT Q95527

ò g

Gaps

ö

ö

ö

90 AA

PRELIMINARY;

ô

õ g

```
[1]
SEQUENCE FROM N.A.
MEDLINE; 87009855.
COPPIN H.L., MCDEVITT H.O.;
"Absence of polymorphism between HLA-B27 genomic exon sequences isolated from normal donors and ankylosing spondylitis patients.";
J. Immunol. 137:2168-2172(1986).
EMBL; M14013; AAA59643.1; -.
HSSP; P10318; 1ROG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                ö
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 86149317.

SEQUENCE FROM N.A.

MEDLINE; 86149317.

SECTS H., RIETHMULLER G., WEISS E., MEO T.;

SCORPLET SEQUENCE OF HIA-B27 CDNA identified through the characterization of structural markers unique to the HLA-A, allelic series.";

Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986).

ENBL; MI2678; AAA59514.1;

HSSP; P10318; 1ROG.

PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                           Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 88.7%; Score 118; DB 7; Length 35
Best Local Similarity 88.0%; Pred. No. 1.2e-10;
Matches 22; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 7;
Pred. No. 9.2e-11;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               069F7E64 CRC32;
                                                                                                                                                                                                                                                                                                                         31659 MW; 9A74A6BA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               359 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 WDRETQICKAKAQTDREDLRILLRY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 1
359 AA; 40042 MW;
                                                                                                                                                                                                                                                                                                                                                                           88.7%;
88.0%;
                                                                                                                                                                                                HSSP; P10318; 1ROG,
PROSITE; PSO0290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TREMBLrel. 12, HLA-B27 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                        274
                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity
                                                                                                                                                                                                                                                                                           1
274 2
274 AA;
                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           029934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    029693
029693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
Q29693
ID Q29693
AC Q29693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
Q29934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                   MEDLINE; 92337445.
HIGGINS C.M., LUND T., SHIPLEY M.E., EBRINGER A.,
SADOWSKA-WROBLEWSKA M., CRAIG R.K.;
Ankylosing spondylitis and HLA-B27: restriction fragment length
polymorphism and sequencing of an HLA-B27 allele from a patient with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.7%; Score 118; DB 7; Length 181; 88.0%; Pred. No. 6.1e-11;
                                                                                                                                                                                                                                                                                                                                      Score 118; DB 7; Length 90;
Pred. No. 3e-11;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STEINER N.K., HURLEY C.K., KOESTER R.P.;
"NOVEL-HLA-B allele.";
Submitted (1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF072764; AAC25779.1;
EMBL; AF072763; AAC25779.1;
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             019692;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
MHC CLASS I HLA-B27 M (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 1
181 181
181 AA; 21079 MW; 24949BOF CRC32;
                                                                                                                                                                                                                                                    1 1
90 90
90 AA; 10571 MW; F22CCB4E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                          ankylosing spondylitis.";
ann. Rheum. Dis. 51:855-862(1992).
EMBL; 839758; CAB27364.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 60 WDRETQICKAKAQTDREDLRTLLRY 84
                                                                                                                                                                                                                                                                                                                                                                                                               1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 88.7%;
Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P10318; 1ROG.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 22; Conserv
                                         (1)
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        078142 078142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              019692
```

ö

Gaps

œ

RESULT 019692

ò g

ပု

ö

Gaps

```
TISSUE-BLOOD;
HASEGAWA T., SUGAHARA Y., MORIYAMA Y., NANZAI H., OGAWA A., TAWARA K.,
KONDO S., TOKUNGAR K.;
"Molecular characterization of a novel HLA-B27 allele.";
Submitted (JAN-1996) to the EMBL/Genbank/DDBJ databases.
EMBL) B3044; BAA11753.1;
HSSP; P10318; IROS
PROSITE; PS00290; IG_MHC; 1.
PFRAM; PF000129; MHC_1: 1.
SEQUENCE 362 AA; 40441 MW; 1D8099BC CRC32;
                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 118; DB 7; Length 362;
Pred. No. 1.2e-10;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 118; DB 7; Length 362;
Pred. No. 1.2e-10;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF026218; AAC42275.1; -.
HSSP; P10318; 1R0G.
                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2B0EF602 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 AA.
 362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEURYNCK K.L., BAXTER-LOWE L.A.; "B27052 W496D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 AA; 40486 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88.7%;
88.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 88.7%;
Best Local Similarity 88.0%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08,
12,
                                 01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 88.7
Best Local Similarity 88.0
Matches 22; Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC CLASS I ANTIGEN.
HLA-B.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                      HLA-B PROTEIN.
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
046693
ID 046693
AC 046693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         078189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
078189
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of a novel HLA-B27 subtype by restriction analysis of a cytotoxic gamma delta T cell clone."; J. Immunol. 153:3093-3100(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-BLOOD;
MEDLINE; 94375872.
DEL PORTO P., D'AMATO M., FIORILLO M.T., TUOSTO L., PICCOLELLA E., SORRENTINO R.;
                                                                                                                                                                            MEDLINE; 96134006.

RUDMALETT M., BOWNESS P., WORDSWORTH P.;
RUDMALETT M., BOWNESS P., WORDSWORTH P.;
The nucleotide sequence of HLA-B*2704 reveals a new amino acid substitution in exon 4 which is also present in HLA-B*2706.";
Immunospenetics 43:160-162(1996).

EMBL; U27668; AAC50444.1; --
HSSP; P10318; IROG.

PROSITE; PS00230; IG_MHC; 1.

PRAM: PF000129; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                            88.7%; Score 118; DB 7; Length 362; Illarity 88.0%; Pred. No. 1.2e-10; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 88.7%; Score 118; DB 7; Length 362; Best Local Similarity 88.0%; Pred. No. 1.2e-10; Matches 22; Conservative 1; Mismatches 2; Indels
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HUMAN LYMPHOCYTE ANTIGEN HLA-B27.
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE 362 AA; 40416 MW; 850432B4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 AA; 40450 MW; CCA23A50 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, Z33453; CAA83876.1; -.
HSSP; P10318; 1ROG.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                             SEQUENCE FROM N.A.
```

029846 RESULT 11

õ g

ö

Gaps

ö

ö

Gaps

ö

SEQUENCE

12

RESULT P79612

g à

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                             ö
                                                                        Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                             Query Match 88.0%; Score 117; DB 7; Length 90; Best Local Similarity 84.0%; Pred. No. 4.3e-11; Matches 21; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.0%; Score 117; DB 7; Length 90; Best Local Similarity 84.0%; Pred. No. 4.3e-11; Matches 21; Conservative 3; Mismatches 1; Indels
                                                                                                                                                     STRAIN=ROSS;
GRINSLEY C., MATHER K.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF022168; AAC99790.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=EVE;
GRIMSLEY C., MATHER K.A., OBER C.;
SUDMILTEQ (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AF022199; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             046694 PRELIMINARY; PRT; >v.r..
046694;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
                                                                                                                                                                                                                                               NON_TER 1 1
NON_TER 90 90
SEQUENCE 90 AA: 10707 MW; EE865717 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
90 90
90 AA; 10707 MW; EE865717 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                           1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WDRETQICKAKAQTDRENLRIALRY 25
                                                                                                                                                                                                                                                                                                                                                                                                            60 WDRNTQICKAQAQTERENLRMALRY 84
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
046694
                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

Search completed: February 8, 2000, 19:16:17 Job time: 21504 sec

60 WDRNTQICKAQAQTERENLRMALRY 84

g

THIS PAGE BLANK (USPTO)

```
4287 : X03945 Human gene for HLA-B
6553 : AR008238 Sequence 1 from pa
271 : AF022168 Pan troglodytes 1so
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/protein_id="aab60357.1"
/protein_id="aab60357.1"
/db_xref="doi:790215"
/db_xref="doi:790215"
/translation="apwledgepeywdretqickakaqtdrenlrialryyngseags
HTLQMXGCPVGPDGRLLRGYHQDAYDGKDY ALNEDLSSWTAADTAAQITQRKWEAA
RVAEQLRAYLEGECVEWLRRYLENGKETLQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä
                                                                                                                                                       HSU18659 399 bp mRNA PRI 30-APR-1995 Human MHC class I HLA-B mRNA (HLA-B-27KSH allele) exons 2 and 3, partial cds. U18659.1 GI:790214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (14-DEC-1994) Effie Petersdorf, Human Immunogenetics,
Fred Hutchinson Cancer Research Center, 1124 Columbia, Seattle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gee="HLA-B"
/note="This submission reports an HLA-B-2702 variant
/HLA-B-27KSH) that differs from the published B-2702
/GenBank Accession Number X03664"
/phenotype="HLA-B-27"
/replace="t"
a 119 c 145 g 48 t
                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae; Homo.
1 (bases 1 to 399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 25
Gaps: 0
Percent Identity: 100.000
  1.2e-10
1.9e-10
8.8e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HLA-B"
/note="HLA-B-27KSH allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="6p21.3"
/cell_type="leukocyte"
/tissue_type="blood"
1. .399
/gene="HIA-B"
/gene="HIA-B"
/mumber=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .399
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular Diversity of HLA-B
  335.04
331.40
355.58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128. .>399
/gene="HLA-B"
  118.00
118.00
117.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 399)
Petersdorf, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1. .>399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: HSU18659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 133.00
Ratio: 5.320
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-32 x HSU18659
                                                                                                   seg_name: gb_pr2:HSU18659
                                                                                                                                             seq_documentation_block:
LOCUS HSU18659
DEFINITION Human MHC Cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
gb_prl:HSHLAB27
gb_pat:AR008238
gb_pr4:AF022168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      variation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 Documentation ...
1 U18659 Human MHC class I HLA-B
39 1 L38504 Homon sapiens (clones 18
11 X03664 Human class I MHC gene
12 1 W05578 Pan paniscus class I Ini
12 X03664 Human class I MHC gene
13 1 W0692 H sapiens HLA-B gene, ex
14 W0693 H sapiens HLA-B gene, ex
15 1 W05578 Pan paniscus class I Ini
15 1 W0692 H sapiens HLA-B gene, ex
15 1 W05516 Homo sapiens isolate class I MHC 2165 Homo sapiens isolate class I MHC 216935 Homo sapiens MHC class I MI344 Human MHC class I processive in MHC 216935 Homo sapiens MHC class I MA-B Homo sapiens HLA-B HOM Homo MHC Class I HLA-B HOMO Sapiens MHC Class I MA-B Homo sapiens MHC class I MA-B Homo sapiens HLA-B HOMO Sapiens MHC class I MA-B Homo Sapiens HLA-B MA-B HOMO Sapiens HLA-B MA-B MR-M SASS I AND S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human MHC class I HLA-B
HLA-B27 (HLA-B*2705)-hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               233453 H.saplens mRNA for hums M12678 Human HLA-B27 mRNA, cor M54883 Human MC class I HLA-1 E01341 Genomic DNA encoding H
                                                                                                                                                                                            -MODEL-frame+_p2n.model -DEV-x1p
-Q-/G9q1_J/USPTO_20500_JV0SR05_329/_runat_04022000_160701_15779/app_query.fasta.2
-DB-GenEmbl -OFMT-fastap -SGFFIX-rge -GAPOP-12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -QGAPOP-4.500
-GAPEXT-0.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL
-OUTPWT-pfs -NORM-ext -MINLEN-0 -MAXIEN-1000000 -USER-US08653294
-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                                                                About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M54883 H
E01341 G
M12967 H
S39758 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 de la companya de l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8e-11
8e-11
3e-09
5e-12
1e-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7e-11
7e-11
7e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340.80
337.62
304.33
355.83
361.53
358.74
358.74
358.74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              346.82
346.79
346.79
346.79
346.79
346.79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349.20
       GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
Query: US-08-653-294-32
Query length: 25
Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176.920000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of: US-08-653-294-32 to:
                                                 Date: Feb 8, 2000 10:25 PM
                                                                                                                                                                      Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95-pri HSHLAKI

95-pri HSHLAKI

95-pri HSHLABHBA

95-pri HSHLABHBA

95-pri HSHLABHBA

95-pri HSHLABHBA

95-pri HSP022161

95-pri HSP022161

95-pri HSP022161

95-pri HSPMC1

95-pri HWMHCRN3

95-pri HWMHCRN3

95-pri HWMHCRN3

95-pri HWMHCRN1

95-pri HSHLAWN1

95-pri HWMHB27A

95-pri HWMHB27A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               score_list:
Sequence
gb_pr2:HSU18659
    ĕ
```

```
class I genes
EMBO J. 5 (3), 547-552 (1986)
86220133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=HLA_mRNA
<79. .151
/gene="HLA-B27K"
/label=ex1
                                                                                                                                                                                                                                               300 GAACCIGGGATCGCGCTCCGCTAC 324
                                                                                                       from: 1
                                                                                                                                                                                                                 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       793. .1068
/gene="HLA-B27K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280. .549
/gene="HLA-B27K"
                                                                                                                                                                                                               17 uAsnLeuArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=ex3
399 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=ex2
                                                                                                       Align seg 1/1 to: HUMHLABC
Ratio: 5.320
Percent Similarity: 100.000
                                                   alignment_block:
US-08-653-294-32 x HUMHLABC
                                                                                                                                                                                                                                                                                      seq_name: gb_pr1:HSHLAK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="major histocompatibility complex"
/protein_id="aAA69724.1"
/db_xref="d1:896271"
/td_xref="d1:896271"
/translatio="MKYTAPPTLLLLIMGAVALIETWAGSHSMRYFHTSVSRPGRGEP
RFITAVSYDDTLFYRDSDAASPREBPRAPWIEQEGPBYWDRETOICKAKAOTDRENL
RIALRYYNQSEAGSHTLQNMYGCDVGPDGRLLRGYHQDAYDGKDYIALNEDLSSWTAA
RDAAQTTQRKWEBARAVREDLRALBEECVEWLRRYLENGKETLQRADPPRTHYHHPI
SDHEATLRCWALGFYPABITITWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVVPSG
EEQRYYCHVQHEGLFRPLTLRRPESSQSTVPIVGINAGLAVLAVVVIGAVVAAVWCRR
KSSGGGGGSYSQAACSDSAQGSDVSLTA"
                                                                                                                                                                              HUMHLABC 1089 bp mRNA PRI 11-JUL-1995
Homo sapiens (clones 18.1, 18.2, 19.2) MHC class I HLA-B*2702 mRNA,
complete cds.
                                                                                                                                                                                                                                                L38504
L38504.1 GI:886270
cell surface glycoprotein; class I gene;
integral membrane protein; major histocompatibility complex.
Homo sapiens (clone: B18.1) cDNA to mRNA; Homo sapiens (clone:
18.2) cDNA to mRNA; and Homo sapiens (clone: 19.2) cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                    1 (bases 1 to 1089)
Parham, P., Arnett, K.L. and Adams, E.J.
On the nucleotide sequences of B*2702 and B*2705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .1089
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="B18.1"
/cell_line="NW"
/cell_type="BBV-transformed B-cell"
/haplotype="HLA A2/3; B7; Cw2,7"
/clone="18.2"
/map="6p21.3"
1. 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          172 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1995)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1022. .1054
/gene="HLA-B*2702"
1055. .100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <1...73
/gene="HLA-B*2702"
74...343
/gene="HLA-B*2702"
344...619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1089
/gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1055. .>1089
/gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                896. .1021
/gene="HLA-B*2702"
                                                                                          HILLIFILIFILITITITITITITE

84 GAACCTGCGGATCGCGCTCCGCTAC 108
                                                                      17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 c
                                                                                                                                           seq_name: gb_pr2:HUMHLABC
                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                           SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
```

```
join 79. 151280. 549,793. 1068,X03667.1:6. 281,
X03667.1:373. 489,X03667.1:930. 962,X03667.1:1069. 1112)
Agene-Wild-B2TK
/codon_start-1
/label-HIA_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(<79. .151,280. .549,793. .1068,x03667.1:6. .281,
x03667.1:373. .489,x03667.1:930. .962,x03667.1:1069. .1116,
x03667.1:1299. .>1639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .1112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA27301.1"
/db_xref="G1:811296"
/db_xref="G1:81296"
/db_xref="G1:81296"
/translation="kkyyapetullilkykyapetullilkykyybptusykyddylkyhybptusykyddagaspreeprapwiegegepeywdretgickakagtdren
Rialryngseagshtlonwygcdovgdgrifkyyddaydckdylalneblsswya
Rialryngseagshtlonwygcdovgdgrifkyyddaydckdylalneblsswyaa
Suprapitrgrkeaarvaegeraylegecvewirriengretgickyythypi
Suprapitrgralithydrogogebotodfilkyybetythypi
Suprapitrgralithydrogogebotodfilkyyby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1241)
Seemann, G. H., Rein, R. S., Brown, C. S. and Ploegh, H. L.
Gene conversion-like mechanisms may generate polymorphism in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   join(79. .151,280. .549,793. .1068,X03667.1:6. .281,
X03667.1:373. .489,X03667.1:930. .962,X03667.1:1069.
/gene="HLA-B27K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS HSHLAKI 1241 bp DNA PRI 28-JAN-1997
DEFINITION Human class I MHC gene HLA-B27K exons 1-3 (BRUG cell line).
ACCESSION X03664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            380 bp of intron III missing. Sequence continued in X03667. Location/Qualifiers
                                                                                                                                                                                                                                                  X03664.1 GI:32236 class I antigen; major histocompatibility antigen; major histocompatibility complex; signal peptide.
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                        to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="BRUG"
```

φ

447

ø 213

BASE COUNT

25

Length:

Quality: 133.00

ORIGIN

```
/codoc_start=1
/product="class I histocompatibility antigen"
/product="class I histocompatibility antigen"
/proteh.ld="AAA50181.1"
/db_xref="cl:48774"
/translation="VLLLLSAALALTETWAGSHSMRYFYTSVSRPGAGEPRFISVGTV
/translation="VLLLLSAALALTETWAGSHSMRYFYTSVSRPGAGEPRFISVGTV
/branslation="VLLLLSAALALTETWAGSHSWRYFYTSVSRPGAGEPRFISVGTV
/translation="VLLLLSAALALTETWAGSHSWRYFYTSVTHPLSHTRYN
OSFAGSHTLQTMYGCDVGFDGFRIRGYRGFAYDGKDYTALNEDLSSWTAADTAAQITG
RKWEAARVAEQQPARLEGLCVFWLRRYLENGKETLGRADPRYTHTHPISDHFATLE
CWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDRTFOKWAAVVVPSGOEGRYTCH
VQHGGLPEPLILRWEPSSQSTIPIVGIVAGLAVLAVVTGAVVAAVWCRRKSSGGRGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                  PPU05578 1065 bp mRNA PRI 08-0CT-1994 Pan paniscus class I histocompatibility antigen Papa-B (Papa-B-02 allele) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 1065).

McAdam, S.N., Boycon, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bontrop, R.E. and Watkins, D.I.

A uniquely high level of recombination at the HLA-B locus Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                      oaps: 0
Percent Identity: 92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 25
Gaps: 0
Percent Identity: 92.000
                                                                                                                             from: 1 to: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Pan paniscus"
/isolate="Bosondjo"
/db_xref="taxon:9597"
1. .1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="HLA-B-02 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSQAASSDSAQGSDVSLTA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. .1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 g
                                                                                                                                                                                                                                                                                                        276 GAACCIGCGGAICGCGCICCGCIAC 300
                                                                                                                                                                                                                                                             17 uAsnLeuArgileAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <í. .1065
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 1065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U05578.1 GI:454773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        327 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pygmy chimpanzee.
Pan paniscus
                                                                                                                             Align seg 1/1 to: PPU05575
Ratio: 4.960
Percent Similarity: 100.000
                                                             alignment_block:
US-08-653-294-32 x PPU05575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio: 4.960
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-32 x PPU05578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 124.00
                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pr1:PPU05578
                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS PPU05578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin Regional Primate Research Center, 1220 Capitol Court, Madison, WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="VLLLLSAALALTETWAGSHSMRYPDTAVSRPGAGEPRFITVGYV
ODDOFVRREDSDAASPREBRARAWEGGSEPEWINTOJCKGAGOTDRENLRIALTYN
OSEAGSHTLQRWYGCDUVGPDGRLLRGYSGSAYDGKDYTALNEDLSSWTAADTAAQITO
RKWEAARVAEGLRAYLEGLCVEWLRRYLEBNGKETLQRADPPRTHYTHPISDHEATLR
VQHEGLPEPLTITWQRROEDDOYDTELVETRRAGDRYFGWAAVVYBSGQEQRYTCH
VQHEGLPEPLTILKWEBSSGSTIPIVGIVAGLAVYTGAVVATGAVVAAVWCRRKSSGGKGG
SYSQAASSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PPU05575 1065 bp mRNA PRI 08-OCT-1994
Pan paniscus class I histocompatibility antigen Papa-B (Papa-B-03 allele) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates: Catarrhini; Hominidae; Pan.

1 (bases I to 1065)
McAdam, S.N., Boyson, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bontrop, R.E. and Watkins, D.I.
A uniquely high level of recombination at the HIA-B locus Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="class I histocompatibility antigen"
/protein_id="AAAS0178.1"
/db_xref="GI:454768"
                                                                                                                                                                                                                                                                                                           1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                               Gaps: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168
                                                                                                                                                                                                                                         from: 1 to: 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Pan paniscus"
/isolate="Lorel"
/db_xref="taxon:9597"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HLA-B"
/note="HLA-B-03 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      1. .1065
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 1065)
Boyson, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U05575.1 GI:454767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <1. .1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pygmy chimpanzee.
Pan paniscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                               Quality: 133.00
Ratio: 5.320
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 124.00
                                                                                                                                                                                                                                         Align seg 1/1 to: HSHLAK1
                                                                                                                                                                      alignment_block:
US-08-653-294-32 x HSHLAK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_pr1:PPU05575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regional Pr
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
```

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS

TITLE JOURNAL

FEATURES

gene CDS BASE COUNT

DEFINITION

ACCESSION

DEFINITION ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE

JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

FEATURES

```
Homos sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 250)
1 (bases 1 to 250)
Molecular evolution of HIA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (07-027-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOMBIA
                                                                                                              10-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCOS AF022159 255 bp DNA PRI 05-JAN-1999
DEFINITION Homo sapiens isolate 026 MHC class I antigen HLA-H (HLA-H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .250
/organism="Homo sapiens"
/isolate="Isabel-26"
/isolate="from amerindian community Nukak-Maku"
/db_aref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 TGGGACCGGAACACACAGATCTGCAAGGCCCAGGCACAGACTGAACGAA 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                            HSHLABHBB 250 bp DNA PRI
H.sapiens HLA-B gene, exon 2, HB(b) allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 120.00 Length: 25
Ratio: 4.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 t
                                                                                                                                                                                       HLA-B gene; human leukocyte antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /der_stage="adult"
/tissue_type="blood"
/cell_type="white"
/lab_host="E.coli TG1"
/clone="cHBC2(b)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="cHBC4(b)"
14. .250
/gene="HLA-B"
<14. .>250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="allel HB(b)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
214 GAACCTGCGGATCGCGCTCCGCTAC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214 GAACCTGCGGATCGCGCTCCGCTAC 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene-"HLA-B"
                                                                                                                                                                    Y08693.1 GI:1619288
                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 250)
Rojas-Munoz,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: HSHLABHBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-32 x HSHLABHBB
                                                         seq_name: gb_pr1:HSHLABHBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_pr4:AF022159
                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                               DEFINITION
ACCESSION
                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota: Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 250)
Rojas-Munoz, A., Mendez, I. and Yunis, I.

Molecular evolution of HLA-B locus in a small population amerindian community: The Nukak-Maku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (07-OCT-1996) A. Rojas-Munoz, National Institute Of
Health, Immunogenetics, Avenida El Dorado, Carrera 50, Santafe De
Bogota / Zona 6, COLOWBIA
Location/Qualifiers
                                                                                                                                                                                                                                                               10-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/isolate="Nancy-28"
/isolate="from amerindian community Nukak-Maku"
//isolate="fraxon:9606"
/chromosome="6"
                                                      HSHLABHBA 250 bp DNA PRI
H.saplens HLA-B gene, exon 2, HB(a) allele.
Y08692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 25
Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                           Y08692.1 GI:1619287
HLA-B gene; human leukocyte antigen
                   Align seg 1/1 to: PPU05578 from: 1 to: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
fissue_type="blood"
/cell_type="white"
/lab_host="E.coli TG1"
/clone="cHBC1(a"
/clone="cHBC2(A)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <14. .>250
/gene="HLA-B"
/note="allel HB(a)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δ
                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14. .250
/gene="HLA-B".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 250)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: HSHLABHBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-32 x HSHLABHBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 120.00
                                                                                                                                                                                                        seq_name: gb_pr1:HSHLABHBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rojas-Munoz, A.
                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS HSHLABHBA
                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
```

BASE COUNT ORIGIN

gene

exon

```
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
              REFERENCE
AUTHORS
TITLE
                                                                      JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                  SBS
                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                      C (bases 1 to 255)
2 (bases 1)
2 (bases 1)
3 (bases 1)
3 (bases 1)
4 (bases 2)
5 (bases 3)
5 (bases 3)
6 (bases 3)
6 (bases 3)
7 (bases 3)
                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 255;
Grimsley,C., Mather,K.A. and Ober,C.
HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AF022161 271 bp DNA PRI 05-JAN-1
DEFINITION Homo sapiens isolate 068 MHC class I antigen HLA-H (HLA-H)
ACCESSION AF022161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                /note="African-American individual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MHC class I antigen HLA-H"/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 255
pseudogene, partial sequence.
AF022159
AF022159.1 GI:2655062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        228 GAACCTGCGGATCGCGCTCCGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AF022159 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                              1. .255
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .>255
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <i. .>255
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                              /map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF022161.1 GI:2655064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 120.00
Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                             /bsendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /bsendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-32 x AF022159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /psendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_pr4:AF022161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                          ORGANISM
                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                          AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                              JOURNAL
                                                                                                                                                                                              MEDLINE
                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
```

```
2 (bases 1 to 271)
2 (bases 1 to 271)
3 (crimsley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairvlew Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
1 (bases I to 271)
Grimsley,C., Mather,K.A. and Ober,C.
HLA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF022163 271 bp DNA PRI 05-JAN-1999
Homo sapiens isolate 138 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
AF022163.1 GI:2655066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 271) (arimaley, C., Mather, K.A. and Ober, C. HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 TGGGACCGGAACACACAGATCTGCAAGGCCCAGGCACAGACTGAACGAGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/isolate="068"
/db_xref="taxon:9606"
/map="6p21.3"
/note="African-American individual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 25
Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HLA-H"
/note="MHC class I antigen HLA-H"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1 to: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85
                                                                                                                                                                                                                                                                                                                                                                                                                            1. .270
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <1. .>271
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1. .>270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AF022161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /bsendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-32 x AF022161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /bsendc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr4:AF022163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AF022163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
```

```
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sonrce
                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                 ORIGIN
2 (bases 1 to 271)
GrimsLey.C., Mather, K.A. and Ober, C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
1. . 271
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 defined to 271)
Grimaley,C., Mather,K.A. and Ober,C.
Grimaley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
1.071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 271)
Grimaley,C., Mather,K.A. and Ober,C.
HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci
Mol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AF022164 271 bp DNA PRI 05-JAN-1.
DEFINITION Homo sapiens isolate 156 MHC class I antigen HLA-H (HLA-H)
pseudogene, partial sequence.
ACCESSION AF022164
VERSION AF022164.1 GI:2655067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                              7 others
                                                                                                                                                                                              /note="African-American individual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 120.00 Length: 25
Ratio: 4.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.000
                                                                                                                                                                                                                                                                            <1. >270
/gene="HLA-H"
/note="MHC class I antigen HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                ų
                                                                                                                                                                                                                                                                                                                                                                                                              36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 271
                                                                                                                                               /db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                 ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AF022163 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                91
                                                                                                                                /isolate="138"
                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                               1. .270
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                             <li.>271
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                            84 C
                                                                                                                                                                                                                                                                /number-2
                                                                                                                                                                                                                                                                                                                                                                                                 /psendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-32 x AF022163
                                                                                                                                                                                                                                               /bsendo
                                                                                                                                                                                                                                                                                                                                                 /psendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_pr4:AF022164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99083426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
   REFERENCE
AUTHORS
                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                  FEATURES
                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
```

```
Chases 1 to 271)
Crimsley,C., Mather,K.A. and Ober,C.
Grimsley,C., Mather,R.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo. 1 (Dases I to 271) (Cases I to 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRI 05-JAN-1999
class I antigen HLA-H (HLA-H)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
/note="African-American individual"
                                                                                                                                                           /map="6p21.3"
/note="African-American individual"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 25
Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                               <1. .>270
//gene="HLA-H"
/note="MHC class I antigen HLA-H"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 271
/organism="Homo sapiens"
/isolate="156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 271
/organism="Homo sapiens"
/isolate="175"
                                                                                    /db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AF022165 271 bp DNA
DEFINITION Homo sapiens isolate 175 MHC
pseudogene, partial sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AF022164 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 GAACCIGCGGAICGCGCICCGCIAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF022165
AF022165.1 GI:2655068
                                                                                                                                                                                                                                               1. .270
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <1..>271
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O
                                                                                                                                                                                                                                                                                                                                                                         /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /pseudo
85 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouality: 120.00
Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                   /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-32 x AF022164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr4:AF022165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
```

```
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 271)
Grimaley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairview Ave. N., M374, Seattle, WA 98109, USA
1. .271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AF022166 271 bp DNA PRI 05-JAN-1999
DEFINITION Homo sapiens isolate 219 MHC class I antigen HLA-H (HLA-H)
PSeudogene, partial sequence.
ACCESSION AF022166.1 GI:2655069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 271)
Grimsley,C., Mather, K.A. and Ober,C.
H.A.H.: a pseudogene with increased variation due to balancing selection at neighboring loci
MOL. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                 others
                                                                                                                                                                                                                                                                                                                                                    1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="African-American individual"
                                                                                                                                                        Φ
                                                                                                                                                                                                                        Length: 25
Gaps: 0
Percent Identity: 88.000
                                       <1. .>270

/orene"HLA-H"
/note="MHC class I antigen HLA-H"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MHC class I antigen HLA-H"
/codon_start=1
                                                                                                                                                        ų
                                                                                                                                                      35
                                                                                                                                                                                                                                                                                                                         to: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/isolate="219"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                        δ
                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                      91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <1. .>270
/gene="HLA-H"
/gene="HLA-H"
/pseudo
                                                                                                            <li..>271
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .270
/gene="HLA-H"
                                                                                                                                                      83 c
                           /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'number=2
                                                                                                                                                                                                                                     Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AF022165
                                                                                                                                         /psendo
                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-32 x AF022165
                                                                                                /psendo
                                                                                                                                                                                                                         120.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /psendo
                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr4:AF022166
                                                                                                                                                                                                                         Quality:
                                                                                                                                                      53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
```

```
/product="MHC class I antigen HLA-H ortholog"
/protein_id="AAC99794.1"
/db_xref="G1:2655080"
/translation="GSHSMRYEYITMSRPGRGEPREISVGYVDDTQFVRFDSDDASPR
EEPRARMERGPEFYRDRNTYGTRAGAGTERENLRIALRYYNQSEG"
84 c 91 g 37 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA PRI 05-JAN-1999
Shamba MHC class I antigen HLA-H ortholog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chases 1 to 271)
Grimaley,C., Mather,K.A. and Ober,C.
Direct Submission
Submitted (03-SEP-1997) Fred Hutchinson Cancer Research Center,
1100 Fairvlew Ave. N., M374, Seattle, WA 98109, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gorilla.

Gorilla gorilla

Gorilla gorilla

Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Gorilla.

1 (Dases I to 271)

Grimaley, C., Mather K.A. and Ober, C.

HIA-H: a pseudogene with increased variation due to balancing selection at neighboring loci

Wol. Biol. Evol. 15 (12), 1581-1588 (1998)
                                                                                                                                                                                                                                                                                                                                                                                          1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                 Length: 25
Gaps: 0
Percent Identity: 88.000
                                                                                  ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Gorilla gorilla"
/isolate="Shamba"
/db_xref="taxon:9593"
                                                                                  38
                                                                                                                                                                                                                                                                                                                               ;
t
                                                                                    b
                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AF022172 271 bp DN.
DEFINITION GOTILLA GOTILLA ISOLATE Sh.
ACCESSION AF022172
VERSION AF022172.1 GI:2655079
                                                                                  91
                                                                                                                                                                                                                                                                                                                               from: 1
/pseudo
<1. .>271
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .270
/gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="HLA-H"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=2
                                                             /pseudo
84
                                                                                                                                                                                 Quality: 120.00
Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AF022166
                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-32 x AF022166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_pr4:AF022172
```

Length:

us-08-653-294-32.rge

```
major histocompatibility complex.
Homo sapiens DNA.
SM Homo sapiens DNA.
Homo sapiens DNA.
SM Homo sapiens DNA.
SM Homo sapiens Characa, Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eutheria; Primates; Catarrhini; Hominidae; Homo.
S Zemmour, J., Koller, B.H., Ennis, P.D., Geraghty, D.E., Lawlor, D.A., Orr, H.T. and Parham, P.
HIA-AR, an inactivated antigen-presenting locus related to HLA-A.
Implications for the evolution of the MHC
L J. Immunol. 144 (9), 3619-3629 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .1096
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="hematopoietic B-lymphoblastoid cell line
LCL721"
                                                                                                                                                                                                                                                                                                                                                                            14-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Authorin copy of sequence [1] kindly submitted by J. Zemmour, 14-FEB-1990.
                                                                                                                                                                  Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 120.00 Length: 25
Ratio: 4.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS HUMMHGAR3 1096 bp DNA
DEFINITION HUMBU MHC HLA-AR gene, inactive antigen.
ACCESSION M32106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. >1096
/note="MHC HLA-AR; putative"
/pseudo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: HUMMHCAR3 from: 1 to: 1096
                                                                                                                                 Align seg 1/1 to: AF022172 from: 1 to: 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
334 c 362 g
                                                                                                                                                                                                                                         Quality: 120.00
Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-32 x HUMMHCAR3
                                                                         alignment_block:
US-08-653-294-32 x AF022172
                                                                                                                                                                                                                                                                                                                        seq_name: gb_pr2:HUMMHCAR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
```

```
Human secreted protein 5' ES
Human nel-related protein t
Mus musculus SOCSIO gene. S
Human nel-related protein t
     Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Such DNA, antigen or antibody
Claim 2; Page 4; 5pp; German.
The DNA may be used as a hybridisation probe for detecting the HLA
B27 gene, e.g. for assessing susceptibility to rheumatic disorders
such as ankylosis spondylitis, or may be used to transform cells
for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27
antibody in human serum, or to produce mono- or polyclonal HLA B27
sequence 1026 BP; 213 A; 307 C; 344 G; 162 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:

ID N70225 standard; DNA; 3874 BP.

AC N70225;
DT 03-APR-1991 (first entry)

DE Sequence of genomic DNA encoding human histocompatibility antigen

DE HLA-B 27.
                                                                                                                                                                                                                                                                               10-APR-1991 (first entry)
Sequence encoding the human histocompatibility antigen HLA B27
Rheumatic disorder; genetic screening; diagnosis;
ankylosing spondylitis; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA coding for antigen HLA B27 - and diagnostic reagents contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       178 TGGGACCGGGAGACACAGATCTGCAAGGCCAAGGCACAGACTGACCGAGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ankylosing spondylitis; rhewmatic disorder; diagnosis;
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 118.00 Length: 25
Ratio: 5.130 Gaps: 0
nilarity: 92.000 Percent Identity: 88.000
     322
2448
2649
3198
13.93
176.22
194.51
246.19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: N70935 from: 1 to: 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04_JUN-1987.
28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERRE AG.
Riethmuller G, Meo T, Weiss E, Szots H;
WPI; 87-157893/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
518. .590
/*tag= a
/*tag= b
1090. .1506
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .1026
128.96
109.17
108.40
106.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                              N70935 standard; DNA; 1026 BP. N70935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 GGACCTGCGGACCCTGCTCCGCTAC
  seq_name: N_Geneseq_36:N70935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:N70225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-32 x N70935
                                                                                                                                                                                               seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
  N_Geneseq_36:X40673
N_Geneseq_36:V01882
N_Geneseq_36:V38678
N_Geneseq_36:V01883
                                                                                                                                                                                                                                                                                                                                                                                                                                                          cds
DE3542024-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                   NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1026 Sequence encoding the human hill 1026 Sequence of genomic DNA encoding 1187 In 1872 Consensus sequence. De 1088 Sequence encoding HLA-BW52 and 1089 HLA-BW52 gene for production C 1089 HLA-BW53 exon. HLA-BW53 gene, 4059 HLA-BW53 exon. HLA-BW53 gene, 11089 HLA-BW53 exon. HLA-BW53 gene, 11089 HLA-BW53 exon. HLA-BW53 gene, 11089 HLA-BW53 exon. HLA-BW53 gene, 1109 HLA-BW53 exon. HLA-BW53 exon. Connoction sequence of a portion of the MH Mucleotide sequence of a portion of the MH MH MLA but 10 Not leotide sequence of a portion of the MH MH MLA but 10 Not leotide sequence of a portion of the MH MH MLA but 10 Not leotide sequence of a portion of the MH MH MLA but 10 Not leotide sequence of a portion of the MH MH MLA but 10 Not leotide sequence of a portion of the MH MH MLA but 10 Not leotide sequence of a portion of the MH MH HA but 10 Not leotide sequence of a portion of the MH MH But 10 Not leotide sequence of a portion of the MH MH But 10 Not leotide sequence of a portion of the MH HA but 10 Not leotide sequence of a portion of the MH HA but 10 Not leotide sequence of a portion of the MH HA but 10 Not leotide sequence of a portion of the MH HA but 10 Not leotide sequence of a portion of the MH HA but 10 Not leotide sequence of a portion of the MH HA but 10 Not leot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expression vector pAP045. Prep
Acetobacter cdg2 operon. Polyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSHV long unique coding reg
                                                                                                                                                                                                                    -MODEL-frame_p2n.model -DEV=xlp
-O=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-O=/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-O=/cgn1_1/USPTO_spool/US08653294/runat_0402000_16000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=6.000 -GCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=11.MATRIX=blocoun62
-TRANS=human40.cdi -LISP=45 -DOCALIGN=200 -THR_SCORE_pct
-ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3150 !
35100 !
137507
2988 !
4558 !
     out_format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.4737
160.00
3.3e+03
1.8e+04
184.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8e-08
3e-05
0e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .3e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.0014
0.0013
0.0074
0.0113
0.0473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.93
74.93
86.48
96.74
255.06
39.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.82
8.62
15.13
25.27
29.30
     OM of: US-08-653-294-32 to: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250076
3355.37
3300.18
3300.18
3300.18
3300.18
3300.18
3300.18
3300.18
3300.18
3310.57
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
2332.77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
search time (sec): 873.190000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
Query: US-08-653-294-32
Query length: 25
                                                                                                                                                                                                  Command line parameters:
                                                          Date: Feb 8, 2000 7:31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:N70225
N_Geneseq_36:106139
N_Geneseq_36:001822
N_Geneseq_36:005701
N_Geneseq_36:005701
N_Geneseq_36:005934
N_Geneseq_36:012114
N_Geneseq_36:012114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:V12763
N_Geneseq_36:V34403
N_Geneseq_36:T29389
N_Geneseq_36:T29389
N_Geneseq_36:T29389
N_Geneseq_36:Q2069
N_Geneseq_36:Q2069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_36:092068
N_Geneseq_36:T86375
N_Geneseq_36:X26690
N_Geneseq_36:Q70152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:070152
N_Geneseq_36:142166
N_Geneseq_36:18977
N_Geneseq_36:004524
N_Geneseq_36:004524
N_Geneseq_36:00080
N_Geneseq_36:00080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _Geneseq_36:N70935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:Q12117
N_Geneseq_36:N80603
N_Geneseq_36:T21345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq_36:V04900
N_Geneseq_36:Q25977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         012115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:Q51474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _Geneseq_36:V32024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:V73804
N_Geneseq_36:V19941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:043661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THREADS-1
```

```
indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID Q01822 standard; DNA; 1086
AC Q01822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:001822
                                                                                                                                                                                                                                                                                       Quality: 118.00
Ratio: 5.130
nilarity: 92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality: 101.00
                                                                                                                                                                                                                                                                                                                                               US-08-653-294-32 x T61639
                                                                               97-192924/17
                                                                                                                                                                                                                                                                                                              Percent Similarity:
            WO9709450-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-354580-A.
                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                     ryan DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
 R 01-JAN 1985; DE-542024.

R 12-DEC-1985; DE-542024.

R 12-BELW ) BERRINGWERKE AG.

Scots H, Westss E. Dorner C, Lang M, Meo T, Riethmuller G;

WPI; 87-171469/25.

R PFDBB; P70155.

T or diagnosis and antigen and antibody prodn.

T for diagnosis and antigen and antibody prodn.

T for diagnosis and second antigen and antibody prodn.

T for man genetic material. The HIA-B 27 gene (opt. mutated) in thuman genetic material. The HIA-B 27 may be used to detect anti-HIA-B 27 antibodies in human serum. The antibodies may be used to detect mine HIA-B 27 antibodies in human serum.

C determine HIA-B 27 levels in human serum.

C sequence 3874 BB; 751 A; 1094 C; 1171 G; 858 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIA B27 consensus sequence.
HIA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
ss; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /noce= "3' flanking region diagnostic for genetic predisposition to SNSA" 4770. 4556 /*teq= b /*teq= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "3' flanking region diagnostic for genetic
predisposition to SNSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "HLA-B27 3' flanking region, downstream
                                                                                                                                                                                                                                                                                                                                                                                                                                       d
"absence of cytosine at this site
                                                                                                                                                                                                                                                                                                                                   Length: 25
Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: N70225 from: 1 to: 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3' untranslated region"
4112. .4556
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
3968. .6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           946 GGACCTGCGGACCCTGCTCCGCTAC 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 uAsnLeuArgileAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID T61639 standard; DNA; 6553 BP.
         /*tag= d
2450. .2566
/*tag= e
/*tag= f
3148. .3191
/*tag= g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                  Quality: 118.00
Ratio: 5.130
nilarity: 92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:T61639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
/note=
                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-32 x N70225
                                                                                                               116139
                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_difference
                                                                                                   24-JUN-1987.
21-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                       EP-226069-A
                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T61639;
                      intron
intron
                                             intron
                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
```

```
Detecting pre-disposition to seronegative spondylarthropathies - Trom the absence of a C residue at a specific position in the from the absence of a C residue at a specific position in the 3'-flanking region of the HLA B27 allele Genetic predisposition to seronegative spondyloarthropathies (SNSA) is detected by determining the absence of a cytosine nucleotide in the 3' flanking region (see also T61647-48) of an HLA-B gene at a position corresponding to nucleotide 4455 of the HLA-B37 consensus sequence given in T61639. Probes and primers (see also T61640-46) chased on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA, romal individuals who are susceptible (but as yet unaffected) to such diseases. Sequence 6553 BP; 1443 A; 1619 C; 2017 G; 1474 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2: ppil-12: 23pp: English.

The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be sequence by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 33 A; 335 C; 358 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 25
Gaps: 0
Percent Identity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: T61639 from: 1 to: 6553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAY-1991 (first entry)
Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .1086
/*tag= a
13-MAR-1997.
11-AUG-1996; U13256.
01-SEP-1995; UG-522942.
(CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107 GACCTGCGGACCCTGCTCCGCTAC 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-FEB-1990.

10-AuG-1998 JP-200758.

(OLYU) Olympus Optical Co., Ltd.

Kano K, Takiguchi;

WPI: 90-046289/07.

P-PSDB: R03142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17 uAsnLeuArgileAlaLeuArgTyr 25
```

m

```
The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 90-255479/34.
Allotype specific monoclonal anti- HLA antibodies prodn. - using hibbridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype.
Disclosure: Fig 1 A-G; 20pp; English.
The human HLA-Bw52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (see Q05693).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 005701;
03-JAN-1991 (first entry)
HIA-BW52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HIA antibodies; hybridomas;
transgenic animals; HIA-BW52 gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ë
                                                                                                                                                                                                               171
  Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359
                                                                                                                                                                from: 1 to: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="alpha 1-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="alpha 2-domain:
520. .895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="alpha 3-domain"
896. .1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q05701 standard; DNA; 1089 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP-383183-A.
22-AUG-1990.
07-FEB-1999; 102424.
08-FEB-1999; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
Takiguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /number=6
1043. .1089
/*tag= g
/number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .013. .1042
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74. .343
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=4
4.391
                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:Q05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101.00
4.391
92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                          Align seg 1/1 to: Q01822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       *tag=
                                                                              alignment_block:
US-08-653-294-32 x Q01822
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALD DOTCHER FEET TO SEE SEED OF SEED O
```

Percent Identity: 80.000

Length: Gaps:

Quality:

Ratio:

Percent Similarity:

```
Transgenic non-human mammalian HLA-Bw 52 gene - useful for analysis of expression of gene structure, and prodn. of nalysis of expression of gene structure, and prodn. of neulaysis of expression of gene structure, and prodn. of neulaysis of expression of the human leukocyte or antigen Bw 52 gene. The complete gene may be introduced into non-human mammals, pref. rat or mouse, or their ancestors at the primary developmental biological step via transplantation into the zygote or embryo to generate transgenic non-human mammals contg. HLA-Bw 52 are useful for the analysis of capression of the gene, its structure, and prodn. of mouse models of capression of the gene, its structure, and prodn. of mouse models of sequence 270 BP; 59 A; 88 C; 86 G; 37 T;
                                                                                                                                                                                                                                                                                                                                                                                                                            09-WAR-1993 (first entry)
HIA-Bw 52 exon 2 alpha-1 domain.
Human leukocyte antigen; transgenic; germ cells; somatic cells;
                                                                                                                                              1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 25
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q29167 from: 1 to: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1991 (first entry)
Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen; ss.
BP354580-A.
                                                                                                                                                                                                                                                            300 GAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             227 GAACCIGCGGAICGCGCICCGCIAC 251
                                                                      from: 1
                                                                                                                                                                                                               17 uAsnLeuArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 uAsnLeuArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID 029167 standard; DNA; 270 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-AUG-1990; 207329.
03-AUG-1990; JP-207329.
(OLYU ) OLYMPUS OPTICAL CO.
WPI; 92-342893/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID_001834 standard; DNA; 1086
                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:Q29167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 100.00
Ratio: 4.348
nilarity: 92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:Q01834
alignment_block:
US-08-653-294-32 x Q05701
                                                                   to: 005701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-32 x Q29167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   001834;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D S K E E E E E
```

```
D 14-FEB-1990.

F 10-AuG-1988; JP-200758.

R 11-AuG-1988; JP-200758.

I Amon K, Takiguchi;

R WPI; 90-046289/07.

New DRA for class I human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.

T transformed cells, useful for DNA typing, as immunogens etc.

Claim 1: Page 11: 23pp; English.

Claim 1: Page 11: 23pp; English.

The HLA class I DNA can be used a source of probes for use in DNA ctyping. Transformed cells, which are useful as immunogens, can be cotyping. Transformed cells, which are useful as immunogens, can be sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-37N-1991 (first entry)
03-37N-1991 (first entry)
HLA-B51 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas;
transgenic animals; HLA-B51 gene; ss.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.00 Length: 25
4.130 Gaps: 0
92.000 Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: Q01834 from: 1 .to: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="alpha 3-domain"
396. .1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="alpha 1-domain'
344. .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="alpha 2-domain"
620. .895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID 005693 standard; DNA; 1089 BP.
AC 005693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/number=5
1013. 1042
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=6
1043. .1089
/*tag= g
/number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
Takiguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .73
/*tag= a
/number=1
74. .343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= d
/number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:Q05693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-32 x Q01834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP-383183-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
         NEETT - EFT - EFT
```

```
Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and hybridomas derived from transgenic animals carrying HLA gene and produced with HLA antigen of different allotype bisclosure; Fig 1 A-G; 20pp; English.

The human HLA-BSI gene was injected into fertilised mouse eggs and then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the chromosome, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-BSI gene. The pransgened. Offspring were immunised with HLA antigen. The spleen lymphocytes were fused with myeloma cells. Hybridomas producing antibodies were selected.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
Homo sapiens.
                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                173
                                                                                                                                                                                                                                Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                357 G;
                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: Q05693 from: 1 to: 1089
                                                                                                                                                                                335 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1089
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                  300 GAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                   17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID 012114 standard; DNA; 1089 BP.
AC 012114;
                                                                                                                                                                                224 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-AUG-1991 (first entry)
                                                                                                                                                                                                                                95.00
4.130
92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:012114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.00
4.130
92.000
                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-32 x Q05693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-32 x Q12114
                                                                                                                                                                                1089 BP;
90-255479/34
                                                                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J03112487-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                Sequence
```

```
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note- "encodes put
HLA-B7 heavy chain"
                                                                                                                                                                                 to reverse of: Q75974
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q75973 standard; cDNA; 4965 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .1853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chain mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              535. .606
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-AUG-1995 (first entry)
                                                                                                                     alignment_block:
US-08-653-294-32 x Q75974/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    peptide"
1621 186
                                                           4.421
                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:Q75973
                                       84.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                         2584 GAGCCTGCGG 2575
                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block
                                                                                                                                                                                                                                                                                                  17 uAsnLeuArg 20
                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                           075973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI: 95-036494/05.
WPI: 95-036494/05.
New vectors for genetic meterial encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s) page 42-43: 50pp; English.
This HLA-B7 antigen encoding hasmid was developed to incorporate many advantageous features, eg. the kanamycin resistance gene. The eradication of two open reading frames encoding portions of SW40 viral proteins lowers the risk of tumourigenicity. The vector may also operate as a cassette into which cistrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest.
                                                                                                                                                                                                                                                                                            23-AUG-1995 (first entry)
pHLA-B7 expression vector.
pHLA-B7; bicistronic mRNA;
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      notes "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'noteّ "Rous sarcoma virus 3' LTR promoter region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/note= "pBR322 backbone contg. bacterial origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1000 T;
                                                           1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                untranslated region of HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "SV40 polyA signal sequence"
complement (1412. .1560)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1033 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "HLA-B7 open reading frame" complement (2886. .3415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  t intron"
to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1410. .1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1051 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (1795. .2880)
                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "SV40 small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the gene is taken
Tn903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (1561.
                                                                                                                                                        300 GAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heavy chain mRNA"
                                                                                                                   17 uAsnLeuArgIleAlaLeuArgTyr 25
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "HLA-B7
                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         975 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                replication"
355. .1170
                                                                                                                                                                                                                                  seq_documentation_block:
ID Q75974 standard; cDNA; 4059
AC Q75974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1994.
27-MAY-1994; U06069.
07-UNN-1993; US-074344.
(UNMI ) UNIV MICHIGAN.
(YICA-) VICAL INC.
Lew D, MARQUET M. Nabel
                                                                                                                                                                                               seq_name: N_Geneseq_36:Q75974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
to: Q12114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4059 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NO9429469-A
                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ltr
```

NE STATE STA

```
/*tag= a
/note= "Rous sarcoma virus LTR promoter domain, derived
                                                                                                                                                                                                                                                                                                                                                                      expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7; light beta-2 microglobulin; class I major histocompatibility complex; MHC; bicistronic mRNA; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nucleotides 255-843 of cloned EMCV genomic DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy chain mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for the Schmidt-Rupin strain nucleotides 8673-9146. This region also includes a 56 bp region of a synthetic oligonucleotide which modifies this regulatory sequence to effect a higher level of expression of downstream sequences. The oligonucleotide removes a polyadenylation signal sequence originally found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA-B7 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= g
/*tag= g
/*tag= multiple cloning site, forms a junction
between the HLA-B7 sequence and the EMCV-CITE
sequence, and is used to facilitate subcloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the
                                                                                                                                                             2634 TGGGACCGGAACACAGATCTACAAGGCCCAGGCACAGACTGACCGAGA 2585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oţ
                                                                                                                                          1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= c
/note= "HLA-B7 heavy chain open reading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   putative signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label consensus_Kozak_signal_sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "3' untranslated sequence of
                                                                                                             to: 4059
Length: 20
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/note= "encodes putative HLA-B7
                                                                                                                                                                                                                                                                                                                                                           pHLA-B7/beta-2 microglobulin expression vector.
                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In the RSV DNA sequence."
```

US-08-653-294-32 x Q75973

```
PR 022-DEC-1994; U06069.

PR 27-MAY-1994; U06069.

PR 27-MAY-1994; U06069.

PR 07-UNN-1993; US-07444.

RUNII ) UNIV MICHIGAN.

PI Lew D, Marquet M, Nabel EG, Nabel GJ;

Lew D, Marquet M, Nabel EG, Nabel GJ;

New vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express proposed for therapeutic peptide(s).

PT New vectors for gene therapy, partic for tumours - comprising genetic material encoding one or more cistron(s) which express for genetic material encoding one or more cistron(s) which express for the knamycoic resistance gene, contains the plasmid DNA encoding the contains by the plasmid DNA encoding the chary (human HLA-B7/beta-2 microglobulin plasmid expression vector, in addition contains the plasmid is class I major hisotocompatibility complex (MHC) antigen. The plasmid is class I major hisotocompatibility complex (MHC) antigen. The plasmid is class I major hisotocompatibility complex (MHC) antigen. The plasmid is cutaryotic cells. Initiation of transcription of the many and sequence deriv. from the bovine growth hormone controlled by the CTIFE. Finally the replication of the plasmid in controlled by the CTIFE. Finally the replication of the plasmid in controlled by the CTIFE. Finally the presence of a bacterial origin of replication. The vector is used partic. for the treatment of neoplastic contains and provides enhanced gene delivery and expression in the contains and provides enhanced gene delivery and expression in the contains and provides enhanced gene delivery and expression in the contains and provides enhanced gene delivery and expression in the contains and provides enhanced gene delivery and expression in the contains and provides enhanced gene delivery and expression in the contains and provides enhanced gene delivery and expression in the contains the contains and provides enhanced gene delivery and expression in the contains the contains and provides enhanced delivery and expression in the contains the contains and provides e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= o
/*tag= 
                                                                                                                                                                            2480. .2839
/*tag= 1
/note= "encodes beta-2 microglobulin; this cDNA is deriv. from chimpanzee (differs to the human cDNA bases)"
2840. .2846
ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HLA-B7 stop codon on this biscistronic mRNA to be recognised by the ribosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= p
/note= "pBR322 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "synthetic linker to facilitate cloning complement (3151. .3967)
                                                                                                                                                                                                                                                                                                                                                                                         /*tag= j
/note= "3' untranslated region of the beta-2
microglobulin mRNA"
2847. 2870
/*tag= k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1338 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "synthetic linker"
'UTR .3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1171 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . 2984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .3151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1014. .4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag=
3112. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9429469-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in vivo
                                                                                                                                                                                                                                                                                                                                                                3'utr
                                                                                                                                                                                   cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cds
```

Length: 20 Gaps: 0 Percent Identity: 80.000

84.00 4.421 95.000

Quality:

alignment\_scores:

Ratio: Percent Similarity:

alignment\_block:

```
19-MAY-1998 (first entry)
Human Class I non-classical HLA gene exon 2 consensus DNA.
Human leukocyte antigen class I gene; non-classical HLA; allele testing;
donor; tissue matching; recipient; graft rejection; class typing; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.
Claim 1; Page 1; 13pp; Japanese.
Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C animals and prodn. of monoclonal antibodies specific for the HIA-C sequence 1101 BP; 211 A; 337 C; 377 G; 176 T;
                                                                                                                                                                                                                                                                          HLA-C exon Cb-1.

Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.

Homo sapiens.
                                                    1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 20
Gaps: 0
Percent Identity: 70.000
to: 4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 1101
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1101
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:

ID V02693 standard; DNA; 268 BP.

AC V02693; standard; DNA; 268 BP.

DT 19-WAY-1998 (first entry)

DE Human Class I non-classical HLA

RW Human leukocyte antigen class I

KW donor; tissue matching; recipies

OS Homo sapiens.

PN W09723467-A1.

PD 03-JUL-1997.

PF 04-JAN-1996; U00362.
from: 1
                                                                                                                                                                                                                                Q12116 standard; DNA; 1101 BP. Q12116;
                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1991.
22-SEP-1989; 247695.
22-SEP-1989; UP-247695.
(OLVU) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
P-PSDB; R12465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.00
4.375
80.000
                                                                                                                                                                                 seq_name: N_Geneseq_36:Q12116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seg_name: N_Geneseg_36:V02693
to: Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-32 x Q12116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: 012116
                                                                                                                                834 GAGCCTGCGG 843
                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300 GAGCCTGCGG 309
                                                                                                           17 uAsnLeuArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 uAsnLeuArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                      29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                  J03112485-A
 Align seg 1/1
```

```
alignment_scores;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Violegies Fig 6; 89pp; English.

VO2693 is a consensus sequence of the human leukocyte antigen (HLA) Class VO2693 is a consensus sequence of the human leukocyte antigen (HLA) Class I non-classical HLA genes exon 2, which is used in a novel method for testing a tissue sample to determine the allelic type of a HLA class I gene in the sample. The HLA Class I gene is selected from among HLA-A, be and c genes. The method comprises of treating the tissue sample to obtain nucleic acid polymers suitable for amplification then combining these polymers with a first primer which hybridises with a different portion of the HLA Class I gene and a second primer which hybridises with a different portion of the HLA Class I gene under conditions suitable for amplification to obtain an amplified product. The product is then evaluated to determine the allelic type of the antigens between donors and recipients and hence for preventing graft
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAY-1991.

F 22-SEP-1989; 247697.

A (OLYU ) OLYMPUS OPTICAL KK.

NPI: 91-182991/25.

R P-FSDB; R12464.

T HLA-B35 gene - used in DNA probe and transformant cells for immunising animals, for developing monoclonal antibody.

Claim 1; Page 1; 11pp; Japanese.

C Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and produ of monoclonal antibodies specific for the cannals and produ of monoclonal antibodies specific for the sequence 1089 BP; 221 A; 336 C; 359 G; 173 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss. Homo sapiens.
04-JAN-1996; WO-U00362.

(SLOK ) SLOAN KETTERING INST CANCER RES.

(SCEPE N. Yang ST:
WPI: 97-351080/32.

DNA-based human leukocyte antigen class I gene typing method -
useful for tissue matching and prevention of graft versus host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 TGGGACCGGGAGACACAGAACTTCAAGGCCCACACACAGACTGACCGAGA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: V02693 from: 1 to: 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID Q12115 standard; DNA; 1089 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouality: 66.00
Ratio: 4.714
Percent Similarity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .1089
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:Q12115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-653-294-32 x V02693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            versus host disease.
Sequence 268 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-B35 exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J03112486-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 G 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 u 17
                                                                                                                                              disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
```

```
HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 2; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and produ. of monoclonal antibodies specific for the HIA-C animals and produ. of see also glaif (same patent) and J03112486 and J03112487. Sequence 1101 BP; 215 A; 335 C; 379 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIA-C exon Cb-2.

Himan leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.

Homo sapiens.
                                                                                                                                                                                                                                                 250 TGGGACCGGGAGACACAGAAGTACAAGCGCCAGGCACAGGCTGACCGAGT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                          1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
66.00 Length: 20
3.667 Gaps: 0
90.000 Percent Identity: 65.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65.00 Length: 20
4.062 Gaps: 0
80.000 Percent Identity: 65.000
                                                                                                                                                                          to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q12117 from: 1 to: 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .1101
/*tag= a
                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID Q12117 standard; DNA; 1101 BP.
AC Q12117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLYU) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
P-PSDB; R12466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:Q12117
                                                                                                   alignment_block:
US-08-653-294-32 x Q12115
                                                                                                                                                                          Align seg 1/1 to: Q12115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-32 x Q12117
                                                                                                                                                                                                                                                                                                                                                                300 GAGCCTGCGG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 GAGCCIGCGG 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                   17 uAsnLeuArg 20
  Quality:
Ratio:
                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 uAsnLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J03112485-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-MAY-199
```

THIS PAGE BLANK (USPTO)

```
! AA227277 zr20h03.rl Stratage
! H23327 ym52e08.rl Soares inf
! AW215398 up03c01.xl NCI_CGAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de;
sequenced by Qiagen within the cDNA sequencing consortium of the
German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to HLA-B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  No standard success of the standard sta
                                                                                                                              AL036690 171 bp mRNA EST 27-SEP-1999
DKFZp564D2463_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKFZp564D2463 5', mRNA sequence.
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 171)
                                                                                                                                                                                                                                                                                                                                   Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                Wiemann,S.
EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced g1:5866258.
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 25
Gaps: 0
Percent Identity: 88.000
   375
479
591
 0.0724
0.0972
0.1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AL036690 from: 1 to: 171
190.89
188.59
186.62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 GGACCTGCGGACCCTGCTCCGCTAC
                                                                                                                                                                                                        AL036690.3 GI:5927859
 65.00
65.00
65.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118.00
5.130
92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-32 x AL036690
                                                                        seq_name: gb_est38:AL036690
                                                                                                            seq_documentation_block:
LOCUS AL036690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS D82221
                                                                                                                                                                                                                                                              Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est6:D82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                     AL036690
                                                                                                                                                                                                                                             human.
                     gb_est4:H23327
gb_est44:AW215398
 gb_est11:AA227277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Documentation ... 6402463_r1 564 (
| 74.036690 DKF2p564D2463_r1 564 (
| D82.21 HUMHBC4626 Human pancrea |
| D82.21 HUMHBC4624 Human pancrea |
| A1124815 am56e06.x1 Johnston fr |
| AA121891 zoo1f06.x1 Johnston fr |
| AA263158 PMY0534 KG1-a Lambda Z |
| AA263158 PMY0534 KG1-a Lambda Z |
| AA369664 wc74hl1.x1 NOI_CGAP_PR |
| AA69664 wc74hl1.x1 NOI_CGAP_PR |
| AA58109 zoo57h10.s1 Stratagene |
| AA121088 zm22d06.r1 Stratagene |
| AA121088 zm22d06.r1 Stratagene |
| AA121088 zm22d06.r1 Stratagene |
| AA13662 zoo57hl1.r1 Stratagene |
| AA143626 zoo57hl1.r1 Stratagene |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T52124 Yb29906.rl Stratagene fe
AA112349 zm27b04.rl Stratagene fe
AA112349 zm27b04.rl Stratagene
R20954 yg06c01.rl Scares infant
AA263135 PMY0598 KG1-a Lambda Z
F13067 HSC31C011 normalized inf
A1466429 vx35b04.yl Stratagene
C03945 C03945 Human heart cDNA
AA352960 EST61101 Activated T-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A10924 hbc122 Human pancreatic
A1826037 wk14903.x1 NCI_CGAP_Ly
AA66896 ac74601.s1 Stratagene
AA979637 vx38b05.r1 Stratagene
AA31489 EST71032 T-cell lymphc
AA449607 zx06h02.r1 Soares_tota
AA451951 zx30a04.r1 Stratagene
AA41643 x16762.x1 Soares_test
AA41643 x16762.x1 Soares_test
AA41643 x16762.x1 Soares_test
C19056 Human placenta cL
AA381090 EST94155 Activated T-c
W50004 zc92e11.r1 Pancreatic Is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA127128 z187d05.r1 Stratagene
AL039796 DKFZp434B1912_r1 434 (
AW208428 uo60c03.x1 NCI_CGAP_Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA352534 EST60562 Activated T-c
AA160317 2056c07.rl Stratagene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA160317 zo56c07.rl Stratagene
W40489 zc84b01.rl Pancreatic Is
                                                                                                                                           -WODEL-frame-pan.model -DEV-x1p
-WODEL-frame-pan.model -DEV-x1p
-WODEL-frame-pan.model -DEV-x1p
-G-Cqqul_J/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB=EST -QFMT=fastap -SUFFIX=rst -GAPOP=12.000 -GAPOP-4.500
-MINMATCH=0.100 -LOOPCL-0.000 -LOOPEXT=0.000 -GAPOP-4.500
-GAPORTT=0.100 -XGAPOP-10.000 -XGAPEXT=0.500 -DELDP=6.000
-FGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500 -DELDP=6.000
-DELEXT=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LST=45 -DOCALIGON=200 -THR_SCORE-pct -ALIGN=15 -WODE-LCCAL
-OUTPMT=pfs -NORM-ext -MINLEN-0 -MAXIEN-1000000 -USER-US08653294
-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0.0232
0.0533
0.0568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0114
0126
0141
0071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0403
0.0464
0.0684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM of: US-08-653-294-32 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                 Query: US-08-653-294-32
Query length: 25
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 7600.090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88888
                                        Æ
                                                                                                                                                                                                                                                                                                                                                    Search information block:
                                      6:23
                                                                                                                              Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est23:A1124815
gb_est10:AA151891
gb_est10:AA151891
gb_est211:A1696864
gb_est31:A1696864
gb_est6:DA1541
gb_est10:AA147151
gb_est10:AA147151
gb_est10:AA121088
gb_est2:AA121088
gb_est1:T52124
gb_est11:T52134
gb_est12:AA310808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_estl3:AA352960
gb_estl:T10924
gb_estl3:AI826037
gb_estl7:AA663896
gb_est20:AA879637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9b_est9:AA100848

9b_est13:AA364489

9b_est13:AA449607

9b_est10:AA449607

9b_est10:AA151951

9b_est10:AA151951

9b_est13:AA381090

9b_est7:W52004

9b_est7:W52004

9b_est10:AA127128

9b_est10:AA127128

9b_est13:AA381090

9b_est13:AA381090

9b_est13:AA381090
                                      Date: Feb 8, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est38:AL036690
gb_est6:D8221
gb_est6:D82189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est2:F13067
gb_est27:A1466429
gb_est8:C03945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est11:AA263135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est10:AA160317
gb_est7:W40489
```

```
Email: jtakeda@sb.gunma-u.ac.jp
                                                                                                                                                                                                                                                                                                   100.00
4.348
92.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est23:A1124815
                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-32 x D82189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg_documentation_block:
                                                                                                                                                                                                                                                                                                                       Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           uman.
                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Human pancreatic islet"
/clone_lib="Human pancreatic islet"
/clone_vector: Lambda ZAPII: Site_1: Eco RI; Site_2: Xho
I: mRNA was prepared from normal adult human islets. CDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. CDNA was size fractionated to remove
sequences <1000 bp in size."
3 others
                                                                                                                                                               Human pancreatic islet ESTs
Unpublished (1995)
Unpublished (1995)
Unpublished (1995)
Con Apr 14, 1993 this sequence version replaced g1:785255.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8896
Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pancreatic islet ESTs
Upupblished (1995)
On Apr 14, 1993 this sequence version replaced g1:785206.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIGH-BY SEAT 09-FEB-1996 HUMHBG4524 Human pancreatic islet Homo sapiens cDNA similar to B42189 HIGH-BY SEAT 09-FEB-1996 HIGH-BY SEAT 09-FEB-1996 HIGH-BY SEAT 1183562
                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 375)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo Saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 415)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 25
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                     Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
1, .375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 GAACCTGCGGATCGCGCTCCGNTAC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                   GI:1183739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106.00
4.417
96.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: D82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-32 x D82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est6:D82189
D82221
D82221.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                 AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                 VERSION
KEYWORDS
                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                          FEATURES
```

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="Vector: Lambda ZAPIT; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."

134 c 133 g 61 t 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E I bases to the fundate; Craniata; Vertebrata; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.
Eutherla; Primates; Catarrhini; Hominidae; Homo.
E I (bases 1 to 414)
S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Rucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., While,T., Walle,T., Walle,T., Walle,T., Walle,T., Walle,T., Walle,T., Walle,T., Walle,T., Contact: Wilson RK Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -4,00n3 fwd. Er from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AII24815 414 bp mRNA EST 11-SEP-1998 am56e06.x1 Johnston frontal cortex Homo sapiens cDNA clone IMAGE:1539586 3' similar to 90:M24038_cds1 HLA CLASS I HISTOCOMPATIBILITY AMTIGEN, BW-44(B-12) B*4402 (HUMAN); contains MER22.t3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ltMAGE:1539586"
/clone_lib="Johnston frontal cortex"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled frontal lobe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;;
Location/Qualiflers
1. .415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 GAACCIGNGGAICGCGCICCGNIAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: D82189 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI124815.1 GI:3593329
```

```
Homo saplens
                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                             57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human .
                                                                                                                                                                                                                                                                                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
              /lab_host="SOLR (kanamycin resistant)"
/note="Organ: brain; Vector: Bluescript SK-; Site_1:
Ecor; Stanley Neuropathology Consortium
(www.stanleylab.org) brains S-58, S-65, S-78.
Random + oligo-dT primed into EcorI site of ZAP II Vector.
Random + oligo-dT primed into EcorI site of IAP II Vector.
Pass excised. Avg insert length 1.9kb. Custom library
provided by Dr. Nancy Johnston [(410) 614-3918,
nlj@welchlink.welch.jhu.eddi).

140 c 136 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Butkaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 255)
Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Hillier,L., Lennon,G., Becker,M., LacyM., Le,M., Le,M., Hawkins,M., Hultman,M., Kucaba,T., LacyM., Le,M., Le,N.,
Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rikin,L.,
Rohlfing,T., Schellenberg,R., Soares,M.B., Tan,F., Thierry-Meg,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS
LOCUS
AA151891
LOCUS
DEFINITION ZOOIGHO.IL Stratagene colon (#937204) Homo sapiens CDNA clone
IMAGE:566435 5' similar to gb.H15497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 8, 1995 this sequence version replaced gi:800234
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 TGGGACCGGGAGACACAGATCTCCAAGACCAACACACAGACTTACCGAGA 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TrpAspargGluThrGlnIleCysLysalaLysalaGlnThraspArgGl 17
                                                                                                                                                                                                                                                                                                                      Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="GDB:4590888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 GAACCIGCGCACCGCGCTCCGCTAC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 uAsnLeuArgIleAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
AA151891
AA151891.1 GI:1720754
                                                                                                                                                                                                                                                                                                                                          Ratio: 4.364
Percent Similarity: 88.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AI124815
                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-653-294-32 x AI124815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est10:AA151891
                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                        80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                        COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                        BASE CO
```

```
seq_documentation_block:
LOCUS AA263158 283 bp mRNA EST 02-JUL-1998
DEFINITION PMY0534 KG1-a Lambda Zap Express CDNA library Homo sapiens CDNA 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutherla, Primates, Catarrhini, Hominidae, Homo.

Eutherla, Primates, Catarrhini, Hominidae, Homo.

I (bases 1 to 283)

Claudio,J.O., Liew,C.C., Dempsey,A.A., Cukerman,E., Stewart,A.K., Na,E., Atkins,H.I., Iscove,N.N. and Hawley,R.G.

Identification of sequence-tagged transcripts differentially expressed within the human hematopoietic hierarchy Genomics 50 (1), 44-52 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="kG1-a Lambda 2ap Express cDNA library"
/cell_type="promyeloblast"
/cell_line="kG1-a"
/note="Wetcor: Lambda 2ap Express (Stratagene); Site_l:
EcoRI: Site_2: XhoI; Unidirectional choning sites:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Tel: 416 3403834
Fax: 416 3403834
Samil: r.hawley@utoronto.ca
Similar to M58636 MHC class I HLA-Bw gene. Clone was randomly
plicked from KGla primary library.
Seq primer: 5, CaAATTAACCTCACTAAAAGGG 3'
High quality sequence stop: 283.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On May 5, 1995 this sequence version replaced gi:797810.
Contact: Hawley RG
Oncology Research Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82 GAACCTGCGGATCGCNCTCCGCTAC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 uAsnLeuArgileAlaLeuArgTyr 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MRNA sequence.
AA263158
AA263158.1 GI:1898964
                                                                                                                                                                                                                                                                                                                                                      95.00
4.524
84.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AA151891
                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-32 x AA151891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est11:AA263158
```

```
alignment_block:
US-08-653-294-32 x AI359260/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   227 c
                                                                                                                                                                                                                                               4.524
                                                                                                                                                                                                                            95.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est31:AI696864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 a
                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                            Quality:
                                                                                                                            128
                                                                                                                                                                                                                                                  Ratio
                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
EcoR1-Xhol. mRNA was purified from KG1-a cell line, cDNA was synthesized using an Xhol-OligodT linker primer. EcoR1 adaptors were ligated, followed by digestion with Xhol for directional cloning into predigested Lambda Zap Express" 91 c 88 g 9 t0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing By: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLML at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 618)

NCI/NINDS-CSAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CSAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                          1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
/clone="taxon:9606"
/clone=lib="NCI_CGAP_Brn23"
/tissue_type="q1ioblastoma (pooled)"
/lab_host="DH108"
                                                                                                                                                                                Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ww-bio.ilní.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Insert Length: 691 Std Error: 0.00 Seg primer: -40UP from Gibco High quality sequence stop: 458. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             to: 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .618
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 GAACCTGCGGATCGCGCTCCGCTAC 149
                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 uAsnLeuArgileAlaLeuArgTyr 25
                                                                                                                                                                                  95.00
4.130
92.000
                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AA263158
                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-32 x AA263158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est26:AI359260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                     Quality:
                                                                                  64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
DEFINITION
                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bass 1 to 7/48)

1 (bass 1 to 7/48)

1 (Northeria; Primates; Catarrhini; Hominidae; Homo.

1 (CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

1 Mational Cancer Institute, Cancer Genome Anatomy Project (CGAP),

1 Tumor Gene Index

1 (1998 this sequence version replaced g1:2961758.

1 On Mar 16, 1998 this sequence version replaced g1:2961758.

1 Contact: Robert Strausbergenih.gov

1 Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

1 Life Technologies catalog #: 11548-013

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.72 kb. Life Technologies catalog #: 11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    è
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS A1696864 748 bp mRNA EST 03-JUN-1999
DEFINITION WC14111.X1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2324421
Similar to gb:M28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-51(B-5) B*5101 ALPHA (HUMAN);, mRNA sequence.
VERSION A1696864 GI:4984764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 TGGGACGAGGACAGGGAAAGTGAAGGCCCACTCACAGACTGACCGAGA 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl
                                                                                                                                                                                                                                                                                                  Length: 25
Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="IMAGE:32441"
/clone=lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -400c 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to reverse of: AI359260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314 GAACCIGGGATCGCGCTCCGCTAC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17 uAsnLeuArgIleAlaLeuArgTyr 25
```

```
/organism="Homo sapiens"
/db_xref="GDB:462329"
/db_xref="GDB:462329"
/db_xref="Izaxon:9606"
/clone="Ixaxon:9606"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.
Eutheria; Primates; Catarrhini; Hominidae; Homo.
E 1 (bases 1 to 495)
S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., While,Y., Wayle,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
L Unpublished (1997)
Con Sep 12, 1996 this sequence version replaced gi:1395000.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314, 286 1810
                                                                                                                                                                seq_documentation_block:

LOCUS AAL58109 495 bp mRNA EST 09-MAR-1998
DEFINITION 2057h10.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone
IMAGE:591043 3' similar to gb:U04245 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, B-7 B+0702 ALPHA (HUMAN);, mRNA sequence.

ACCESSION AA158109
VERSION AA158109.1 GI:1732894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Insert Length: 1581 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality: sequence stop: 43.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 20
Gaps: 0
Percent Identity: 85.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AA158109 from: 1 to: 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 g
311 GAACCTGCGGATCGCGCTC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91.00
4.789
95.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-32 x AA158109
                                                                                            seq_name: gb_est10:AA158109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274 GGGCCTGCGG 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 uAsnLeuArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dclone_lib="Human pancreatic islet"
/note="vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."

49 t 4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human pancreatic islet ESTs
Unpublished (1995)
Unpublished (1995)
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785191.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D82177 330 bp mRNA EST 09-FEB-1996
HUMHBC4504 Human pancreatic islet Homo sapiens cDNA similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 330)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TrpAspargGluThrGlnIleCysLysalaLysalaGlnThraspargGl 17
                                                                                                                                                                                                                                                                                                                                                                                                          1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                Gaps: 0
Percent Identity: 76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 78.261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                       to: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: jtakedaesb.gunma-u.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: D82177 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B, mRNA sequence.
D82177
D82177.1 GI:1183645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 uAsnLeuArgileAlaLeu 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.00
4.273
95.652
                                                                                            95.00
4.130
92.000
                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AI696864
                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-32 x AI696864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-32 x D82177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est6:D82177
                                                                                                                                   Ratio:
                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uman.
                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
```

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT REFERENCE AUTHORS

FEATURES

6 others

Align seg 1/1

BASE COUNT ORIGIN

12-APR-1995

seq\_name: gb\_est10:AA147151

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE COMMENT

```
Wilson, R.
The WashUr Marck EST Project
In Unpublished (1995)
Contact: Wilson RK
WashIngton University School of Medicine
WashIngton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 1875
High quality sequence stops: 384 Source: IMAGE Consortium, LINL
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1875 Std Error: 0.00
Seq primer: MIJRP1
High quality sequence stop: 384.
                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 459)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hulman,M., Kucaba,T., Leh,M., Lemnon,G., Marra,M.
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                     R13904 459 bp mRNA EST 12-APR-199
YAG2003.r1 Soares infant brain INIB Homo sapiens DNA clone
YMAGE:26601 5' similar to gb:M64742_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) A*2301 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="GDB:399148"
/db_xref="taxon:9606"
/clone="IMAGE:26801"
/clone_lib="Goares infant brain INIB"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: R13904 from: 1
                                                                                                                           R13904
R13904.1 GI:766980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-32 x R13904
seg_documentation_block:
LOCUS R13904
DEFINITION yf62c03.rl So
                                                                                                                                                                                                               Homo saptens
                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                        2032006.rl Stratagene colon (#937204) Homo sapiens CDNA clone
IMAGE:588587 5' similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, A-24(A-9) A*2402 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 581)

Hillar, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Markins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Scholshoberg, K., Soares, M.B., Teange, C., Rikin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Teange, C., Rikin, L., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                               Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 272.
                                             05-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Sep 12, 1996 this sequence version replaced gi:1393699.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0 Gaps: 0 Percent Identity: 72.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .581
/organism="Homo sapiens"
/db_xref="GDB:4620899"
/db_xref="taxon:9606"
/clone="IMAGE:588587"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1 to: 581
                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA147151.1 GI:1716526
                                           581 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            162 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AA147151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-32 x AA147151
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                      and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                               AA147151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
```

source

FEATURES

COUNT

BASE CC

24

17 uAsnLeuArgIleAlaLeuArg

seq\_name: gb\_est2:R13904

```
/db_xref="GDB:4623179"
/db_xref="GDB:4623179"
/db_xref="GDB:4623179"
/db_xref="Ixaxon:9606"
/clone="Ixaxon:9606"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:

LOCUS AA143626 338 bp mRNA EST 08-NOV-1997

DEFINITION 2065h01.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:591793 5' similar to gb:U04245 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN. B-7 B*0702 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

L (bases 1 to 338)

Hillder, L. Allen, M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Tanite, Y., Wolte, T., Wolfelenberg, K., Steptoe, M., Tan, F., WashU-NCI human EST Y., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
On Nov. 29, 1993 this sequence version replaced gi:634605.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feat: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 31 282 182
Fax: 31 282

     AA143626.1 GI:1713058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 84.00
Ratio: 5.250
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-32 x AA143626
                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est10:AA143626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                               286 GGCCTGCGG 295
                                                                                                                                                               17 uAsnLeuArg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="GDB:3917806"
/db_xref="GDB:3917806"
/db_xref="GDB:3917806"
/db_xref="Inaxon:9606"
/dlone="Inaxon:9606"
/clone="Inaxon:9606"
/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Figure 1: estewatson wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone tontains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin; Hominidae; Homo.

(Dases 1 to 41)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Rucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moore,B., Moorris,M., Parsons,J., Prange,C., Rithn,L.,
Rohling,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 18, 1995 this sequence version replaced gi:811358.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 20
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AA121088 from: 1
291 GAACCTGCGGATCGCGCTCCGC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA121088
AA121088.1 GI:1678632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               133 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-653-294-32 x AA121088
                                                                                                                                                               seq_name: gb_est9:AA121088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

```
from: 1
Align seg 1/1 to: AA143626
                                                        seq_name: gb_est1:T52124
```

1 TrpAspArgGluThrGlnIleCysLysAlaLysAlaGlnThrAspArgGl 17

Length: 16 Gaps: 0 Percent Identity: 93.750

```
T52124 06-FEB-1995

YD299G6.rl Stratagene fetal spleen (#937205) Homo saplens cDNA

Clone IMAGE:72634 5' similar to similar to qb:M24032_cds1 HLA CLASS

I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 (HUMAN), MRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High qality sequence stops: 330 Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: MI3RP1
High quality sequence stop: 330.
Location/Qualifiers
                                                                                                                                                                                                                                             Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;

Butharia; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 367)

1 (hases 1 to 367)

1 (hases 1 to 367)

Chissoe, J. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, M., DuBuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Randis, E., Moore, B., Moris, M., Parsons, J., Prange, C., Rikin, L.,

Rohlifing, T., Schellenberg, K., Soares, M.B., Tan, F., Thlerry Weg, J.,

Treyaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
/clone="IMAGE:72634"
/clone_lib="Stratagene fetal spleen (#937205)"
/tissue_type="fetal spleen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81.00 Length: 20
4.263 Gaps: 0
95.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. 367
/organism="Homo sapiens"
/db_xref="GDB:494299"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 48
                                                                                                                                                 T52124
T52124.1 GI:653984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-32 x T52124
seq_documentation_block:
LOCUS T52124
DEFINITION Yb29906.rl S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

17 uAsnLeuArg 20 |:::|||||| 286 GAGCCTGCGG 295

Align seg 1/1 to: T52124 from: 1 to: 367

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model Run on:

February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 2.660 Million cell updates/sec

US-08-653-294-33 74

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 KAQTDRENLRIALRY 15 Scoring table:

188963 segs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	CTL mod	N	. H	HLA-B2702 CTL modu	-:	B2702.6	Human HLA-B27-(62-	Peptide fragment o	HLA-B2702 CTL modu	HLA-B2705.60-84. C	Sequence of the hu	ö	Peptide fragment o	HLAB38 CTL modulat	HLAB38.6084. Comps	Peptide Seg ID No:	Sequence of HLA-Bw	e of HLA	Bw53	CTL modulating pep	HLA B27 hypervaria	[Phe74]	Human HLA-B27 alph	Peptide fragment o	CIL mo	-helix	T-cell modulating	Immunomodulatory p	Peptide B2702.75-8	HLA-B2702 CTL modu	HLA-B2702 CTL modu	4-75-8	Immunomodulating d	.84
SUMMARIES		Ð		W33795	R41205	R83090	R95416	W33794	R71442	R41221	R83091	R95417	P70590	P70155	R48286	R83093	R95422	X06801	R03142	R03144	R12463	R83071	R50266	R71443	W58992	R41208		R95413			W33784	O.	U١	R95428		
		Length DB	Z.	S	S.	'n	Z.	'n	7	'n	S	S	7	62	Z.	2	Z,	84	62	~	62	9	9	۲.	_	0	0	0	0	0	0	0	0	20 1	0	0
	Query	Match L	8	100.0	8	8	8	8	79.7	7.67	79.7	79.7	7.67	79.7	75.7	75.7	75.7	75.7	75.7	75.7	75.7	71.6	70.3	9.79	9. 79	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2	66.2
		Score	74	74	74	74	74	74	59	59	59	29	59	29	26	56	26	26	56	26	26	53	52	20	20	49	49	49	49	49	49	49	49	49	49	49
	Result	NO.	1	7	e	4	Ŋ	Q	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34

HLA-B7.60-84. Comp HLA-B2702 CTL modu	HLA-B2702 CTL modu HLA-B2702 CTL modu HLA-B2702,75-84(D)	HLA-B2702.75-84(T) T-cell modulating Immunomodulatory p	Immunomodulatory p Peptide B2702.75-8 Peptide B2702.75-8
R95431 R83094	R83095 R83096 R95425	R95426 W07513 W47267	W47269 W33788 W33787
44		ннн	
25	222	222	1000
æ.ι.	เกเก	היהיה	សសល
		5000	
4 4 4 4 5	4 4 4 4 4	4 4 4 4 4 4	<b>7 7 7</b>
35 36	38	4 4 4 4 2 1 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	4 4 4 5 4 4 3

|--|

Query Match 100.0%; Score 74; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 2e-07; Matches 15; Conservative 0; Mismatches 0; Indels

ô

Gaps

ö

1 KAQTDRENLRIALRY 15 ò

1 KAQTDRENLRIALRY 15 g

~

W33795 standard; peptide; 15 AA.

W33795;
19-JUN-1998 (first entry)
19-JUN-1998 (first entry)
Peptide B2702.70-84 tested for immunomodulating activity.
Immunomodulating dimer: Immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; 

rejection. Synthetic. Homo sapiens. W09744351-A1. 27-NOV-1997.

R83090 standard; peptide; 25 AA.

RESULT

g

12

1 KAQTDRENLRIALRY 11 KAQTDRENLRIALRY

ö

16-MAY-1996 (first entry)

```
WALLY, $48.0802304048.

New immunomodulating dimer peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

For treating autoimmune diseases.

Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity, A peptide-type compound or variant is claimed which has a minomodulating activity, including the N-terminal acylated and/or creminal anidated or esterified forms of up to 60 amino acids, where to the peptide-type compound comprises the formula: A-B, where A, B = creminal anidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = creminal amino acid; aa80 = R or G; aa80 = I or N; aa81, aa81 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions or 19-84). They can be used to inhibit cytotoxat. T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They are also inhibit the proliferation of T cells in a combination and interest can also be used for taetection and diagnosis. The products can also be used for detection and diagnosis. The products can also be sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mew populate(s) based on class I HLA antigen domains - used for modulating cytocoxic T-lymphocyte activity towards targets T-lamphocyte activity towards targets Tolaim 8; Page 53; 61pp; English.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, and thinbition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia; parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 74; DB 1; Length 15; 100.0%; Pred. No. 2e-07; ive 0; Mismatches 0; Indels
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C. Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1993.
25-FEB-1993: U01758.
02-MRR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
(STAD) STANFORD JUNIOR.
(STAD) 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R41205 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 15; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ᠬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R41205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 13; Page 32; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-R2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIA-B2702.60-84...
HIA-B2702.60-84...
HIA-B2702.60-84...
HIA-B2702.60-84...
HIA-B2702.60-84...
HIA-B 74...
HIA-B 7
                                                                                                                 HIA-B2702 CTL modulating peptide (B2702.60-84).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HIA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clayberger C, Krensky AM;
WPI; 95-194027/25.
Compsns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.
Example: Page 9; 29pp; English.
R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                     clayberger C. Krensky AM, Parham P;
WPI; 95-358862446.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represent palindromes and fragments of antigens. This sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 74; DB 1; L
100.0%; Pred. No. 3.6e-07;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human-leucocyte-associated antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                       12-CT-1995.
05-APR-1995.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R95416 standard; peptide; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 KAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    patient
                                                                                                                                                                                                                                                                                                                                    12-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R95416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
RESULT
R95416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

ö

Gaps

ö

Length 25; Indels

100.0%; Score 74; DB 1; I 100.0%; Pred. No. 3.6e-07; ative 0; Mismatches 0;

Query Match 100. Best Local Similarity 100. Matches 15; Conservative

```
from a T-cell lysather of the state of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound Hi-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with this sequence, induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate composition containing the amount of antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74. Modulation of certacellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PER PERION K, Liapperger C, Michary AM;
WHI: 98-086530708

New immunomodulating dimer peptide(s) - based on a Class I HLA-B
alpha-1 domain, used for preventing rejection of transplants or
reating autoimmune diseases

Example 1; Page 19; 41pp; English.

PER CALIVITY A Peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or
C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, Sor N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or
Small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise at any peptide type bond within the brackets. The compounds comprise or at any peptide type bond within the brackets. The compounds comprise or any peptide type bond within the brackets or a class I HLA-B alphal domain (Positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CDS. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes,

C used for detection and diagnosis. The products can also be used for detection and subanes of subanes and subanes or any expensive the mand of the detection and diagnosis. The products can also be used for detection and subanes are also inhibit the products can also be used for detection and diagnosis. The products can also be used for detection and diagnosis. The products can also be used for detection and diagnosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
  These sequences can be used to isolate the protein p74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1998 (first entry)

Peptide B2702.60-84 tested for immunomodulating activity.

Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 74; DB 1; I 100.0%; Pred. No. 3.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STR ) UNIY LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W33794 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-B2702.60-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W33794
qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New poptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets Example 13; Page 39; 61pp; English.

The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 45; 103pp; English.

R71439-R71443 are human major histocompatibility complex class 1
R71439-R71443 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.

They were used to modulate interactions between MHC 1/HLA and cell
surface receptors. Via competitive inhibition the peptides diminish
the receptors response, this feature may be useful for the treatment
of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                              12-0cT-1995 (first entry)
Human HLA-B27-(62-85) antigen derived peptide.
Human HLA-B27-(62-85) antigen derived peptide; cell receptor;
Interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-WAR-1994 (first entry)
Peptide fragment of HLA-B2705 antigen.
Human leukocyte antigen; HLA: peptide: transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                      ô
                                                                                                                                                                                                                                                                                                                                                                                                           Goldstein A, Goodenow RS, Olsson L;
WPI; 95-089577/13.
Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 59; DB 1; Length 17;
Pred. No. 0.00012;
1; Mismatches 2; Indels
                                    Indels
100.0%; Score 74; DB 1; 1
100.0%; Pred. No. 3.6e-07;
                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-1993. 001758. 25-FEB-1993. 001758. (SZ-MAR-1992; US-844716. (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R41221 standard; peptide; 25 AA.
R41221;
                                  0;
                                                                                                                                                                                                 ¥.
                                                                                                                                                                                             R71442 standard; peptide; 17
R71442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clayberger CA, Krensky AM; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 12; Conservative
                                    Conservative
                                                                                                                                                                                                                                                                                                                                                      12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KAQTDREDLRILLRY 16
                                                                       1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KAQTDRENLRIALRY 15
                                                                                                      11 KAQTDRENLRIALRY 25
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 AA;
                                                                                                                                                                                                                                                                                                        Homo sapiens.
WO9505189-A.
                                                                                                                                                                                                                                                                                                                                           23-FEB-1995.
 Query Match
Best Local Simi
Matches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                              7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                                              RESULT
R71442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R41221
                                                                                                                                                                                                 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
```

which may

```
Compsons, comprising lymphoid surface membrane proteins - which mainhibit cytolytic activity and differentiation of CTLs. Example; Page 9; 29pp; English. R95413, and R95415-R95431 represent palindromes and fragments of
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
P70590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 13; Page 32; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to fare the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-B2702 CTL modulating peptide (B2702.60-84).
Cytotoxic I lymphocyte, CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                 This peptide is derived from the HLA-B2705 antigen and corresponds to the amino acid positions 60 \cdot 84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC unmatched
the recipient
                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                          Score 59; DB 1; Length 25; Pred. No. 0.00019; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 59; DB 1; Length 25;
Pred. No. 0.00019;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from
donor hosts - using Class I B75-84 MHC antigen of
                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MONSACTORY
12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R95417 standard; peptide; 25 AA. R95417;
                                                                                                                                                                                                                                                                                                                                                             R83091 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.7%;
80.0%;
                                                                                                                            79.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                       16-MAY-1996 (first entry)
                                                                                                          Ouery Match
Best Local Similarity 80.07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                            1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                       11 KAQTDREDLRTLLRY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the patient
Sequence 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
WO9513288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                   R83091;
                                                                                                                                                                                                                                                                                                                   RESULT
R83091
                    ខ្លួខ្លួ
                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                     NAME OF THE PART O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
```

```
The sequence and the sequence and transments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the HLA-B2705.60-84. These sequences can be used to isolate the protein of from a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on a panited number of cell types, but is particularly expressed on amphoteric detergent, and then passed through an affinity column amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic cativity of CT-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete containing the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Such DNA, antigen or antibody
Disclosure: Page 5: 5pp; German.
The DNA may be used as a hybridisation probe for detecting the HLA
B27 gene, eg for assessing susceptibility to rheumatic disorders
such as ankylosis spondylitis, or may be used to transform cells
for prodn. of HLA B27. The HLA B27 may be used to detect HLA B27
antibody in human serum, or to produce mono- or polyclonal HLA B27
sequence 337 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA coding for antigen HLA B27 - and diagnostic reagents contg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59; DB 1; Length 337;
Pred. No. 0.0033;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of the human histocompatibility antigen HLA B27. Rheumatic disorder; genetic screening; diagnosis; markylosing spondylitis. Homo sapiens.

DE3542024-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79.7%; Score 59; DB 1; Length 25; 80.0%; Pred. No. 0.00019; tve 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-542576.
(BEHW ) BEHRINGWERKE AG.
Rethmuller G, Meo T, Weiss E, Szots H; WPI; 87-157893/23.
N-PSDB; N70935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P70590 standard; protein; 337 AA.
P70590;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.7%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 79.7
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KAQTDRENLRIALRY 15
```

a

```
Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
                                                                  ;
0
                                                                                                                                                                                                                                                                                                                                     R83093 standard; peptide; 25
R83093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R95422 standard; peptide; 25
R95422;
      75.7%;
92.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1996 (first entry)
HLAB38.6084.
                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                 15
                                                                                                                                                                                             25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity
      Ouery Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                 3 QTDRENLRIALRY
                                                                                                                                                                         Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                         SOULT SEED STATE S
                                                                                                                                                                                             ద
                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N PSDB; N70225.

DNA coding for human histocompatibility antigen HLA-B 27 - useful for diagnosis and antigen and antibody prodn.

Disclosure; p6; 13pp; German.

THe DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, eg for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mew peptide(s) based on Class I HIA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets
Example 13; Page 39; 61pp; English.
The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
The peptide is used to modulate cytotoxic T-lymphocyte (CTL)
Inhibiting CTL toxicity in transplantations, for inducing CTL
activity in parasitic diseases and neoplasia and in studies on viral
infection. The peptide can also be used for identifying CTLs which
bind to it and removing subsets of CTLs from a T-cell composition.
This peptide is derived from the HLA-B38 antigen and corresponds
Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human leukočyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                         03-APR-1991 (first entry)
Sequence encoded by genomic DNA encoding human histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 59; DB 1; Length 362;
Pred. No. 0.0036;
.; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Szots H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller G; WPI; 87-171469/25.
                                                                                                                                                                                                                                                                                                                                                     antigen HLA-B 27.
Ankylosing spondylitis; rheumatic disorder; diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-SEP-1993. U01758. 02-MRR-1992; UN1758. (STRD) UNIV LELAND STANFORD JUNIOR. CLAYDBEGER CA, Krensky AM; WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-MAR-1994 (first entry)
Peptide fragment of HLA-B38 antigen.
                                                                                                                                                                                             P70155 standard; protein; 362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R48286 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 79.7
Best Local Similarity 80.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-NOV-1986; 116139,
01-JAN-1985; DE-542024,
21-DEC-1985; DE-545576,
(BEHW ) BEHRINGWERKE AG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KAQTDRENLRIALRY 15
                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 KAQTDREDLRILLRY
70 KAQTDREDERTEERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP-226069-A.
24-JUN-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9317699-A.
                                                                                                                                                                                                                                                        10-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                              RESULT 12
```

g

ŏ

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; Page 32; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HLAB38. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLAB38 CTL modulating peptide (B38.6084).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLAB38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
Synthetic.
W09513288-A1.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1995.
10.NOV-1994; U12985.
10.NOV-1993; US-150493.
10.NOV-1993; US-150493.
(STRD ) UNIV LELAND STARFORD JUNIOR.
Clayberger C, Krensky AM;
WPI: 95-194027/25.
Compens. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.
Example; Page 9; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-1995.

05-APR-1995; U04349.

05-APR-1994; US-222851.

(STRD ) UNIV LELAND STANFORD JUNIOR.

WPI: 95-35882/46.

Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
Length 25;
                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
Score 56; DB 1; 1 Pred. No. 0.00065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75.7%; Score 56; DB 1; I 92.3%; Pred. No. 0.00065; tive 0; Mismatches 1;
                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
R95422
AC R95422
DT R95422
DT 12-NOV
DE HLAB18
KW T-cell
KW B cell
KW B Cell
KW G Synthe
PD 18-MAY
PF 10-NOV
PR 10-NOV
PR (2TRD
PA (2TRD
```

```
human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the HIAB18.6084. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the hear shock protein H870.0 p74 is found in a cross lamited number of cell types, but is particularly expressed on B and T cells. p74 can be isolated by lysis of a suitable cell with an amplication comprising then passed through an affinity column compositions comprising then passed through an affinity column compositions comprising the extracellular fragment of p74 combined with HIA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the with p74 for the binding of the p74 in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                 888888888888888888888888888
```

Gaps ö Ouery Match 75.7%; Score 56; DB 1; Length 25; Best Local Similarity 92.3%; Pred. No. 0.00065; Matches 12; Conservative 0; Mismatches 1; Indels

3 QTDRENLRIALRY .15 || ||||||||||| 13 QTYRENLRIALRY 25 ò g

Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

	igen Ltd.
4.5	Compr
	- 2000
enCore	) 1993
Ger	ŝ
	Copyright

sw model	February 7, 2000, 18:04:41; Search time 111.22 Seconds (without alignments) 6.362 Million cell updates/sec
guisn	2000,
ż	7,
OM protein - protein search, using sw model	February
OM protein	Run on:

1 KAQTDRENLRIALRY 15 US-08-653-294-33 74 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 segs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_62:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SUMMAKIES	
Result		Query			٠	
No.	Score	Match	Length	BB :	OF CE	Description
Н	70		354	Ŋ	593	class I histocompa
7	70	4.	354	~	180167	class I histocompa
m	70	94.6	362	~	JH0541	class I histocompa
4	70	₹.	362	~	JH0539	н
Ŋ	70	4.	362	7	JH0540	class I histocompa
φ	69	93.2	355	~	180169	H
7	69	93.2	355	~	180171	class I histocompa
80	69	93.2	363	7	807113	class I histocompa
o,	69	93.2	363	~	S03537	class I histocompa
10	99	89.2	359	Н	HLHU12	MHC class I histoc
11	99	89.5	365	~	S77963	MHC class I histoc
12	99	89.2	365	~	154416	HLA-AW24 protein -
13	99	89.2	365	~	I54493	MHC class I histoc
14	61	82.4	274	щ	нгниз2	н
15	61	82.4	364	~	A35997	н
16	9	81.1	137	~	180174	class I histocompa
17	9	81.1	354	7	180168	class I histocompa
. 18	9	81.1	362	П	HLHUB8	MHC class I histoc
19	9	81.1	362	~	162045	gene HLA B-1517 pr
20	9	81.1	362	~	I84490	te te
21	9	ä	362	~	137521	
22	9	81.1	364	~	D35997	B
23	29	79.7	338	~	156116	MHC HLA-B27-HS - h
24	59	79.7	362	н	HLHUB2	MHC class I histoc
25	59	79.7	362	~	137485	human lymphocyte a
56	59	79.7	362	~	137515	MHC class I histoc
27	29	79.7	362	7	I54289	MHC HLA-B27d - hum
28	26	75.7	273	~	385	clas
53	26	75.7	274	7	5446	MHC HLA-B38 chain
30	26	75.7	362	7	B30345	MHC class I histoc

362 2 A45834 362 2 184486 362 2 159633 362 2 159633 362 2 137120 318 2 137120 318 2 137516 362 2 161865 362 2 A4585 362 2 154442 365 2 154442 365 2 154442 365 2 1141	MHC class I histoc transmembrane glyc	MHC Class I histoc MHC HLA-B transmem class I histocompa	MHC class I histoc	HLA-B alpha-chaln class I histocompa MHC class I histoc	MHC HLA-B44.2 chai MHC class I histoc class I histocompa	MHC class I heavy class I histocompa
77225555555555555555555555555555555555	A45834 184486	A30345 I59633 S24434	137120	137516 S25415 A45850	161861 154442 JH0537	167482 S11141
	222	7 7 7 7 8 7 8 7 8 9 8 9 8 9 8 9 8 9 8 9	18 5	555 625 626	2 2 2 2 2 2 2 2 2 3	57 2
	75.7	75.7	75.7	2000 2000 2000	6.89 6.89 6.69	62.2
77777777777777777777777777777777777777	500	200	23.0	21 21 21	51 51 7	4 4 6
0047111113000000	31	2 8 8 2 4 6	36 37	2 6 4 2 0 0	41 43 43	44 45

## ALIGNMENTS

Gaps ö Score 70; DB 2; Length 354; Pred. No. 3.5e-05; 1; Mismatches 0; Indels Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative

ö

1 KAQTDRENLRIALRY 15 ò g

RESULT

Class I histocompatibility antigen - pygmy chimpanzee (fragment)
Class I histocompatibility antigen - pygmy chimpanzee, bonobo)
Class 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 23-Jul-1999
Classion: 180167
R.McAdam, S. N.; Boyson, J. E.; Julu, X.; Garber, T. L.; Hughes, A.L.; Bontrop, R.E.; Wat R.McAdam, S. N.; Boyson, J. E.; Julu, X.; Garber, T. L.; Hughes, A.L.; Bontrop, R.E.; Wat A. Title: A uniquely high level of recombination at the HLA-B locus.
A.Reference number: 159308; MUID:94286544
A.Accession: 180167
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRMA
A.Residues: 1-354
A.Residues: 1-354
A.Residues: 1-354
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology

94.6%; Score 70; DB 2; Length 354; 93.3%; Pred. No. 3.5e-05; ive 1; Mismatches 0; Indels Query Match 94.6 Best Local Similarity 93.3 Matches 14; Conservative 1 KAQTDRENLRIALRY 15 ŏ

a

ö

Gaps

ö

154

gorilla

```
C;Accession: JH0540
R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to huma A;Reference number: JH0534; MUID:92078860
A;Accession: JH0540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               class I histocompatibility antigen - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 23-Jul-1999
C;Accession: 18017!
R;McAdam, S.N.; Boyson, J.E.; Liu, X.; Garber, T.L.; Hughes, A.L.; Bontrop, R.E.; Wat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.L.; Bontrop, R.E.; Wat
                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
A;Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Reywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0102 #status
F;25-114/Domain: alpha-1 <ALL>
                        class I histocompatibility antigen Gogo-B0102 heavy chain precursor - lowland C;Species: Gorilla gorilla gorilla (lowland gorilla)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: U05580; NID: 9454777; PIDN: AAA50183.1; PID: 9454778
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:X60693; NID:922867; PIDN:CAA43101.1; PID:922868
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;299-362/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 69; DB 2; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 70; DB 2; Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-355 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; 5
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.6%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;115-206/Domain: alpha-2 <AL2>
F;207-298/Domain: alpha-3 <AL3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 QAQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                          A; Residues: 1-362 < LAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 14;
                                                                                                                                                                                                                                                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics:
Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
Superfamily: class I histocompatibility antigen; immunoglobulin homology
Reywords: transmembrane protein
1-24/Domain: signal sequence #status predicted <SIG>
25-362/Product: class I histocompatibility antigen heavy chain, Gogo-B0101 #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pre
                                                      C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C; Accession: Julo341
B; Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A; Title: Gorilla class I major histocompatibility complex alleles: comparison to human 8 A; Reference number: JH0534; MUID: 92078860
A; Accession: JH0541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491–1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human
A;Reference number: JH0534; MUID:92078860
class I histocompatibility antigen Gogo-B0103 heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla gorilla (lowland gorilla) C;Date: 30-Jun-1992 *sequence_revision 30-Jun-1992 *text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      class I histocompatibility antigen Gogo-BO101 heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla gorilla (lowland gorilla) C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                            Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
Superfamily: class I histocompatibility antigen; immunoglobulin homology
Keywords: transmembrane protein
1-24/Pomain: signal sequence #status predicted <SIG>
1-24/Pomain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                      A;Molecule type: DNA
X;Residues: 1-362 <LLMA>
A;Cross-references: EMBL:X60254; NID:g22869; PIDN:CAA42806.1; PID:g22870
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-362 <LAW>
A;Cross-references: EMBL:X60255; NID:g22865; PIDN:CAA42807.1; PID:g22866
A;Experimental source: EBV-transformed B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70; DB 2; Length 362;
Pred. No. 3.6e-05;
.; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: transmembrane protein
C; Keywords: transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-362/Product: class I histocompatibility antigen hea
F;25-114/Domain: alpha-1 <ALL>F;15-206/Domain: alpha-3 <ALL>F;207-298/Domain: alpha-3 <ALL>F;207-288/Domain: alpha-3 <ALS>F;207-285/Domain: immunoglobulin homology <IMM>F;299-362/Domain: intracellular #status predicted <INT>F;299-362/Domain: intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-114/Pomain: alpha-1 <ALI>
115-206/Domain: alpha-2 <ALI>
200-208/Domain: alpha-3 <ALI>
2200-208/Domain: almunoglobulin homology <IMM>
2209-362/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 70; DB 2; Le
Pred. No. 3.6e-05;
l; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94.6%;
ilarity 93.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OAQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OAQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: JH0539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S:
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

94

g ó

ö

ö

ö g

```
C; Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C; Date: 05-Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C; Accession: Apr-1983 #sequence_revision 05-Apr-1983 #text_change 22-Jun-1999
C; Accession: Mo2189
R; Mailssen, M.; Mailssen, B.; Jordan, B.R.
Proc. Natl. Acad. Sci. U.S.A. 79, 893-897, 1982
A; Title: Exon/intron organization and complete nucleotide sequence of an HiA gene.
A; Reference number: A02189; MUD: 82151002
A; Rocession: A02189
A; Molecule type: DNA
A; Restdues: 1-359 - AAAL>
A; Accession: A02189
A; Molecule type: DNA
A; Restdues: 1-359 - AAAL>
A; Cross-references: GB:J000191; GB:V00526; NID: 9187600; PIDN:AAA36218.1; PID: 9386873
C; Comment: The seven exons correspond approximately to the domain structure of this c
C; Genetics:
A; Map position: 6p21.3
A; Intros. 221.1127, 204/1; 296/1; 335/1; 346/1
C; Superfanily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterodimer: transmembrane sequence #status predicted <EXT>
F; 12-21/Domain: alpha-1 <EXI>F; 12-239/Pomain: alpha-2 <EXI>F; 21-230/Domain: alpha-2 <EXI>F; 21-230/Domain: alpha-2 <EXI>F; 21-230/Domain: intracellular #status predicted <INN>F; 335-359/Domain: intracellular #status predicted <INN>F; 307/Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 224-280/Disulfide bonds: #status predicted
F; 224-280/Disulfide bonds: #status predicted
                                                                         A. Molecule type: mRNA
A. Residues: 1-363 < MAYS
A. Cross references: EMBL:X13115
C. Superfamily: class I histocompatibility antigen; immunoglobulin homology
C. Reywords: transmembrane protein
C. Reywords: transmembrane #status predicted < SIG>
C. Sel / Domain: extracellular #status predicted < NM>
C. 259 - 285 / Domain: transmembrane #status predicted < NM>
C. 250 - 285 / Domain: intracellular #status predicted < NM>
C. 250 - 285 / Domain: intracellular #status predicted < NM>
C. 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 250 - 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC class I histocompatibility antigen HLA-A alpha chain precursor - human (isolate C; Species: Homo sapiens (man)
A; Variety: isolate A*2402
A; Variety: isolate A*2402
C; Variety: i3-Jan-1995 #sequence_revision 15-Aug-1997 #text_change 23-Jul-1999
C; Accession: S77963
R; Belich, M.P.; Madrigal, J.A.; Hildebrand, W.H.; Zemmour, J.; Williams, R.C.; Luz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHC class I histocompatibility antigen HLA alpha chain precursor (clone pHLA 12.4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.2%; Score 66; DB 1; Length 359;
86.7%; Pred. No. 0.00019;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.2%; Score 69; DB 2; L¢
100.0%; Pred. No. 5.4e-05;
1ve 0; Mismatches 0;
    A; Reference number: S01171; MUID: 89030641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 QAQTERENLRIALRY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 AQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 13; Conserv
                                              A; Accession: S03537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                쉱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Notecule type: mRNA
A; Residues: 1-363 < RES.>
C; Superfamily: class I histocompatibility antigen: immunoglobulin homology
C; Superfamily: class I histocompatibility antigen chain #status predicted
E; Reywords: glycoprotein; membrane protein
F; 1-24 Pomain: signal sequence #status predicted < SIG>
F; 25-363/Product: class I histocompatibility antigen chain #status predicted
F; 25-363/Promain: alpha-1 #status predicted < EXI>
F; 200-285/Domain: alpha-2 #status predicted < EXI>
F; 200-285/Domain: immunoglobulin homology < INM>
F; 307-332/Domain: intracellular #status predicted < INT>
F; 333-363/Domain: intracellular #status predicted < INT>
F; 110-1081 high site: carbobydrate (Asi) (covalant) #status predicted
F; 125-188, 227-283/pisulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 7, 2765-2774, 1988
A;Title: Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-sped
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Class I histocompatibility antigen Ch39 alpha chain precursor - chimpanzee N; Alternate names: MHC ChIA chain C; Species: Pan troglodytes (chimpanzee) C; Dacte: 19-Mar-1997 **Requence_revision 19-Mar-1997 **text_change 23-Jul-1999 C; Accession: S07113; 13657 **R.Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P. Nature 335, 268-271, 1988 **A:Title: HLAA and B polymorphisms predate the divergence of humans and chimpanzees. A; Reference number: S06424; MUID:88319000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 $03537
class I histocompatibility antigen ChLA-B1 alpha chain precursor - chimpanzee
class: Pan troglodytes (chimpanzee)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Oct-1996
C;Accession: $03537
R;Mayer, W.E.; Jonker, M.; Klein, D.; Ivanyi, P.; van Seventer, G.; Klein, J.
EMBO J. 7, 2765-2774, 1988
                                                                                                                                                                                                                   A;Molecule type: mRNÅ
A;Residues: 1-355 CRES>
A;Cross-references: EMBL:U05582; NID:9454781; PIDN:AAA50185.1; PID:9454782
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Proc. Natl. Acad. Sci. U.S.A. 91, 5893-5897, 1994
A;Title: A uniquely high level of recombination at the HLA-B locus.
A;Reference number: 159308; MUID:94286544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.2%; Score 69; DB 2; Length 363; 100.0%; Pred. No. 5.4e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Molecule type: mRNA
A; Residues: 1-363 <LAW>
F; Parham, P: Lawlor, DA; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A; Tille: Diversity and diversification of HLA-A,B,C alleles.
A; Reference number: 136956; MUID:89235215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 69; DB 2; L
Pred. No. 5.3e-05;
); Mismatches 0;
                                                                                                                            A.Accession: 180171
A.Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 93.2%; Sco
Best Local Similarity 100.0%; Pi
Matches 14; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

æ

```
R;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A;Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: freque A;Reference number: A35997; MUID:90207291
A;Accession: A35997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Seywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;196-261/Domain: immunoglobulin homology <IRM>
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
           R;Krangel, M.S.
J. Exp. Med. 163, 1173-1190, 1986
A;Title: Secretion of HLA-A and -B antigens via an alternative RNA splicing pathway.
A;Recence number: 155659; MUID:86198522
A;Accession: 155659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 271-365 <RE2>
A;Cross references: GB:M12377; NID:9187607; PIDN:AAA17889.1; PID:9187608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHIC class I histocompatibility antigen HLA-A32 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
C;Accession: A26088
R;Wan, A.M.; Ennis, P.; Parham, P.; Holmes, N.
J Immunol. 137, 3671-3674, 1986
A;Title: The primary structure of HLA-A32 suggests a region involved in formation of A;Reference number: A26088; MUID:87058961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 15
A35997
MHC class I histocompatibility antigen HLA-A25 alpha chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 16-Nov-1990 #sequence_revision 16-Nov-1990 #text_change 16-Feb-1997
C;Accession: A35997
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
A;Introns: 25/4; 115/1; 207/1; 299/1; 338/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
        A; Cross-references: GB:M64741; NID:9187615; PIDN:AAA59601.1; PID:9187616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB 2; Ler
Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 61; DB 1;
Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.28;
92.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 89.2
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 82.4
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein A; Residues: 1-274 < WAN>
                                                                                                                                                                                                                                                                                                                  A; Gene: GDB: HLA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: HLA-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLHU32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H
                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-365/Product: MHC class I histocompatibility antigen HLA-A alpha chain #status predi
F;220-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence, surroundings and comparison with the HLA-A2 and
                                                                                                                                                                                               A;Cross-references: EMBL:M64740; NID:g403142; PIDN:AAA59600.1; PID:g187614
A;Experimental source: cell line KRC 032; isolate A*2402
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 154416
E;N'Guyen, C.; Sodoyer, R.; Trucy, J.; Strachan, T.; Jordan, B.R.
Immunogenetics 21, 479-489, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: I54493; I55659
R;Little, A.M.; Madrigal, J.A.; Parham, P.
Immunogenetics 35, 41-45, 1992
A;Title: Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3.
A;Reference number: I54493; MUID:92104637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHC class I histocompatibility antigen HLA-A alpha chain precursor - human C;Species: Homo saptens (man) C;Date: 07-Jun-1996 #text_change 23-Jul-1999 C;Date: 07-Jun-1996 #text_change 23-Jul-1999 C;Accession: I54403; I55659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arithe: The HLA-AW74 gene: sequence, surroundings and comparison with the A; Reference number: 154416; MUID:85206128
A; Reference number: 154416
A; Reference number: 154416
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-365 < RES>
A; Residues: 1-365 < RES>
A; Cross-references: GB:M15497; NID:g187644; PIDN:AAA59611.1; PID:g386877
C; Genetics:
A; Introns: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1; 365/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
Nature. 357, 326-329, 1992
A/Title: Unusual HLA-B alleles in two tribes of Brazilian Indians. A/Reference number: 137120; MUID:92269955
A/Accession: 877963
A/Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.2%; Score 66; DB 2; Le 92.9%; Pred. No. 0.00019; tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 66; DB 2; 1
Pred. No. 0.00019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-365 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.2%;
92.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 89.2
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-AW24 protein - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AQTDRENLRIALRY
                                                                                                                                                                        A; Residues: 1-365 <BEL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 13; Conserv
                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                     A; Gene: GDB: HLA-A
                                                                                                                                          A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12
```

ò g ö

ò g

ö

A; Residues: 1-364 <ENN>
A; Cross-references: GB:N32321
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology C; Reywords: transmembrane protein
F; 219-284/Domain: immunoglobulin homology <IMM>

0; Gaps Query Match
82.4%; Score 61; DB 2; Length 364;
Best Local Similarity 85.7%; Pred. No. 0.0015;
Matches 12; Conservative 2; Mismatches 0; Indels

0

2 AQTDRENLRIALRY 15 :|||||:|||||||||||| 95 SQTDRESLRIALRY 108 ò

Search completed: February 7, 2000, 18:04:41 Job time: 22207 sec

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model Run on:

February 8, 2000, 01:26:01; Search time 68.63 Seconds
(without alignments)
6.527 Million cell updates/sec

US-08-653-294-33 74 1 KAQTDRENLRIALRY 15

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

di .	
Description	P10317 homo sapien P30379 gortilla gor P30380 gortilla gor P30380 gortilla gor P30380 gortilla gor P30381 gortilla gor P30381 pon troglod P01893 homo sapien P1845 homo sapien P1845 homo sapien P10314 homo sapien P10319 homo sapien P10373 homo sapien P30487 homo sapien P30487 homo sapien P30481 homo sapien P30480 hom
SUMMARIES	1815_ HUMAN 1801_GORGO 1802_GORGO 1801_FORGO 1801_PANTR 1801_PANTR 1802_HUMAN 1802_HUMAN 1802_HUMAN 1862_HUMAN 1862_HUMAN 1862_HUMAN 1862_HUMAN 1862_HUMAN 1862_HUMAN 1862_HUMAN 1816_HUMAN
<b>B</b> B	
Length	8000 H H B 600 D D D D D D D D D D D D D D D D D D
% Query Match	0444m0000001111110000000000000000000000
Ma.	04 04 04 04 04 04 04 04 04 04 04 04 04 0
Score	47 C C C C C C C C C C C C C C C C C C C
Result No.	

P30492 homo sapien P30493 homo sapien P30494 homo sapien P30496 homo sapien P30496 homo sapien O56464 paracoccus P30385 gorilla gor P30501 homo sapien P30502 homo sapien
1B55_HUMAN 1B56_HUMAN 1B57_HUMAN 1B59_HUMAN 1B59_HUMAN MAUJ_PARVE 1C03_GORGO 1C03_GORGO 1C03_GORGO 1C03_HUMAN 1C04_GORGO
папапапапапа
99999999999999999999999999999999999999
00000000000000000000000000000000000000
4444448888 444440000000
WWWWW444444 WWCWWOUUW4W

## ALIGNMENTS

```
40170 MW; 2E33E2B8 CRC32;
                                                                                                                                                                                                                                                                                                                                                     MICROGLOBULIN).
 362 AA;
                               Ouery Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
362 AA;
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                1B02_GORGO
P30380;
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                           RESULT 3
                                                                         à
                                                                                             셤
                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@labs.ib.ch).
                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92078860.
LAWLORD D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLORD D.A., WARREN E., TAYLOR P., PARHAM P.;
GGTILLA class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0101 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland GOTILLA).
ELWARYOTA: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
ELWARYOTA: Primates; Catarrhini; Hominidae; Gorilla.
  CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P03989; 1HSA.
PROSTER: PSO0290; IG_MHC; 1.
PRAM: PF00047; ig; 1.
PFAM: PF00129; MHC_I; 1.
PFAM: PF00129; MHC_I; 1.
SIGNAL 25 362 CLASS I HISTOCOMPATIBILITY ANTIGEN,
CHAIN
                                                                                                                                                                     ö
                                                                                                                                              100.0%; Score 74; DB 1; Length 362; 100.0%; Pred. No. 2.6e-06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
HLA CLASS I HISTOCOMPATIB:
B-27 B*2702 ALPHA CHAIN.
EXTRACELLOLAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GOGO-BO101 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                        CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONNECTING PEPTIDE
                                                                                                      SIMILARITY.
9798F0BB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY
                                                                                                                40397 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X60255; CAA42807.1; -. PIR; JH0539; JH0539.
                                                                                                                                                                    Conservative
                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                        1 KAQTDRENLRIALRY 15
                                                                                                               362 AA;
                                                                                                                                                         Best_Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                   25
207
209
3309
3333
110
125
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
1115
2207
2299
3309
333
333
125
125
110
                                                                                                                                                                                                                                                                1B01_GORGO
P30379;
                                                                       DOMAIN
CARBOHYD
DISULFID
DISULFID
                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                               SEQUENCE
                                                                                                                                                Query Match
                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                            RESULT 2
1B01_GORGO
  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---
  g
                                                                                                                                                                                         ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE, 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.,
"Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.
                                                                                                                                                                                                                                     01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-B0102 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA (LOWHAND GOTILLA)
BUKATYOLA: Metazoa: Chordata; Creniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 362;
Score 70; DB 1; Length 362
Pred. No. 1.4e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 1; Le
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
3CF119AD CRC32;
                                                                                                                                                                                                      362 AA
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40204 MW;
ch 94.6%;
1 Similarity 93.3%;
14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.68;
93.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KAQTDRENLRIALRY 15
```

ო

```
å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ROCOSEDERATION
                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN GOGO-B0103 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA GOTILLA CHAIN PRECURSOR.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                             MEDLINE; 92078860.
LAMADO D.A., WARREN E., TAYLOR P., PARHAM P.;
LGANLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
GOTILLA Class I major histocompatibility complex alleles: comparison to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1801_PANTR STANDARD; PRT; 359 AA.
P13750;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASS I HISTOCOMPATIBLLITY ANTIGEN,
GOGO-BOll3 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                      -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 70; DB 1; Length 362;
Pred. No. 1.4e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; FEA6A941 CRC32;
                              362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Signal
                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40248 MW;
                                                                                                                                                                                                                                                                                                                                    EMBL; X60254; CAA42806.1; -. PIR; JH0541. HSSP; P03989; 1HSA. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Conservative
                              STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                            1114
206
2298
3308
332
332
362
110
                                                                                                                                                                                                                                                                                                                                                                                                     MHC I; Transmembrane;
SIGNAL 1 24
                                                                                                                                                                                                                                                                                                                                                                                                                                            25
115
207
209
339
333
125
227
210
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                   SEQUENCE FROM N.A.
                             1B03_GORGO
P30381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
1B01_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                  1B03_GORGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                        a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                      KLEIN J.;
"Nucloctide sequences of chimpanzee MHC class I alleles: evidence for
trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-1 ALPHA CHAIN.
B-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                               Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.
-!- SUBDNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN H PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
Chordata, Craniata, Vertebrata, Mammalia,
Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
                                                               SEQUENCE FROM N.A.
MEDILINE: 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANXI P., VAN SEVENTER G.,
KLEIN J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 69; DB 1; Ler
; Pred. No. 2.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
7; 5395FFC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X13115; CAA31507.1; -
PIR; $03537; $03537.
HSSP; $03989; BRSA.
PROSITE; $500290; IG_MHC; 1.
PFAM; PF00147; 1g; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93.2%;
.1larity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AQTDRENLRIALRY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HLA-AR) (HLA-12.4).
HLA-H OR HLAH.
  Eukaryota; Metazoa;
                      Sutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223
106
359 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLAH_HUMAN
P01893;
                                                                                                                                                                                                                                        REVISIONS.
                                                                                                                                                                                                                                                                 MAYER W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLAH_HUMAN
```

ö

4

```
SHOWN HERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JORDAN B.R.
                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                     CHAIN
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation. the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
SEQUENCE FROM N.A.
MEDIJUE: 82151002.
MALISSEN M., MALISSEN B., JORDAN B.R.;
"Exon/intron organization and complete nucleotide sequence of an HLA
gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                    Proc. Natl. Acad. Sci. U.S.A. 79:893-897(1982).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMUNE SYSTEM. COULD BE THE PRODUCT OF A PSEUDOGENE.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-AUL-1999 (Rel. 38, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo saptens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- SUBGNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66; DB 1; Length 362;
Pred. No. 7.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHA CHAIN H.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
5E610F63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                       EMBL; JONGER 1 LONGER 1 LONGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                  EMBL; J00191; AAA36218.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.2%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333
110
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
1115
207
299
309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1A23_HUMAN
ID 1A23_HUMAN
AC P30447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LITTLE A.-M., MADRIGAL J.A., PARHAM P.; "Molecular definition of an elusive third HLA-A9 molecule: HLA-A9.3."; Immunogenetics 35:41-45(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-23(A-9) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A*2401).
MEDLINE; 85206128.
N'GUYEN C., SODOYER R., TRUCY J., STRACHAN T., JORDAN B.R.;
N'HE HILA-MAY4 qenee; sequence, surroundings and comparison with the HILA-A2 and HILA-A3 genes.;
Immunogenetics 21:479-489(1985).
POLYMORPHISM: THE ONLY ALLELE OF A-23 KNOWN IS A*2301 WHICH IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 8

10. 1A24_HUMAN

ID 1A24_HUMAN

STANDARD;

AC P05534;

AC P05534;

BD 10.NOV-1988 (Rel. 09, Last sequence update)

DT 15.JUL-1999 (Rel. 38, Last annotation update)

DE HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN

GN HIA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66; DB 1; Length 365; No. 7.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (XXX-1988) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; BIC21094 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66; DB :
Pred. No. 7.9e :
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A*2402/A*2403).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                              HSSP; P01892; 1AQD.
MIM; 142800; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89.2%;
92.9%;
                                                                                                                                                                                                                                                                                   EMBL; M64742; AAA03662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 89.2
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 SQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299
309
110
125
227
365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS (A*2401).
```

```
Conservative
                                                                                                                                                                                                                                                                    95 SQTDRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              365
                         206
                                                                                                                                                                                                                                           2 AQTDRENLRIALRY 15
                                                                                                                                                      Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                         365 AA;
                         206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-A OR HLAA.
                                                                                         SEQUENCE
                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                  g
      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

G -> A (IN A*2402, A*2403 AND A*2408).

FTIG-VAR_004355.

E -> G (IN A*2408).

FTIG-VAR_004355.

G -> R (IN A*2408).

FTIG-VAR_004355.

G -> R (IN A*2408).

FTIG-VAR_004357.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) ALPHA CHAIN. EXTRACELULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF A-24 ARE KNOWN: A*2401, A*2401, A*2401, A*2401.
                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC 3:9-14(1996).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
SEQUENCE FROM N.A. (A*2402).
MEDLINE; 92269955.
BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J.,
WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P.;
WILLIAMS H.A.B alleles in two tribes of Brazilian Indians.";
Nature 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                         KASHIWASE K., TOKUNAGA K., ISHIKAWA Y., QIU L., FURUYA M., SAWANAKA K., AKAZA T., TADOKORO K., JUJI T.;
"A new A9 sequence HLA-A9HH from Japanese.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal; Polymorphism.
SIGNAL
                                                                                                                                                SEQUENCE FROM N.A. (A*2402).
LAFORET M., TONGIO M.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                  GAO X., MCCLUSKEY J.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O -> W (IN REF. 6).
/FIId-VAR_004358.
DG -> EW (IN A*2403).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M64740; AAA59600.1; --
EMBL; M64741; AAA59600.1; --
EMBL; U19733; AAB60651.1; --
EMBL; U18987; AAB60651.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z72422; CAA96532.1; -. EMBL; D83516; BAA11936.1; -. HSSP; P01892; IAQD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M15497; AAA59611.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIM; 142800; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                           SEQUENCE OF 26-206 FROM N.A.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (A*2408).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  206
208
3308
3345
288
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
1115
207
209
309
333
1110
1125
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     190
                                                                                                                                                                                                                                                                                                                                                         TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /ARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                         9
  RARAR RARAR
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
A-25(A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
/FIId=VAR_004359.
A -> T (IN A*2402, A*2403, A*2408 AND REF: 6).
/FIId=VAR_004360.
DE23D06E_CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ဝို
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MICROGLOBULIN).
-!- POLYMORPHISM: THE FOLLOWING ALLELES OF A-25 ARE KNOWN: A*2501
AND A*2502. THE SEQUENCE SHOWN IS THAT OF A*2501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1A25_HUMAN STANDARD; PRT; 365 AA.
AC P18462; Q95362;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1999 (Rel. 16, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-25(A-10) ALPHA CHAIN
DE PRECURSOR.
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                 Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM: PF00047; 19; 1.
PFAM: PF00129; MHC_I; 1.
MHC_I: Transmembrane; Glycoprotein; Signal; Polymorphism.
SIGNAL 1.24
                                                                                                                           0; Indels
                                                                                               Score 66; DB 1;
Pred. No. 7.9e-05;
                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M32321; AAA36234.1; -.
EMBL; X97802; CAA66389.1; -.
PIR; A35997, A35997.
HSSP; P01081; 2HLA.
MIM; 142800; -.
PROSITE; PS00299; IG_MHC; 1.
                                                       40644 MW;
                                                                                              89.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (A*2501). MEDLINE; 90207291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114
206
298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
1115
207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
```

```
DOMAIN
CARBOHYD
DISULFID
                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                       VARIANT
                                                                                                                                          DOMAIN
                                                                                                                                                                                        DOMAIN
  NAME OF THE PERSON NAME OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- POLYMORPHISM: THE FOLLOWING ALLELES OF A-32 ARE KNOWN: A*3201 AND AND A*3202. THE SEQUENCE SHOWN IS THAT OF A*3201.
                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1A32_HUMAN STANDARD; PRT; 365 AA.
P10314; Q28838;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-32(AW-19) ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Sequencing of a new HLA-A*32 subtype (A*3202).";
Immunogenetics 45:76-77(1996).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 87058961.
WAN A.M., ENNIS P., PARHAM P., HOLMES N.;
"The primary structure of HLA-A32 suggests a region involved cornation of the BW4/BW6 epitopes.";
J. Immunol. 137:3671-3674(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                          Length 365;
                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 97045038.
ZINO E., SEVERINI G.M., MAZZI B., BORDIGNON C., BENAZZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOWENA J.D.;
Submitted (DEC-1993) to the EMBL/GenBank/DDBJ databases.
                                           CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
H.-> Q (IN A*2502).
FITG-VAR_004361.
  CONNECTING PEPTIDE
                                                                                                                                                                                                                                                        Score 61; DB 1;
Pred. No. 0.00066;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 25-298 FROM N.A. (A*3201).
                                                                                                                                                                                        MK.
                                                                                                                                                                                                                                                          82.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U03907; AAA03605.1; -. EMBL; X97120; CAA65786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (A*3202)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 142800; -. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (A*3201)
                                                                                                                                                                                      41218
                                                                                                                                                                                                                                                        Query Match 82.4
Best Local Similarity 85.7
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                          308
332
365
1110
188
283
94
                                                                                                                                                                                                                                                                                                                                                  2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLHU32
                                                                                                                                                                                        365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLEISCHHAUER K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; A26088;
                                           DOMAIN
CARBOHYD
DISULFID
DISULFID
DOMAIN
TRANSMEM
                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1A32_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                           g
  FT
FT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                                                  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 90207291.

ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;

"Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";

Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                              HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A 32 (AN-19) ALERA CHAIN.
EXTRACELLULAR ALPHA 1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPAIDBLITIT ANTIGEN, B-57(B-17) B*5701 ALPHA
CHAIN PRECURSOR (BW57.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 91067476.
ISAMAT M., GIRDLESTONE J., MILSTEIN C.;
"Nucleotide sequence of an HA-Bw57 gene.";
Nucleic Acids Res. 18:6702-6702(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 365;
                                             Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.4%; Score 61; DB 1; Length 365
85.7%; Pred. No. 0.00066;
ive 2; Mismatches 0; Indels
                                                                                                                                                                                               EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
R -> H (IN A*3202).
FTIG-VAR,00473.
L -> Q (IN A*3202).
                                                                                                                                                                                                                                                                                                                                                                                                                                       /FIId=VAR_004374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M32318; AAA36231.1; -. EMBL; X55711; CAA39244.1; -. PIR; S12622; S12622.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 AA; 41048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AQTDRENLRIALRY 15
                                                MHC I; Transmembrane; SIGNAL 1 24 CHAIN 25 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                              25
2007
2007
3333
3333
1110
125
175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1860_HUMAN
AC 191860_HUMAN
AC 01-NOV-1990
DT 01-NOV-1990
DE CHART PECUR
RN EDLINE; 902
RN EDLINE; 902
RN EDLINE; 916
RN EDLINE; 916
RN MEDLINE; 916
CC This SWISS-CC THIS SISSI
```

```
TISSUE-BLOOD
                                                                                                                                              TRANSMEM
DOMAIN
CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                          DOMAIN
                                                                       DOMAIN
                                                                                                                               DOMAIN
                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                       g
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHIA BARKER SERVICE COCCOCCOC SERVICE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN
PRECURSOR (BW57.2)
                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MADELINE, 9305560B.
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARYELL R.W., DU TOIT E.D., PARHAM P.;
"Distinctive HLA-A.B antigens of black populations formed by
interallelic conversion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                            B-57(B-17) B*5701 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                     81.1%; Score 60; DB 1; Length 362; 92.9%; Pred. No. 0.001; 1.ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                          CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                   D91DF8DD CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 AA.
                                                                                                            Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X61707; CAA43876.1; -. PIR; S16774; S16774. HSSP; P30491; IAIM. MIM; 142830; -. PROSITE; PS00290; IG_MHC; 1.
             HSSP; P30491; IAIM.
MIM; 142830; -.
PROSITE: PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC__I; 1.
MHC I; Transmembrane; Glycoprosident.
                                                                                                                                                                                                                                                                                                                                                   ..
Μ
                                                                                                                                                                                                                                                                                                                                                   40224
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 AQTYRENLRIALRY 108
                                                                                                                                                                                                  206
298
308
362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AQTDRENLRIALRY 15
PIR; D35997; D35997
                                                                                                                                                                                 25
115
207
209
3309
333
110
125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-B OR HLAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1B61_HUMAN
P30497;
                                                                                                                                                                                                  DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                          DOMAIN
CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                   DOMAIN
                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1B61_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  õ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-57(B-17) B*5702 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INOUE T., OGAWA A.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
115-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-58(B-17) B*5801 ALPHA
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                       Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 628C2156 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 86008247.
WAYS J.P., COPPIN H.L., PARHAM P.;
The complete primary structure of HLA-Bw58.";
J. Biol. Chem. 260:11924-11933(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M11799; AAA59628.1; --
EMBL; AB008102; BAA22916.1; --
PIR; A23895; HLHUB8.
HSSP; P30491; 1A1M.
MIM; 142830; --
PROSTE; P500290; IG_MRC; 1.
PFAM; PF00147; 19; 1.
PFAM; PF00129; MRC_I; 1.
MRC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
1 24
CHAIN
25 362 HLA CLASS I HISTO
                                                                                                                                                                                                                                                                                                                                                     Score 60; DB 1;
Pred. No. 0.001;
0; Mismatches
  Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                         MM;
                                                                                                                                                                                                                                                                                                                                                       81.1%;
92.9%;
                                                                                                                                                                                                                                                                                       40342
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AQTDRENLRIALRY 15
MHC I; Transmembrane;
SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MICROGLOBULIN).
                                                                                25
115
207
299
339
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1B62_HUMAN
ID 1B62_HUMAN
AC P10319;
```

Length 338;

```
Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                    HLA-B OR HLAB
                                                                                                                                                                                                                    1B14_HUMAN P03989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- DISEASE:
                                                                                                                                                                                 RESULT 15
1914_HIMAN

10 19194_HIMAN

11 13-OCT

11 15-UUL

12 16 HLA CLI

13 HLA CLI

14 HIMAN

15 HLA CLI

16 HLA CLI

17 HIMAN

18 HLA CLI

18 HLA CLI

18 HLA CLI

19 HLA CLI

19 HLA CLI

10 CC

11 HA CLI

11 HA CLI

12 HLA CLI

13 HLA CLI

14 HA MEDLINI

18 HA MEDLINI

18 HA SZOETS

19 HA SZOETS

10 HA SZ
                                                                                          à
                                                                                                                           셤
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE; 91268545.
CHOO Y.S., FAN L.A., HANSEN J.A.;
"A novel HLA-B27 allele maps B27 allospecificity to the region around position 70 in the alpha 1 domain.";
J. Immunol. 147:174-180(1991).
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INMUNE SYSTEM.
-!- SUBDINT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-ARR-1993 (Rel. 25, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 B*2707 ALPHA CHAIN (B27-HS).
                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
B*5801 ALPHA CHAIN.
                                                                                                                                                                                                                                         DB 1; Length 362;
0.001;
                                                                                                                                                                                                                                                                              1; Indels
             EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                           Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

3E5E7534 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
33FB8134 CRC32;
                                                                                                          CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                         Score 60; DB 1
Pred. No. 0.001
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                338 AA.
 BW-58(B-17)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM, 142830, -... IG_MHC; 1. PROSITE; PS00290; IG_MHC; 1. PFAM; PF00047; ig; 1. PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                       Œ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37804 MW;
                                                                                                                                                                                                                                           81.1%;
92.9%;
                                                                                                                                                                                   40337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M62852; AAA59647.1;
HSSP; P03989; 1HSA.
                                                                                                                                                                                                                                       Query Match 81.1
Best Local Similarity 92.9
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD:
                                                                                                                                                                                                                                                                                                                                    95 AQTYRENLRIALRY 108
                                                                                                                                                                                                                                                                                                                   2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
203
338 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                           1B20_HUMAN
ID 1B20_HUMAN
                              DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RANSMEM
                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
 FT
FT
FT
FT
SO
SO
                                                                                                                                                                                                                                                                                                                                                        g
```

,

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its make by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                 ö
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE, 86149317.
SZOETS H., RIETHMUELLER G., WEISS E., MEO T.;
Complete sequence of HLA-B27 cDNA identified through the
characterization of structural markers unique to the HLA-A, -B, and
                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1986 (Rel. 02, Created)
13-ANG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-27 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92018187.

MADDEN D. R., GORGA J.C., STROMINGER J.L., WILEY D.C.;

The structure of HIA-B27 reveals nonamer self-peptides bound in a extended conformation.";

Nature 35:321-325(1991).

-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMONE SYSTEM.

-I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 85226361.
EZQUERRA A., BRAGADO R., VEGA M.A., STROMINGER J.L., WOODY J.,
LOPEZ DE CASTRO J.A.;
"Primary structure of papain-solubilized human histocompatibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92405152.

MADDEN D.R., GORGA J.C., STROMINGER J.L., WILEY D.C.;

"The three-dimensional structure of HLA-B27 at 2.1-A resolution suggests a general mechanism for tight peptide binding to MHC.";

Cell 70:1035-1048(1992).
                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEISS E.H., KUON W., DOERNER C., LANG M., RIETHMUELLER G.; "Organization, sequence and expression of the HLA-B27 gene: a molecular approach to analyze HLA and disease associations."; Immunobiology 170:367-380(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THIS PROTEIN CORRELATES WITH THE DEVELOPMENT OF
                                                                 Indels
Score 59; DB 1; Le
Pred. No. 0.0014;
.; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 83:1428-1432(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 25-300.
                                                                                                                                                                                                                                                                                                                                                                           361 AA
                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen HLA-B27.";
Biochemistry 24:1733-1741(1985).
79.7%;
larity 80.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 25-361 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANKYLOSING SPONDYLITIS.
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                   1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY.
                                                                                                                                                                         SEQUENCE OF 25-295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROGLOBULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 86138405.
```

Ė

150 S. C.

ö

Gaps

ö

Query Match 79.7%; Score 59; DB 1; Length 361; Best Local Similarity 80.0%; Pred. No. 0.0015; Matches 12; Conservative 1; Mismatches 2; Indels

```
Db 94 KAQTDREDLRTLLRY 108
```

1 KAQTDRENLRIALRY 15

ò

Search completed: February 8, 2000, 01:26:01 Job time: 1561 sec

THIS PAGE BLANK (USPTO)

homo sapien pan troglod pan sapien homo sapien homo sapien homo sapien homo sapien homo sapien homo sapien

0062923 00299210 00299210 00299329 00299841 00299841 00299841 00298841 00298841 00298841 00298841 00298841 00298833 0029833 0029833 0029833 0029833 0029833

062923 029910 029910 029963 029841 029881 029881 029881 029881 029881 029881 04669 046696 04669 04669 04669 04669 04669 04669 04

```
O19189;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HISTOCOMPATIBILITY ANTIGEN-B (HLA-B-27KSH) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
TISSUE-LEUKOCYTE;
PETERSDORF E.;
Submitted (50C-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; 142830; -...
MIM; 142830; -...
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-VOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I A ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 74; DB 7; 1
Best Local Similarity 100.0%; Pred. No. 6.5e-06;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1
133
15491 MW; 3A3BC802 CRC32;
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 KAQTDRENLRIALRY 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KAQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
133 1
133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                    019189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          019354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
019354
ID 01
AC 01
DT 01
DT 01
DE MH
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gorilla gor
pan paniscu
pan paniscu
hylobates 1
pan troglod
pan troglod
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O19189 homo sapien
                                                                February 8, 2000, 19:16:17; Search time 176.54 Seconds (without alignments) 5.891 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homo
homo
homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  рошо
рошо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      095412
095529
030988
019607
019609
019610
029724
029689
046697
        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                            225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                            summaries
                                              protein search, using sw model
                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                               4: $p_human:*
5: $p_human:*
6: $p_nammal:*
7: $p_hnc:*
8: $p_organelle:*
9: $p_plage:*
10: $p_plage:*
11: $p_rodent:*
12: $p_virus:*
13: $p_virus:*
14: $p_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          019354
095524
095524
095527
095527
095608
019608
019608
019610
019610
029629
029689
                                                                                                        US-08-653-294-33
74
1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                       1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                  DB seq length: 0
DB seq length: 1000000
                                                                                                                                                                                                                                                                               SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
Sequence:
                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM protein
                                                                                                                                                                                                                                                                                ..
                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                               Database
                                                                                                                                                                                                                 Minimum
                                                                                                                                                                                                                              Maximum
                                                                  Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Result
```

133 AA.

ö

Gaps

ö

181 AA.

Length 133;

```
"Molecular cloning of orangutan and gibbon MHC class I cDNA. The HLA-A and -B loci diverged over 30 million years ago."; J. Immunol. 148:2547-2554(1992).
                                                                                                                                                                                                               STRAIN-BOSONDJO;
MEDLINE; 94286544.
MCADINE; 94286544.
MCADAM S.N., BOYKON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;
A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. 561, U.S.A. 91:5893-5897(1994).
EMBL; U05578; AAASO181.1;
HSSP; P30491; IAlM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   095412 PRELIMINARY; PRT; 354 AA.
095412;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I (FRACMENT).
Hylobates lar (Common gibbon).
Bukaryota; Metacos; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
                                                                             Pan paniscus (Pygmy chimpanzee) (Bonobo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE; 9218857.
CHEN Z.W., MCADAM S.N., HUGHES A.L., DOGON A.L., LETVIN N.L.,
WATKINS D.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 70; DB 7; Length 354;
Pred. No. 9.6e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.2%; Score 69; DB 7; Length 354; 100.0%; Pred. No. 0.00014; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
CHEN 2.W., MCADAM S.N., HUGHES A.L., WATKINS D.I.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
EMBL, U50091; AAB08074.1; -
HSSP; P30491; 1A1M.
01-NOV-1999 (TrEMBLrel. 12, Last annotation update) CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1
354 AA; 39401 MW; 6E38CFFE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       354 AA; 39748 MW; 43EDEC6F CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94.6%;
93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86 QAQTDRENLRIALRY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 AQTDRENLRIALRY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AOTDRENLRIALRY 15
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
  á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A PART REPORTED THE PROPERTY OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                    MEDLINE; 96408732.
CEREB N. KNOR Y., LEE S., MAYE P., YANG S.Y.;
NUCLEOCIGE sequences of MHC class I introns 1, 2, and 3 in humans and intron 2 in nonhuman primates.";
Tissue Antigens 47:498-511(1996).
EMBL: U37323; AAB49915.1;
HSSP; P10318; 1ROG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-LOREL;
MEDLINE; 94286544.
MEDLINE; 94286544.
MCDAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.,
A uniquely high level of recombination at the HLA-B locus.";
Proc. Mall. Acad. Sci. U.S.A. 91:5893-5897(1994).
ENBL; U05575; AAA50178.1; -..
HSSP; 730491: 1A1M.
PROSITE; PS00290; IG_MHC; 1.
PFRAM; PF00129; MHC_I: 1.
                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan paniscus (Pygmy chimpanzee) (Bonobo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 94.6%; Score 70; DB 7; Length 181; Best Local Similarity 93.3%; Pred. No. 4.7e-05; Matches 14; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 02, Created)
(TrEMBLrel. 02, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 70; DB 7; I
Pred. No. 9.6e-05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                  181 181
181 AA; 20981 MW; FFB51D78 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1 354 AA; 39227 MW; 5D75939D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 AA
  Gorilla gorilla gorilla (Lowland gorilla).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                    PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KAQTDRENLRIALRY 15
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q95527 F
Q95527;
01-FEB-1997 (
01-FEB-1997 (
                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     095524
095524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
Q95527
ID Q95527
AC Q95527;
DT 01-FEB
DT 01-FEB
```

RESULT 095524

ACCOC OCT REP REP DE RE

ò g

ò a

ö

Gaps

ö

ö

Gaps

ö

ö

Gaps

ö

Indels

9

RESULT Q95529

```
SEQUENCE FROM N.A. SIRIKONG M., LUANGTRAKOOL K., SRINAK D., RUNGROUNG E., BEJCHANDRA S., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF030920; AAB87056.1; -. EMBL, AF030919; AAB87056.1; -. HSSP; P01891; ITMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 90.5%; Score 67; DB 7; Length 180; Best Local Similarity 86.7%; Pred. No. 0.00016; Matches 13; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.5%; Score 67; DB 7; Length 180; Best Local Similarity 86.7%; Pred. No. 0.00016; Matches 13; Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     01-JNN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1
180 180
180 AA; 20811 MW; CECC3537 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
180
20811 MW; CECC3537 CRC32;
                                                                                                                                                                                                                                                                                                                                       180 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 AA.
Mismatches
                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
ö
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P01891; ITMC.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00129; MHC_I; 1
                                                                                                             95 AQTDRENLRIALRY 108
                                                                          2 AQTDRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   019607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             019608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    019608
                                                                                                                                                                                                                                                             œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                             RESULT
019607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
019608
                                                                          δŏ
                                                                                                                                                                                                                                                                                                                                                                              ACCOCCO OCT THE TENT OCT THE THE TENT OCT THE THE TENT OCT THE TENT OC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SETT THE REPORT OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 94286544.

MEDLINE: 94286544.

MCADAM S.N., BOYSON J.E., LIU X., GARBER T.L., HUGHES A.L.,
BONTROP R.E., WATKINS D.I.;

A uniquely high level of recombination at the HLA-B locus.";
Proc. Natl. Acad. Sci. U.S.A. 91:5893-5897(1994).

EMBL: 005580; AAA50183.1; -..

HSSP: 930491: 1A1M.

PROSITE: PS00290; IG_MHC; 1.

PRAM: PF0047; 1g: II.

PFAM: PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                         Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 93.2%; Score 69; DB 7; Length 355; Best Local Similarity 100.0%; Pred. No. 0.00014; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 7; Length 363; 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENNIS P.D.;
Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 23-363 FROM N.A.
MEDLINE: 89235215.
PARHAM P., LAWLON D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
EMBL; MA24045; AAA35424.1; -.
HSSP; P30491; IALM.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                    095529 PRELIMINARY; PRT; 355 AA.
095529;
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-FEB-1997 (TrEMBLrel. 12, Last sequence update)
CLASS I'HISTOCOMPATIBILITY ANTIGEN (FRAGMENT).
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q30988 PRELIMINARY; PRT; 363 AA.
Q30988;
01-NOV-1996 (TYEMBLYEL 01, Created)
01-NOV-1999 (TYEMBLYEL 01, Last sequence update)
01-NOV-1999 (TYEMBLYEL 12, Last annotation update)
CHIMPANZEE MHC CLASS I CHLA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8AD2B984 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133979D1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.2%; Score 69;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    355 AA; 39772 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 AA; 40540 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
```

RESULT 7

ò

030988

ö

Gaps

ö

ö

Gaps

ö

Best Local Similarity

```
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.5%; Score 67; DB 7; Length 365; 86.7%; Pred. No. 0.00034; 1.ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SELVAKUMAR A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; UZ5971; AAA73518.1;
HSSP: P01802; 1HHH.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
CHOPEK M., NIELSEN J., ZHANG H.;
SUDMITTED (SEP-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, U36914; AAA80238.1; -.
HSSP, P01891; ITMC.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN HLA-A2407.
                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 90.5%; Score 67; DB 7; I
Best Local Similarity 86.7%; Pred. No. 0.00016;
Matches 13; Conservative 2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1

NON_TER 181 181

SEQUENCE 181 AA; 20912 MW; D475FCD7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 365 AA; 40679 MW; A23C2F19 CRC32;
                                                                                                                                                                                        181 AA
                                                                                                                                                                                                                                              01-NOV-1996 (TIEMBLREL 01, Created) 01-NOV-1996 (TIEMBLREL 01, Last seq 01-NOV-1999 (TIEMBLREL 12, Last annumHC CLASS I ANTIGEN HLA-A (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 90.5
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KAQTDRENLRIALRY 15
::!!!!!!!!!!!!!!!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                 029724
029724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
029689
029689
DC 029689
DT 01-NOV-
DT 01-NOV-
DE MHC CL/
GN HLAA-A.
OC EUKATY
COC EUKATY

                                                                                                                     RESULT 12
029724
AC 029724
AC 029724
DT 01-NOV
DT 01-NOV
DF MHC-CLi
GN HLA-A.
OC EURARY
CC EURAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
CHANDARYTRGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
Submitted (OCT.1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030924; AAB87425.1; -
EMBL; AF030923; AAB87425.1; -
HSSP; P01891; 1TMC.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEZTHANDRA S.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF030925; AAB87058.1; -.
EMBL; AF030925; AAB87058.1; JOINED.
PFRM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 67; DB 7; Length 180;
Pred. No. 0.00016;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                             019609;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-A (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67; DB 7; Pred. No. 0.00016; 2; Mismatches 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 AA; 20811 MW; CECC3537 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 AA; 20811 MW; CECC3537 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 AA
                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.5%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 90.5%;
Best Local Similarity 86.7%;
Matches 13; Conservative ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.7
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  019610
                                                                                                                                                                                                                                                       019609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 11
019610
                                                                                               q
                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

ö

Gaps

ö

Length 181; 0; Indels ö

Gaps

ö

RESULT 14

1 KAQTDRENLRIALRY 15

ò,

Ç

. .

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "An intronic mutation responsible for a low level of expression of an HLA-A*24 allele.";
Tissue Antiques 50:340-346(1997).
EMBL: Z72423; CAA96533.1; -PFAM; PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 98007772.
LAFORET M., FROELICH N., PARISSIADIS A., BAUSINGER H., PPEIFFER
TONGIO M.M.;
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                Gorilla gorilla gorilla (Lowland gorilla).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 89.2%; Score 66; DB 7; Length 138; Best Local Similarity 92.9%; Pred. No. 0.00018; Matches 13; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                        Score 66; DB 7; Length 90;
Pred. No. 0.00011;
2; Mismatches 0; Indels
                                                                                                                                                                                                       GRIMSLEY C., WATHER K.A., OBER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO1217; AAC99794.1; -.
PFAM: PFO0129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O78209 PRELIMINARY; PRT; 138 AA. 078209; 01-NOV-1998 (TrEMBLrel. 08, Created) 01-NOV-1999 (TrEMBLrel. 08, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) HUMAN LEUKOCYTE ANTIGEN PRECURSOR (FRAGMENT).
                                         01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last Sequence update)
01-MX-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I ANTIGEN HLA-H ORTHOLOG (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 24 POTENTIAL.
138 138
138 AA: 15610 MW; B8417FAO CRC32;
                                                                                                                                                                                                                                                                               NON_TER 1 1
NON_TER 90 90
SEQUENCE 90 AA; 10689 MW; 5E5F2495 CRC32;
               90 AA.
                PRT;
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 86.7%;
Matches 13; Conservative
                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  1 KAQTDRENLRIALRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AQTDRENLRIALRY 15
                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=SHAMBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal; MHC
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
078209
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
```

Search completed: February 8, 2000, 19:16:17 Job time: 21504 sec

:111111111111 95 SQTDRENLRIALRY 108

g

THIS PAGE BLANK (USPTO)

'n

us-08-653-294-33.rge

```
AF030929 Homo sapiens MHC cl
AF030915 Homo sapiens MHC cl
U59699 Human MHC class I (HL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/protein_id="AAB60357.1"
/protein_id="AAB60357.1"
/db_xref="G1:790215"
/db_xref="G1:790215"
/translation="APWIEQEGPEYWDRETQICKAKAQTDRENLRIALRYYNQSEAGS
/translation="APWIEQEGPEYWDRETQICKAKAQTDRENLRIALRYYNQSEAGS
HTLQNMYGCDVGPDGRELRGYHQDAYDGKDYTALNEDLSSWTAADTAAQITQRKWEAA
RYAEQLRAYLEGECVEWLRRYLENGKETLQR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 399)
Petersdorf, E.
Direct Submission
Submisted (14-DEC-1994) Effie Petersdorf, Human Immunogenetics, Fred Hutchinson Cancer Research Center, 1124 Columbia, Seattle,
                                                                                                                                               seq_documentation_block:
LOCUS HSU18659 399 bp mRNA PRI 30-APR-1995
DEFINITION Human MHC class I HLA-B mRNA (HLA-B-27KSH allele) exons 2 and ACCESSION U18659
VERSION U18659.1 GI:790214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HLA-B"
/note="This submission reports an HLA-B-2702 variant
/note="This submission reports an HLA-B-2702
sequence, GenBank Accession Number X03664"
/phenctype="HLA-B-27"
/replace="t" 145 g 48 t
                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 15
Gaps: 0
Percent Identity: 100.000
  3.0e-05
3.0e-05
3.0e-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="HLA-B-27KSH allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_type="leukocyte"
/tissue_type="blood"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualiflers
1. .399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-B
  238.18
238.18
238.18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ō
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128. .>399
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HLA-B
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecular Diversity
Unpublished
  66.00
66.00
66.00
                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 399)
Petersdorf, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             >399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number=3
372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1. .127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: HSU18659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.933
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-33 x HSU18659
                                                                                                      seq_name: gb_pr2:HSU18659
                                                                                                                                                                                                                                                                                                                                                   Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98104, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                       human.
  gb_pr3:HS639HLA1
gb_pr3:HS8151HLA1
gb_pr4:HSKM315S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         variation
                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Documentation | Documentation | Documentation | 1018659 Human MHC class I HLA-B | 1138504 Human applies (clones 18 | 1238504 Human class I MHC gene | 137323 Gorilla gorilla MHC clas | 1037323 Gorilla gorilla MHC clas | 1005575 Pan paniscus class I hi | MC0255 G.gorilla MHCGOGO-B0101 | MCGOGO-B0101 | MCGOGO-BOTILI | MCGOGO-BOTILI | MCGOGO-BOTILI | MCGOGO-BOTILI | MCGOGO-BOTILI 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U35914 Human MHC class I antige
1025971 Human MHC class I antige
108692 H.saplens HLA-B gene, ex
108693 H.saplens HLA-B gene, ex
108693 H.saplens HLA-B gene, ex
AF022159 Homo saplens isolate C
114590 Sequence 67 from patent
114591 Sequence 68 from patent
114592 Sequence 69 from patent
114593 Sequence 70 from patent
114593 Sequence 70 from patent
114594 Sequence 70 from patent
114593 Sequence 70 from patent 114593 Sequence 70 from patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF030923 Homo sapiens MHC class
AF030921 Homo sapiens MHC class
AF030919 Homo sapiens MHC class
AF140723 Homo sapiens MHC class
AF140723 Homo sapiens MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U37110 Human HLA-A24 gene, aile
U37114 Human HLA-A24 gene, alle
U37112 Human HLA-A24 gene, alle
U18987 Human MHC class I antige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens MHC class
Homo sapiens MHC class
Homo sapiens MHC class
Homo sapiens MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L43528 Homo sapiens (clone K620
                                                                                                                                                                                          -MODEL-frame-p20.model -DEV-x1p
-Q-/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
-Q-/cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
-Q-/cgn1_1/USPTO_spool/US08653294/runat_0402000_160701_15779/app_query.fasta.2
-DB-Genembl -Q-FM-fastap -SUFFIX-rege -G-ROP-12.000 -GAPEXT-4.000
-QGAPEXT-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -FGAPOP-4.500
-GAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL
-OUTFWT-pfs -NORM-ext -MINLEN-0 -MAXIEXEN-1000000 -USER-US08653294
-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF030931 H
AF067436 H
AF030911 H
                                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF030927
     out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
22700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176.920000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM of: US-08-653-294-33 to:
                                                   M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search information block:
Query: US-08-653-294-33
Query length: 15
                                                                                                                                                                           Command line parameters:
                                                   Date: Feb 8, 2000 10:25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_pr2:ниминидар
gb_pr3:нA1109нLA1
gb_pr3:нS507нLA1
gb_pr3:нS522HLA1
gb_pr3:нS5342HLA1
gb_pr4:нS2301HL1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_pat:114593
gb_pr1:HSHLAAL1
gb_pr2:HSA011699
gb_pr2:HSA239035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pr2:HSHL24JV01
gb_pr2:HSHL24SA01
gb_pr2:HSHL24YM01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_pr2:L43528
gb_pr3:HS1109HLA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_pr3:HS2402HLA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_prl:HSHLAKI
gb_pr2:GGU37323
gb_pr1:PPU05575
gb_pr1:PPU05578
gb_pr1:GGB0101
gb_pr1:GGB0103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_pr1:PTU05582
gb_pr4:AF115460
gb_pr2:PTCHLAB1
gb_pr1:CHPMHCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_pr2:HSU36914
gb_pr2:HSU25971
gb_pr1:HSHLABHBA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_pr3:HS538HLA1
gb_pr3:HS611HLA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pr1:GGB0103
gb_pr2:HLU50091
gb_pr1:PTU05580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_pr1:HSHLABHBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JD_pr2:HSHLA24S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_pr4:AF022159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pr2:HSU18659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_pat:I14590
gb_pat:I14591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_pat:114592
gb_pat:114593
```

¥

a

```
US-08-653-294-33 x HUMHLABC
                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                  seq_name: gb_prl:HSHLAK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213
                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                Align seg 1/1
                                                                                                                                                                                               DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REITVGYVDDTLEYNDSDAASPEEPRAPHEOEGFEWNDERMILEN SARVONER
RIALRYYNQSEAGSHTLONMYGCDVGPDGRLIRGYHQDAYDGKDY IALNEDLSSWTAA
DTAAOITORKWEAARYAEOLRAYLEGECVEWLRRYLENGKETLORADPRTHYTHHPI
SDHEATLRCWALGFYPAEITLTWQROEDGYDDTELVETRPAGDRTFOKWAVVVPSG
EEDRYYTHVOHSGLEYRLITRWEDSSOSTVPIVGIVAGLAVLAVVYIGAVVAAVWCRR
KSSGGKGGSYSQAACSDSAGGSDVSLTA"
                                                                                               HUMHLABC 1089 bp mRNA. PRI 11-JUL-1995
Homo sapiens (clones 18.1, 18.2, 19.2) MHC class I HLA-B*2702 mRNA,
complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'translation-"MRVTAPRTLLLLLWGAVALTETWAGSHSMRYFHTSVSRPGRGEP
                                                                                                                                                               L38504
L38504.1 GI:896270
cell surface glycoprotein; class I gene;
integral membrane protein; major histocompatibility complex.
Homo sapiens (clone: B18.1) cDNA to mRNA; Homo sapiens (clone:
18.2) cDNA to mRNA; and Homo sapiens (clone:
HOMO sapiens
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="major histocompatibility complex"
/protein_id="AAA69724.1"
/db_xref="G1:896271"
                                                                                                                                                                                                                                                                                                                1 (bases 1 to 1089)
Parham,P., Arnett,K.L. and Adams,E.J.
On the nucleotide sequences of B*2702 and B*2705
Unpublished (1995)
 Length: 15
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_line="NV"
/cell_type="EBV-transformed B-cell"
/haplotype="HLA A2/3; B7; Cw2,7"
/clone="18,2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 t
                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1.1089
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="B18.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1022. .1054
/gene="HLA-B*2702"
1055. .>1089
/gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         620. .895
/gene="HLA-B*2702"
896. .1021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74. .343
/gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /qene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 344. .619
/gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396. .1021
/gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <1. .73
/gene="HLA-B*2702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="19.2"
/map="6p21.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 4.933
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74.00
                                                               seq_name: gb_pr2:HUMHLABC
                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
FEATURES
                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                   SOURCE
```

```
join(79. .151,280. .549,793. .1068,X03667.1:6. .281,
X03667.1:373. .489,X03667.1:930. .962,X03667.1:1069. .1112)
/gene="HLA-B27K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .1241,

/do_xansh="Homo sapiens"

/do_xref="taxon:9606"

/cell_line="BRUG"

/loh(c/9: .151,280. .549,793. .1068,X03667.1:6. .281,

X03667.1:373. .489,X03667.1:930. .962,X03667.1:1069. .1116,

X03667.1:1299. .>1639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAA27301.1"
| Datein_id="Cara7301.1"
| Datein_id="Gara71801.20"
| Datei="Sara71801.0317"
| Abaref="Sara71801.0317"
| Cranslation="MRVTAPRTLLLLIMGAVALTETWAGSHSMRYFHTSVSRPGRGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFITVGYVDDTLFVRFDSDAASPREEPRAPWIEQEGPEYWDRETQICKAKAQTDRENL
RIALRYYNQSEAGSHTLQNWYGCDVGPDGRLLRGYHQDAYDGKDYIALNEDLSSWTAA
DTAAQIIQRKWEAARVAEQLRAYLEGECVEWLRRYLENGKETLQRADPPKTHYTHHPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDHEATLROWALGFYPAEITLFWQRDGEDQTQDTELVETRPAGDRTFQKWAAVVVPSG
EEQRYTCHVQHEGLPKPLTLRWEPSSQSTVPIVGIVAGLAVLAVVVIGAVVAAVMCRR
KSSGGKGGSYSQAACSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(79. 151,280. 549,793. .1068,X03667.1:6. .281,
X03667.1:373. 489,X03667.1:930. .962,X03667.1:1069.
/gene="HIA-B27K"
                                                                                                                                                                                                                      HSHLAKI 1241 bp DNA PRI 28-JAN-1997
Human class I MHC gene HLA-B27K exons 1-3 (BRUG cell line)
X03664
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases I to 1241)

2 Seemann, G.H., Reln, R.S., Brown, C.S. and Ploegh, H.L.

Gene conversion-like mechanisms may generate polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             380 bp of intron III missing. Sequence continued in X03667. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                           X03664.1 GI:32236 class I antigen; histocompatibility antigen; major histocompatibility complex; signal peptide.
                                                                                 280 AAGGCACAGAGTGGACGAGAGAACCTGCGGGATCGCGCTCCGCTAC 324
                                                     1 LysalaGlnThraspargGluAsnLeuArgIlealaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 class I genes
EMBO J. 5 (3), 547-552 (1986)
86220133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ρ
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <79. .151
/qene="HLA-B27K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /ys. .lubs
/gene="HLA-B27K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280. .549
/gene="HLA-B27K"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label-HLA_mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1/label=HLA CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-ex2
793. .1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=ex3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 74.00
Ratio: 4.933
Percent Similarity: 100.000
  to: HUMHLABC
```

```
/traislation="Villesaalaltetwagshsmryfdtavsrpgagepreitvgyv
DDTOGVREDSDASSREEPRAPWMEDEGPEYWDRNYGICKAQAQTDRENLRTALRYYN
GEAGSHILDRAYGDVGDORGLICK SYGSAYDGROYIALBLESYNAADTAAQITO
RKWEARVAEQLRAYLGGLOYPGWLRRYLENGKTLORADPRYTHVTHPISDHEATLE
CWALGFYPAEITLTWRDGEDOTQDTELVETRRAGDRTFOKWAAVVPSGQEORYTCH
VQHEGLPEPLILRWEPSSGSTIPIVGIVAGLAVLAVVTGAVVAAVWCRRKSSGGRGG
                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPT005578 1065 bp mRNA PRI 08-OCT-1994
Pan paniscus class I histocompatibility antigen Papa-B (Papa-B-02 allele) mRNA, partial cds.
U05578 U05578.1 GI:454773
                                                     PPU05575 1065 bp mRNA PRI 08-OCT-1994 Pan paniscus class I histocompatibility antigen Papa-B-03
                                                                                                                                                                 pygmy chimpanzee.
Pan paniscus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Euthoria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1065)
McAdam,S.N., Boyson,J.E., Liu,X., Garber,T.L., Hughes,A.L.,
Bontrop,R.E. and Watkins,D.I.
A uniquely high level of recombination at the HLA-B locus
Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="class I histocompatibility antigen"
/protein_id="AAA50178.1"
/db_xref="G1:454768"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               256 CAGGCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 LysalaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 15
Gaps: 0
Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1065
/organism="Pan paniscus"
/isolate="Lorel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="HLA-B"
/note="HLA-B-03 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SYSQAASSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9597"
1. .1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 g
                                                                                          allele) mRNA, partial cds.
U05575
U05575.1 GI:454767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'gene-"HLA-B"
                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1065)
Boyson, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            328 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: PPU05575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-33 x PPU05575
seq_name: gb_pr1:PPU05575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_pr1:PPU05578
                                     seq_documentation_block:
LOCUS PPU05575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS PPU05578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ಥ
                                                                                                                                                                                                                                                                                                                            Proc. Nat
94286544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
                                                         LOCUS
DEFINITION
                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                            ACCESSION
                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="SHSMRYFDTAVSRPGRGEPRFITVGYVDDTQFVRFDSDAASPRW
EPRAPWIEQEGPEYWDREIQTSKAQAQTDRENLRIALRYYNGSEAGSHTIQMWYGCDM
GPDGRLLRGYSQSAYDGKDYIALNEDLSSWTAADTAAQITQRKWEAAREAEQLRAYLE
GTCVEWLRRYLENGRRILQRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Memorial
New York, NY
                                                                                                                                                                                                                                                                                                                                      Gorilla gorilla
Bukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Primates; Catarrhini; Hominidae; Gorilla.
1 (bases 1 to 792)
Cereb.N., Kong.Y., Lee,S., Maye,P. and Yang,S.Y.
Nucleotide sequences of MHC class I introns 1, 2, and 3 in humans
and intron 2 in nonhuman primates
                                                                                                                                                                                                                        GGU37323 792 bp DNA PRI 21-MAR-1997
Gorilla gorilla MHC class I B antigen gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tang, S.Y. and Cereb, N.
Direct Submission
Submitted (29-SEP-1995) Soo Yang, Immunology Program, Sloan-Kettering Cancer Center, 1275 York Ave, Box 41, 10021, USA
                                                                                          207 CAGGCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 LysalaGlnThraspargGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(1. .270,517. .>792)
/codon_start=3
/product="MRC class I A antigen"
/protein_id="AAB49915.1"
/db_xref="G1:1654123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .792
/organism="Gorilla gorilla"
/db_xref="taxon:9593"
/cell_line="ROK B cell line"
/clone="ROK1/2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                         to: 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: GGU37323 from: 1
                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome=
                                                                                                                                                                                                                                                                                 U37323.1 GI:1654122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number=2
271. .516
/number=2
517. .792
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-33 x GGU37323
                                                       Align seg 1/1 to: HSHLAK1
alignment_block:
US-08-653-294-33 x HSHLAK1
                                                                                                                                                                   seq_name: gb_pr2:GGU37323
                                                                                                                                                                                                        seq_documentation_block:
LOCUS GGU37323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96408732
                                                                                                                                                                                                                                                                                                                      gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
```

Tare.

```
/translation="MRVTAPPTLLLLLSAALALTETWAGSHSMRYFDTAVSRPGRGEP
RFITVGYVDDTQFVRFDSDAASPRWEPRAPWIEQEGPEYWDRETQTSKAQAQTDRENL
RIALRYYNQSEAGSHTIQRWFGCDVGPDGRLLRGYSQSAYDGKDYIALNEDLSSWTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DTAAQITQRKWEAAREAĒQLRAYLEGTCVEWLRRYLĒNGRETLQRADTPKTHVTHHPI
SUBBATLRKORALGFYPAEITLIWWORDEDQTQDTELVEERRAGGGTFQKWAAVVVPSG
EERRYTCHVQHEGLFKPLTLRWEPSSQSTIPIVGIVAGLAVLAVVVIGAVVTAVICRR
KSSGGKGGSYSQAALSBSAQGSDVSLTA"
Medicine, Dept of Cell Biology, Stanford CA 94305, USA
2 (bases 1 to 1089)
S Lawlor, D.A., Warren, E.
Gorilla class I major histocompatibility complex alleles:
Comparison to human and chimpenzee class I
J. Exp. Med. 174 (6), 1491-1509 (1991)
E 92078860
See x60248-59 & x60692-3.
Location/Qualifiers
I. 1270
//organism="Gorilla gorilla"
                                                                                                                                                                                                                                      /db_xref="taxon.9593"
/cell_type="lymphoblast"
/cell_line="Banga B lymphoblastoid cell line"
/clone_lib="BaB192"
1...1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MhcGogo-B0101"
/product="Mhc class I heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 15
Gaps: 0
Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="Mhc class I heavy
/protein_id="CAA42807.1"
/db_xref="GI:22866"
/db_xref="SWISS-PROT:P30379"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene-"MhcGogo-B0101"
73. .1086
                                                                                                                                                                                                                                                                                                                                                /gene-"MhcGogo-B0101"
                                                                                                                                                                                                                                                                                                                                                                                  'gene="MhcGogo-B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene-"MhcGogo-B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1046. .1089
/gene="MhcGogo-B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344. .619
/gene="MhcGogo_B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620. .895
/gene="MhcGogo_B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        896. .1012
/gene="MhcGogo-B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1013. .1045
/gene="MhcGogo-B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="cytoplasmic 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MhcGogo-B0101"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="transmembrane'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="cytoplasmic
/number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410
                                                                                                                                                                                                                             /isolate="Banga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="alpha 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="alpha 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"alpha
                                                                                                                                                                                                                                                                                                                                                                                                         /number-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'number=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "number"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 70.00
Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3'UTR
BASE COUNT
ORIGIN
                       REFERENCE
AUTHORS
TITLE
                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                  COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                         Boyson, J.E.
Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Frectional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"VLLLLSAALALTETWAGSHSMRYFYTSVSRPGAGEPRFISVGYV
DDTOGYNEDSDAASRPEEPRAPWAGSCPEYWDNYGJCKAGAGTDERULRTALRYYN
OSEAGSHTLOTMYGCDVGFDGRFLRGYRGFAYDGRNYGJCKAGAGTDERULRTALRYYN
OSEAGSHTLOTMYGCDVGFDGRFLRGYRGFAYDGRNYGLNEDLSSWTAADTAAGITG
RKWEAARVAEOGNAYLEGLCVEWLRRYLENGKRTLCARADPRKTHVTHHISDHEATLK
CWALGFYPAEITLTWGRDGEDCTQDTELVETRPAGDRTFQKWAAVVVPSGGEGRYTCH
VYGRGLPEPLILRWEPSSQSITPIVGIVAGLAVVTGAVVAAVMCRRKSSGGRGG
SYGGASSDSAGSSSSAGTA"
171 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B locus allele; Class I major histocompatibility gene; heavy chain; major histocompatibility gene; peptide binding protein; transplantation antigen.
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.

1 (bases 1 to 1270)
Lawlor, D.A.

Direct Submission
Submitted (25-JUN-1991) D.A. Lawlor, Stanford Univ School of
                                                                                                      McAdam, S.N., Boyson, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bortrop, R.E. and Warkins, D.I.
A uniquely high level of recombination at the HLA-B locus Proc. Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGB0101 1270 bp mRNA PRI 01-JUL-
G.gorilla MhcGogo-B0101 gene for Mhc class I heavy chain.
X60255
X60255.1 GI:22865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"class I histocompatibility antigen"
/protein_id-"AAA50181.1"
/db_xref-"GI:454774"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 15
Gaps: 0
Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1065

    1065
    /organism="Pan paniscus"
/isolate="Bosondjo"
/db_xref="taxon:9597"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="HLA-B-02 allele"
                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HLA-B"
                                                                                                                                                                                                        (bases 1 to 1065)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1065
      pygmy chimpanzee.
Pan paniscus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 70.00
Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: PPU05578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-33 x PPU05578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gorilla gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _documentation_block:
US GGB0101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr1:GGB0101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
    SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                              TITLE
JOURNAL
MEDLINE
REFERENCE
                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                     REFERENCE
                                                                                                          AUTHORS
                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
```

```
gorilla.
                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                      3'UTR
                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                     exon
                                   exon
                                                                                                    exon
                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   x60693.1 GI:22867
B locus allele: Class I major histocompatibility gene; heavy chain;
major histocompatibility gene; peptide binding protein;
transplantation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation = "MRVTAPRTLLLLLSAALALTETWAGSHSMRYFDTAVSRPGRGEP"
                                                                                                                                                                                seq_documentation_block:
LoCUS GGB0102 1270 bp mRNA PRI 07-FEB-1992
DEFINITION G.gorilla MhcGogo-B0102 gene for Mhc class I heavy chain.
ACCESSION X60693
                                                                                                                                                                                                                                                                                                                                             Eukaryota; ------ Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhin; Hominidae; Gorilla.
1 (bases 1 to 1270)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-70N-1991) D.A. Lawlor, Stanford Univ School of Medicine, Dept of Cell Biology, Stanford Ca 94305, USA 2 (bases 1 to 1089)
Lawlor, D.A., Warren, E., Taylor, P. and Parham, P. Comparison to human and chimpanzee class I comparison to human and chimpanzee class I J. Exp. Med. 174 (6), 1491-1509 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /isolate="calabar yorinia"
/db.aref="taxon:9593"
/cell_type="lymphoblast"
/cell_tine="calabar B lymphoblastoid cell line"
/clone_lib="CaB181"
                                                                                                  280 CAGGCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                 1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'product="Mhc class I heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MhcGogo-B0102"
/codon_start=1
/product="Mnc class I heavy c
/protein_id="CAA43101.1"
/db_xref="G1:22868"
/db_xref="SWISS-PROT:P30380"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSSGGKGGSYSQAASSDSAQGSDVSLTA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           See X60248-59 & X60692-3.
Location/Qualifiers
1 1270
/organism="corilla gorilla"
                                                 from: 1 to: 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MhcGogo-B0102"
/note="alpha 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="MhcGogo-B0102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="MhcGogo-B0102"
/number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73. .1086
/gene="MhcGogo-B0102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="MhcGogo-B0102
                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                               to: GGB0101
                                                                                                                                                                                                                                                                                                                                      Gorilla gorilla
               US-08-653-294-33 x GGB0101
                                                                                                                                                  seq_name: gb_pr1:GGB0102
                                                                                                                                                                                                                                                                                                                                                                                                           Lawlor, D.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Exp. M
92078860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mat_peptide
alignment_block
                                               Align seg 1/1
                                                                                                                                                                                                  LOCUS
DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                      SOURCE
```

```
B locus allele; Class I major histocompatibility gene; heavy chain; major histocompatibility gene; peptide binding protein; transplantation antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (25-JUN-1991) D.A. Lawlor, Stanford Univ School of Medicine, Dept of Cell Biology, Stanford CA 94305, USA 2 (bases 1 to 1089)
Lawlor, D.A., Warren, E., Taylor, P. and Parham, P. Gorilla class I major histocompatibility complex alleles: comparison to human and chimpanzee class I
J. Exp. Med. 174 (6), 1491-1509 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Vertebrata; Mammalía; Eutheria;
Primates; Catarrhini; Hominidae; Gorilla.
1 (bases 1 to 1270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:

LOCUS GG90103 1270 bp mRNA PRI 07-FEB-
DEFINITION G-gozilla MhcGogo-B0103 gene for Mhc class I heavy chain.

VERSION X60254
VERSION X60254.1 GI:22869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 CAGGCACAGACTGACGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 15
Gaps: 0
Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             See X60248-59 & X60692-3.
Location/Qualifiers
1.1270
/organism="Gorilla gorilla"
                                                                                                                                                                                                                                                                                                                                                                                                            217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 1270
                                                                                                                                                                                                                                                            /note="cytoplasmic 1"
/number=6
1046..1089
/gene="MhcGogo-B0102"
/gene="MhcGogo-B0102"
/note="alpha`2"
                                                                                                                                       896. .1012
/gene="MhcGogo-B0102"
/note="transmembrane"
                                                                                                                                                                                                                      1013. .1045
/gene="MhcGogo-B0102"
                                                                                                                                                                                                                                                                                                                                               /note="cytoplasmic 2"
                                                               620. .895
/gene="MhcGogo-B0102"
                                                                                                                                                                                                                                                                                                                                                                                                            Б
                                                                                                                                                                                                                                                                                                                                                                                                          410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /isolate="Banga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: GGB0102 from: 1
                                                                                                   /note="alpha 3"
                                                                                                                                                                                                                                                                                                                                                                                   0. .>1270
388 c
                                          'number=3
                                                                                                                           'number-4
                                                                                                                                                                                                       'number=
                                                                                                                                                                                                                                                                                                                                                                    'number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 70.00
Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-33 x GGB0102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gorilla gorilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr1:GGB0103
                                                                                                                                                                                                                                                                                                                                                                                                            255 a
```

exon

CDS

```
CWALGFYPAEÏTLTWQRDGEDQTQDTELVETRPAGĎRTFQKWVAVVPSGEEGRYTCH
VQHEGLPEPLTLRWEPSSQSTIPIVGIVAGLAVLAVVVTGAVVAAVWWRRKSLGGKGG
                                   Hylobates lar
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
1 (bases 1 to 1065)
Chen, Z.W., McAdam, S.N., Hughes, A.L., Dogon, A.L., Letvin, N.L. and Watkins, D.I.
                                                                                                                                            Molecular cloning of orangutan and gibbon MHC class I cDNA. The HLA-A and -B loci diverged over 30 million years ago J. Immunol. 148 (8), 2547-2554 (1992)
                                                                                                                                                                                                                         Chen.Z.W., McAdam.S.N., Hughes,A.L. and Watkins,D.I.
Chen.Z.W., McAdam.S.N., Hughes,A.L. and Watkins,D.I.
Direct Submission
Submitted (27-FEB-1996) Pathology, Wisconsin Regional Primate
Research Center, 1220 Capitol Court, Madison, WI 53703, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McAdam, S.N., Boyson, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bohtrop, R.E. and Warkins, D.I.
A uniquely high level of recombination at the HLA-B locus
Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
94286544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pan troglodytes class I histocompatibility antigen Patr-B (Patr-B-09 allele) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 14
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       259 GCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 AlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                          1. .1065
/organism="Hylobates lar"
/db_xref="taxon:9580"
<1. .1065
/note="Hyla B*01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSKAASSDSAQGSDVSLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: HLU50091 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
Locus PTU05580 1068 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 1068)
Boyson, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 69.00
Ratio: 4.929
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-33 x HLU50091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chimpanzee.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_pr1:PTU05580
                                                                                                                                                                                                          92218857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                              source
                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                          MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                        JOURNAL
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                      cos
                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                  TITLE
                                                                                                                                                                                                                           RF ITVGYVDDTQFVRFDSDAASPRMEPRAPWIEQEGPEYWDRETQTSKAQAQTDRENL
RIALRYYNQSEAGSHTIQWMYGCDMGPDGRLLRGYSQSAYDGKDYIALNEDLSSWTAA
                                                                                                                                                                                                                                                           DTAAOITORKWEAAREAEOLBAYLEGTCVEWIRRYLENGRETLORADPRYTHYHPI
SDHEATLRCWALGFYPAEITLTWQRDGEDQTQDTELVETRPAGDGTFQKWAAVVVPHD
EEERYTCHVQHEGLPKPLTLRWEPSSQSTIPIVGIVAGLAVLAVVJGAVVTAVICRR
KSSGGKGGSYSQAASSDSAQGSDVSLTA"
                                                                                                                                                                                                          'translation = "MRVTAPRTLLLLSAALALTETWAGSHSMRYFDTAVSRPGRGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLU50091 1065 bp mRNA PRI 14-SEP-1996
Hylobtes lar MHC class I (Hyla B*01) mRNA, partial cds.
U50091 GI:1545833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 CAGGCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LysalaGlnThraspargGluasnLeuargIlealaLeuargTyr 15
                                                                                                                              /product="Mhc class I heavy chain"
/protein_id="CaA42866.1"
/db_xref="G1:22870"
/db_xref="SMISS-PROT:P30381"
                                                                                                                                                                                                                                                                                                                                                                                73. .1086
/gene="MhcGogo-B0103"
/product="Mhc class I heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Leuyin: 15
Gaps: 0
Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: GGB0103 from: 1 to: 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1013. 1045
/gene="MhcGogo-B0103"
/note="cytoplasmic 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 444. .619
'gene="MhcGogo_B0103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     896. .1012
/gene="MhcGogo-B0103"
'gene-"MhcGogo-B0103"
                                 /gene="MhcGogo-B0103"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /4. .343
/gene="MhcGogo-B0103"
/note="alpha 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="MhcGogo-B0103"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1046. .1089
/gene="MhcGogo-B0103"
                                                                                                                                                                                                                                                                                                                                                              'gene="MhcGogo-B0103"
                                                                                           'gene="MhcGogo-B0103'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="cytoplasmic 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note-"transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note-"alpha 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="alpha 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     388
                                                     'number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'number=4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 70.00
Ratio: 4.667
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-33 x GGB0103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_pr2:HLU50091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS HLU50091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3'UTR
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
```

exon

exon

ORIGIN

exon

```
/COUNTAINER |
//COUNTAINER |
//COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="MHC class I antigen"
/product="de="Aa402439.1"
/db_xref==GI:6049043"
/tb_xref==GI:6049043"
/translation="MQVTAPRTVLLLSAALALTETWAGSHSMRYFYTAVSRPGRGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AF115460 1089 bp mRNA
DEFINITION Pan troglodytes isolate 35B-1 MHC class I antigen (HLA-B) mRNA,
complete cds.
ACCESSION AF115460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 1089).
Matsul,M., Machida,S., Feinstone,S.M. and Akatsuka,T.
Molecular analyses of five new chimpanzee MHC class I alleles:
implications for differences between evolutional mechanisms of
HIA-A, -B, and -C loci
Blochem. Blophys. Res. Commun. 261 (1), 46-52 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 1089)
Matsui,M., Machida,S., Feinstone,S.M. and Akatsuka,T.
Direct Submission
Direct Submission
Moroyama-Cho, Iruma-Gun, Saitama 350-0495, Japan
Location/Qualifiers
1. 1089
/organism="Pan troglodytes"
/isolate="358-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 14
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1068
                                                                                                                           /note-"HLA-B-10 allele"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                            <1. .1068
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .1089
/gene="HLA-B"
      1. .1068
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF115460.1 GI:6049042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 69.00
Ratio: 4.929
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: PTU05582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-33 x PTU05582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_pr4:AF115460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chimpanzee.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="class I histocompatibility antigen"
/protein_id="AAA50183.1"
/db_xref="d1:454778"
/db_xref="d1:454778"
/translation="VLLLSAALALFEWAGSHSMRYFYTSVSRPGRGEPRFITVGYV
/translation="VLLLSAALALFEWDREFRNMKASAQTDRENLRIALRYIN
OSEAGSHIIDQRWYGCDMGPDGRLLRYYQYQYDGRORGENTANEDLSSWFADTAAQITQ
RKWEARAAADGRAALEGTCVEWLRRYLENGKETLCRAADPRATHTHPISDHEATLR
CWALGFYPAEITLTWQRDGEDQTQDTELVETRPEGDRTFOKWAAVVVPSGEEQRYTCH
GSYSGAASSDSAGGSTSIPIVGIVAGLAVLVYTVAVVAAVVAAVLCRRKSSGGRG
GSYSGAASSDSAGGSTSIPIVGIVAGLAVLVYTVAVVAAVVAAVLCRRKSSGGRG
GSYSGAASSDSAGGSTSIPIVGIVAGLAVLTVATVAVVAAVVAAVLCRRKSSGGRG
327 c 354 g 175 t
   Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boyson, J.E.
Direct Submission
Submitted (25-JAN-1994) Jonathan E. Boyson, Watkins Unit, Wisconsin
Regional Primate Research Center, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTU05582 1068 bp mRNA PRI 08-0CT-1994 Pan troglodytes class I histocompatibility antigen Patr-B (Patr-B-10 allele) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan. 1 (bases I to 1068) MacAdam, S.N., Boyson, J.E., Liu, X., Garber, T.L., Hughes, A.L., Bontrop, R.E. and Watkins, D.I. A uniquely high level of recombination at the HIA-B locus Proc. Natl. Acad. Sci. U.S.A. 91 (13), 5893-5897 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 14
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             259 GCACAGACTGACCGAGAACCTGCGGATCGCGCTCCGCTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 AlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. 1068
/organism="Pan troglodytes"
/isolate="Renee"
/db_xref="taxon:9598"
                                                                                                                                                                           /organism="Pan troglodytes"
/isolate="Teppie"
/db_xref="taxon:9598"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 1068
                                                                                                                                                                                                                                                                                                                                                                                                /note="HLA-B-09 allele"
/codon_start=1
                                                                                                                        Location/Qualiflers
1. .1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                       /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                       <i. .1068
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (bases 1 to 1068)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U05582.1 GI:454781
                                                                                                                                                                                                                                                                                 .1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 69.00
Ratio: 4.929
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: PTU05580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           us-08-653-294-33 x PTU05580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pr1:PTU05582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS PTU05582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chimpanzee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment block:
                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
```

```
RIALRYYNOSEAGSHYWOTMYCCDVGPDGRLLRGYGOFAYDGKDYIALNODLSSWTAA
DTAAOITORKWEAARVAEQLRAYLEGTCVEWLRRYLENGKETLORADPPKTHVTHHPI
SDHEATLRCWALGFYPALITLWWRDGEDQTODTELVETRPAGDRTFOKWAAVVVPSG
EEQRYTCHVOHEGLFRPLTLRWEPSGSTIPIVGIVAGLAVLAVVVIGAVVAAVWGRR
KSSGGKGGSYGOSEDSAGSBDVSLLA"
338 c 363 g 173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SWISS-PROT:P13750"
/translation="APRTVLLLLSAALALTETWAGSHSMRYFYTSVSRPGRGEPRFIT
VGYVDDTQFVRFDSDAASPRWEPRAPWIEQEGPEYWDRETRNWKASAQTDRENLRIAL
rfitvgyvddtofvrfdsdaasprmeprapwieoegpeywdretrnvkasaotdrenl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (03-077-1988) W.E. Mayer, Stanford University, Dept. of
Submitted (03-077-1988) W.E. Mayer, Stanford CA 94305-5020, USA
2 (bases 1 to 1507)
Mayer, W.E., Jonker, M., Klein, D., Ivanyi, P., van Seventer, G. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution EMBO J. 7 (9), 2765-2774 (1988) 89030641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalía; Eutheria;
Primates; Catarrhin; Hominidae; Pan.
1 (bases 1 to 1507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="ChLA-B1 protein precursor (1 is 2nd base in (AA -21 to 339)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission Submission Submitted (17-FEB-1989) to the EMBL/GenBank/DDBJ databases Position 607 is c in [1], [3] and u in [2]. Location/Qualifiers 1.1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTCHLABI 1507 bp mRNA PRI 27-MAR-19 Chimpanzee mRNA for class I antigen ChLA-B1. X13115 X12781 X13115.1 G1:38205 antigen; cell surface glycoprotein; class I antigen; major histocompatibility complex; surface antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="Hugo-EBV"
/cell_line="Hugo-EBV"
/clone="plB1, plB4."
<1. .62
/product="leader peptide (AA -21 to -1)"
                                                                                                                                                                                                                                                 Length: 14
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Pan troglodytes"
/db_xref="taxon:9598"
/chromosome="5."
                                                                                                                                                                                                                                                                                                                                                                                                      to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /proteIn_id="CAA31507.1"
/db_xref="G1:755776"
                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 1507)
                                                                                                                                                                                                                                                 Quality: 69.00
Ratio: 4.929
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AF115460
                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-33 x AF115460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chimpanzee.
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pr2:PTCHLAB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS PTCHLAB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mayer, W.E.
                                                                                                                                    215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mayer, W.
                                                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
COMMENT
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                           ORIGIN
```

```
QITQRKWEAAREAEGRRAYLEGTCVEWLRRYLENGKETLQRADPPKTHVTHHPISDHE
TRCWALGPYPAEITLYWQROGEDQTQDTELVETRPEGDRTPCKWAAVVPSGGEGQR
YTCHVQHEGLPKPLILEWEPSSQSTIPIVGIVAGLAVLVVTVAVVAVWAVWGRRKSS
GGRGGSYSQAASSDSAQGSDVSLTA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89235215
Draft entry and computer readable sequence for [2] kindly submitted
RYYNQSEAGSHTWQTMYGCDMGPDGRLLRGYGQYAYDGKDYIALNEDLSSWTAADTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHPMHCAA 1537 bp mRNA PRI 27-SEP-1993
Chimpanzee MHC class I ChlA chain mRNA, complete cds, clone 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M24045 M24029
M24045.1 GI:176814
cell surface glycoprotein; class I gene;
integral membrane protein; major histocompatibility complex.
Chimpanzee (Tank) EBV-transformed B lymphoblastoid cell, cDNA mRNA, clone 39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 87; 1180 to 1537)
                                                                                                     /product-"ChLA-B1 mature protein (AA 1-339)" 63. 332 /note-"alpha-1 domain" 333. .608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 88 to 1179)
Parhan, P., Lawlor, D.A., Lomen, C.E. and Ennis, P.D.
Diversity and diversification of HLA class I alleles
J. Immunol. 142, 3937-3950 (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 14
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 GCACAGACTGACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr
                                                                                                                                                                                                                       /note="alpha-3 domain"
885. 1001
/note="transmembrane domain"
1002. 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
/db_xref="taxon:9598"
/map="5"
                                                                                                                                                                                                                                                                                   1002. .1079
/note="cytoplasmic domain"
1486. .1491
                                                                                                                                                                                                                                                                                                                                                                                                    302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20. .1111
/note="MHC ChlA chain"
/codon_start=1
                                                                                                                                                                                          /note="alpha-2 domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"MHC Chla mRNA"
20. .1111
                                                                                                                                                                                                                                                                                                                                 /note="polyA signal" 1507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P.D.Ennis, 14-APR-1989.
Location/Qualifiers
1. .1537
                                                                                                                                                                                                                                                                                                                                                                              note="polyA site"
435 c 452 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                               63. .1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 69.00
Ratio: 4.929
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: PICHLAB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-33 x PTCHLAB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_pr1:CHPMHCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seg_documentation_block:
LOCUS CHPMHCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ennis, P.D.
                                                                                                                                                                                                                                                                                                                                                                                                    318
                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                    misc_feature
                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                              polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
```

A COLOR OF THE REAL PROPERTY.

```
/protein_id="AAA35424.1"
/db_xref="d1:176812"
/db_xref="d1:176812"
/db_xref="d1:176812"
/db_xref="d1:176812"
/db_xref="d1:176812"
/db_xref="d1:176812"
/db_xref="d1:176812"
RFITVGYVDDTOFVRFDDAASPRMEPRAPWIEQEGEPEWDRETRNVKASAQTDRENL
RIALRYYYDGSEAGSHTWQTMFGCDMPPOFALLARYQYYQYATORSDYILDBLSSWTAA
RIALRYYYDGSEAGSHTWQTMFGCDMPPOFALLARYCKBTLQRADPPKTHWTHPT
SDHEATITGKKWEAARAQCILRAYLEGTCVBWLRYLENGKETLQRADPFKTHWTHPT
SDHEATILRCWALGFYPAEITLTWQRAGEDQTQDTELVETRPEGDRTFGKWAAVVVPSG
EQRYTCHYQHEGLPRPTLRRREPSSQSTIPIVGIVAGLAVLVVTVAVVAVVAVVAVCR
RKSSGGRGGSSGGSSDVSLTA"
445 c 455 g 309 t.
```

324 BASE COUNT ORIGIN

alignment\_scores:

Quality: 69.00 Length: 14
Ratio: 4.929 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 100.000

alignment\_block: US-08-653-294-33 x CHPMHCAA

Align seg 1/1 to: CHPMHCAA from: 1 to: 1537

THIS PAGE BLANK (USPTO)

```
Sequence encoding cephalosp S.aureus topoisomerase IV g S.aureus mutant grlA coding Enterococcus faecalis genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA coding for antigen HLA B27 - and diagnostic reagents contg. such DNA, antigen or antibody
Claim 2; Page 4; 5pp; German.

Claim 2: Page 4; 5pp; German.

The DNA may be used as a hybridisation probe for detecting the HLA B27 gene, e.g. for assessing susceptibility to rheumatic disorders such as ankylosis spondylitis, or may be used to transform cells for prodn of HLA B27. The HLA B27 may be used to detect HLA B27 antibody in human serum, or to produce mono- or polyclonal HLA B27 antibodies for use in immunoassay.

Sequence 1026 BP; 213 A; 307 C; 344 G; 162 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-3-1991 (first entry)
Sequence of genomic DNA encoding human histocompatibility antigen
HLA-B 27.
                                                                                                                                                                                                                                                                      10-APR-1991 (first entry)
Sequence encoding the human histocompatibility antigen HLA B27.
Sequence encoding the human histocompatibility antigen HLA B27.
Sheumatic disorder; genetic screening; diagnosis;
ankylosing spondylitis; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ankylosing spondylitis; rheumatic disorder; diagnosis; Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 AAGGCACAGACTGACCGAGAGCTCCTGCGGACCCTGCTCCGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 15
Gaps: 0
Percent Identity: 80.000
  2325
2403
2403
5330
410.23
426.62
426.62
1.1e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                     cds
DE3342024-A.
DE3342024-A.
28-NOV-1985; 542024.
28-NOV-1985; DE-542024.
21-DEC-1985; DE-542576.
(BEHW ) BEHRINGWERKE AG.
Riethmuller G, Meo T, Weiss E, Szots H; WPI; 87-157893/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: N70935 from: 1 to: 1026
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cocation/Qualifiers
102.58
102.28
102.28
94.91
                                                                                                                                                                                                                     N70935 standard; DNA; 1026 BP. N70935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID N70225 standard; DNA; 3874 BP.
AC N70225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518. .590

*tag= a

/*tag= b

1090. .1506

/*tag= c

1932. .2357

/*tag= d

2450. .2566

/*tag= e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.00
4.538
86.667
  36.00
36.00
36.00
                                                                                                                                     seq_name: N_Geneseq_36:N70935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:N70225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-33 x N70935
                                                                                                                                                                                            seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
Percent Similarity:
N_Geneseq_36:N60607
N_Geneseq_36:T12562
N_Geneseq_36:T12573
N_Geneseq_36:X13261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                           NAME OF THE PART O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Len | Documentation | 1006 | 1206 | 1204 | 1205 | 1204 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1205 | 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 Carcinoembryonic antigen CEA-0
39 Carcinoembryonic antigen CEA-0
39 Carcinoembryonic antigen CEA-0
28 Carcinoembryonic antigen GEA-0
28 Human carcinoembryonic antigen gene of Leishmania chaqasi
19 K39 gene of Leishmania chaqasi
10000 Leishmania chaqasi
171 Streptococcus pneumoniae gene
171 Streptococcus pneumoniae gene
1 Open reading frame F from GS re
1 Open reading frame F from GS re
1 Open reading frame F from GS re
2 Complete GS region DNA sequence
804 Chicken embryo lethal orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Beta-glucuronidase-contg inser
1 Promoter sequence and N-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ! Complete genome sequence of fbpl cDNA for reverse genetic
                                                                                                                                                                                                                -MODEL-frame-p2n.model -DEV-x1p
-Q=/Cqn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/Cqn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q=/Cqn1_1/USPTO_spool/US08653294/runat_04022000_16000
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000
-GAPEXT=4.000 -MINMATCH=0.100 -KGAPOP=10.000 -KGAPEXT=0.500
-FGAPOP=4.500 -QGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE-pct
-ALIGN=15 -MODE-LOCAL -OUTFWT=Pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28171 !
110000
801 ! OF
     out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4435
4435
7995
43804
43804
780
1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0038
0.0182
0.0339
0.0339
0.0031
0.0161
0.0161
0.0161
0.0161
0.0161
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
1.0000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.95
556.18
1.1e+03
8.4e+03
OM of: US-08-653-294-33 to: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 873:190000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search information block:
Query: US-08-653-294-33
Query length: 15
                                                                                                                                                                                            Command line parameters:
                                                      Date: Feb 8, 2000 7:31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_36:T58840_3 + N_Geneseq_36:T74469 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_36:067868
N_Geneseq_36:138500
N_Geneseq_36:18184
N_Geneseq_36:092780
N_Geneseq_36:054352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:Q75974
N_Geneseq_36:Q75973
N_Geneseq_36:T05843
N_Geneseq_36:N92449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:T75431
N_Geneseq_36:Q70152
N_Geneseq_36:T42166
N_Geneseq_36:V52155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_36:T74479
N_Geneseq_36:T74478
N_Geneseq_36:T86375
N_Geneseq_36:X26690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:N70935
N_Geneseq_36:N70225
N_Geneseq_36:T61639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_36:029167
N_Geneseq_36:001834
N_Geneseq_36:001822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_36:Q71567
N_Geneseq_36:T36495
N_Geneseq_36:Q82807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:T46062
N_Geneseq_36:V70153
N_Geneseq_36:N81611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:T74470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:Q55089
N_Geneseq_36:N80055
N_Geneseq_36:Q05916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_36:005693
N_Geneseq_36:005701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:005701
N_Geneseq_36:012114
N_Geneseq_36:051474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36:067869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THREADS-1
```

```
SOCOCOCOCO STANDAR A MAD DA MARA DA MA
                                                                                                                                                                                                                                                                                                                                    Claim 1; p6; 13pp; German.

THE DNA may be used to detect the HLA-B 27 gene (opt. mutated) in human genetic material. The HLA-B 27 may be used to detect anti-HLA-B 27 antibodies in human serum. The antibodies may be used to determine HLA-B 27 levels in human serum, e.g. for diagnosis of rheumatic disorders, esp. ankylosing spondylitis.

Sequence 3874 BP; 751 A; 1094 C; 1171 G; 858 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "3' flanking region diagnostic for genetic predisposition to SNSA" 4270. .4556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "3' flanking region diagnostic for genetic predisposition to SNSA"
                                                                                                                                                                                                                                                                                               - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA B27 consensus sequence.
HLA B27; seronegative spondylarthropathy; ankylosing spondylitis;
Reiter's syndrome; arthritis; acute anterior uveitis; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/note= "HLA-B27 3' flanking region, downstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= d
/note= "absence of cytosine at this site is
indicative of a predisposition to SNSA"
                                                                                                                                                                                                                                                                                             DNA coding for human histocompatibility antigen HLA-B 27 for diagnosis and antigen and antibody prodn.
                                                                                                                                                      01-JAN-1985; DE-542024.
21-DEC-1985; DE-545576.
(BEHW ) BEHRINGWERKE AG.
S20: H, Weiss E, Dorner C, Lang M, Meo T, Riethmuller WPI; 87-17469/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                               litis.
1171 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 15
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: N70225 from: 1 to: 3874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3' untranslated region"
4112. .4556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-SEP-1995; US-522942.
(CEDA-) CEDARS SINAI MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _documentation_block:
T61639 standard; DNA; 6553 BP.
3009. .3041
/*tag- f
3148. .3191
/*tag- g
                             - f
.3191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3968. .6653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59.00
4.538
86.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:T61639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-33 x N70225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1997.
16-AUG-1996; U13256.
                                                                                                                                         116139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 97-192924/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9709450-A1.
                                                                                                                                         21-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                           EP-226069-A
                                                                                                                    24 -JUN-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ryan DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T61639;
         intron
                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ss; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mrna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
```

```
Detecting pre-disposition to seronegative spondylarthropathies - Trom the absence of a C residue at a specific position in the 3'-flanking region of the HLA B27 allele
Claim 1; Page 52-56; 68pp; Bng1sh.
C Genetic predisposition to seronegative spondyloarthropathies (SNSA) is detected by determining the absence of a cytosine nucleotide in the 3' flanking region (see also T61647-48) of an HLA-B gene at a position corresponding to nucleotide 4495 of the HLA-B27 consensus sequence given in T6163. Probes and primers (see also T61640-46) based on this region can be used in diagnostic assays to detect the genetic predisposition to SNSA, and permit the distinction of B27+ individuals who are resistant to SNSA from B27+ normal individuals who are resistant to SNSA from B27+ normal individuals sequence 6553 Bp; 1443 A; 1619 C; 2017 G; 1474 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysis of expression of gene structure, and prodn. of mouse model of human disease

mouse model of human disease

Disclosure: Fig 1; 8pp; Japanese.

The sequence shows the exon 2 alpha-1-domain of the human leukocyte antigen-Bw 52 gene. The complete gene may be introduced into non-human mammals, pref. rat or mouse, or their ancestors at the primary developmental biological step via transplantation into the zygote or embryo to generate transgenic non-human mammals incorporating the HiA-Bw 52 gene in both their germ cells and somatic cells. Transgenic non-human mammals contg. HIA-Bw 52 are useful for the analysis of expression of the gene, its structure, and prodn. of mouse models of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAR-1993 (first entry)
HLA-BW 52 exon 2 alpha-1 domain.
Human leukocyte antigen; transgenic; germ cells; somatic cells; expression; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transgenic non-human mammalian HLA-Bw 52 gene - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1087 AAGGCACAGACTGACCGAGAGGACCTGCGGACCCTGCTCCGCTAC 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 59.00 Length: 15
Ratio: 4.538 Gaps: 0
Percent Similarity: 86.667 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 13
Gaps: 0
Percent Identity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       See also 029166-72
9 A; 88 C; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q29167 from: 1 to: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: T61639 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID 029167 standard; DNA; 270 BP.
AC 029167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-1992.
203-MUG-1990; 207329.
03-AUG-1990; JP-207329.
(OLVU ) OLYMEDS OPTICAL CO.
WPI: 92-342893/42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:Q29167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.667 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-33 x T61639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-653-294-33 x Q29167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
```

14-FEB-1990.

ID DAY KE BOLD DE BOLD

alignment\_scores:

```
Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and immunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; Z0pp; English.

The human HLA-B51 gene was injected into fertilised mouse eggs and then these introduced into the uterus of a pseudo pregnant mouse. The young were tested to ensure incorporation of the gene into the chromosome, and one of them mated 3 times with a normal male to produce 16 young, seven of which carried the HLA-B51 gene. The transgeneic offspring were immunised with HLA-B51 gene. The spleen lymphocytes were fused with myeloma cells. Hybridomas
                                                                                                                                                                                                                                                                                                                                                        OCCUPAN 1991 (first entry)
HLA-B51 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas;
transgenic animals; HLA-B51 gene; ss.
Key
Location/Qualifiers
avon
1. 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 13
Gaps: 0
Percent Identity: 92.308
  Percent Identity: 92.308
                                                                                                                                                                                      285 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 323
                                                                                                                                                            3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              357
                                                                                                               to: 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="alpha 1-domain" 344. .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note-"alpha 3-domain"
96. .1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note-"alpha 2-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producing antibodies were selected.
                                                                                                               from: 1
                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID Q05693 standard; DNA; 1089 BP.
AC Q05693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number=6
1043. .1089
/*tag= g
/number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1013. .1042
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-AUG-1990.
07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= e
/number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=1
74. .343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.00
4.667
92.308
  Percent Similarity: 92.308
                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:Q05693
                                                                                                               to: Q01822
                                          alignment_block:
US-08-653-294-33 x Q01822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1089 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takiguchi M;
WPI; 90-255479/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   See also 2057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP-383183-A.
                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                       New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc. Claim 1; Page 11; 23pp; English.

The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells. Sequence 1086 BP; 224 A; 334 C; 356 G; 172 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New DNA for class 1 human leucocyte antigens and derived probes and transformed cells, useful for DNA typing, as immunogens etc.
Claim 2: ppil-12: 23pp: English.
The HLA class I DNA can be used a source of probes for use in DNA typing. Transformed cells, which are useful as immunogens, can be obtained by introducing these DNAs into eucaryotic cells.
Sequence 1086 BP; 33 3, 335 C; 336 G; 170 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 13
Gaps: 0
Percent Identity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13
213 CAGACTTACCGAGAGACCTGCGGATCGCGCTCCGCTAC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: Q01834 from: 1 to: 1086
                                                                                                                                                                               Sequence encoding HLA-B51 antigen.
Probe; HLA class I DNA; immunogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAY-1991 (first entry)
Sequence encoding HLA-Bw52 antigen.
Probe; HLA class I DNA; immunogen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1086
/*tag= a
                                                                                                                                                                                                                                                                                        10-AUG-1989.
11-AUG-1988: JP-200758.
(OLXU) Olympus Optical Co., Ltd.
Rano K. Takiguchi;
WPI; 90-046289/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-AUG-1988; JP-200758.
(OLVU) Olympus Optical Co., Ltd.
Kano K, Takiguchi;
WPI; 90-046289/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID Q01822 standard; DNA; 1086 BP.
                                                                                   seq_documentation_block:
ID Q01834 standard; DNA; 1086
                                                                                                                                                       19-MAR-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.00
4.667
92.308
                                          seq_name: N_Geneseq_36:Q01834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:Q01822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-33 x Q01834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R03142
                                                                                                                                                                                                                            Homo sapiens.
EP354580-A.
```

Homo sapiens

EP-354580-A. 10-AUG-1989

alignment\_scores:

Ë 173

```
19-MAY-1994 (first entry)
Journal probe with photoremovable protecting group.
Probe: hybridisation; scareening; target sequence; protecting group;
photoactivation; photochemical deprotection; ss.
                                                                                                                                                                                                                                                                                 Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Predetermined region formation on support reactive with predetermined region formation on support reactive with biological polymer - by attaching thiol cpd. and photochemical deprotection, for immobilising oligo-nucleotide probe array on polyvinylidene fluoride support, mol. electronic devices and sepn. stationary phases Example 7; Page 27; 34pp; English.

This oligonucleotide probe was immobilised on a solid support. probe carries a thiol group which is covalently coupled to a photochemically removable protecting group. Many probes can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HIA-BW53 game, DNA probe and transformant cells - used for immunisation, identifying specificity of antiserum etc. Claim 1; Page 1; 11pp; Japanese.

Probes comprising part of the sequence can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-BW53 antigen. See also J03112485 and J03112486. Sequence 1089 Bp; 222 A; 337.C; 356 G; 174 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 13
Gaps: 0
Percent Identity: 92.308
286 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286 CAGACTTACCGAGAGAACCTGCGGGATCGCGCTCCGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. .1089
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-ARR-1993; U03767.
24-ARR-1992; US-874849.
AFRY-) AFRYMAX TECHNOLOGIES NV.
FOGOT SP, MCGA11 GH, Sheldon EL;
WPI; 93-368981/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Q12114 from: 1
                                                                                                                                                                                    H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1991.
22-SEP-1989; 247697.
22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182991/25.
P-PSDB; R12463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q51474 standard; DNA; 30 BP.
AC Q51474;
                                                                                                                                                                       012114 standard; DNA; 1089 012114;
                                                                                                                                                                                                                                           29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 56.00
4.667
92.308
                                                                                          seq_name: N_Geneseq_36:012114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:Q51474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-33 x Q12114
                                                                                                                                                        seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                          HLA-Bw53 exon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-NOV-1993.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J03112487-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The spleen lymphocytes were fused with myeloma cells (P3x63-Ag8.653). Hybridomas producing antibodies were selected. Sequence 1089 BP; 223 A; 336 C; 359 G; 171 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Allotype specific monoclonal anti- HLA antibodies prodn. - using hybridomas derived from transgenic animals carrying HLA gene and limmunised with HLA antigen of different allotype Disclosure; Fig 1 A-G; 20pp; English. The human HLA-BW52 gene was introduced into mouse L cells and then these cells used to immunise one of the transgenic mice (see Q05693)
                                                                                                                                                                                                                                                                                                                                                                                                                   03-JAN-1991 (first entry)
HLA-Bw52 gene for production of monoclonal antibodies.
Alloptype specific monoclonal anti-HLA antibodies; hybridomas; transgenic animals; HLA-Bw52 gene; ss.
Location/Qualifiers
exon 1.73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 13
Gaps: 0
Percent Identity: 92.308
                                                                                                                                                                                286 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 324
                                                                                                                                                    3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                             to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="alpha 1-domain"
344. .619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="alpha 2-domain"
520. .895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-"alpha 3-domain"
196. .1012
                                                                                          Align seg 1/1 to: Q05693 from: 1
                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID Q05701 standard; DNA; 1089 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1013. .1042
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1043. .1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-1990.
07-FEB-1990; 102424.
08-FEB-1989; JP-029313.
(OLYU ) OLYMPUS OPTICAL KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/number=1
74. .343
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= e
/number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= g
/number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=4
                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:Q05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.00
4.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
alignment_block:
US-08-653-294-33 x Q05693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-653-294-33 x Q05701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 90-255479/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rakiguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP-383183-A
```

intron

exon

exon

exon

exon

exon

to: 1089

The

3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15

from: 1 to: 1089

Align seg 1/1 to: Q05701

alignment\_block:

STATE OF

```
PHIA-B7 expression vector.
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the gene is taken from the transposable element Tn903"
                   remove the protecting group and allow the probe to hybridise with a complementary sequence. Selective irradiation in defined regions will activate only those probes required/chosen to be used in a given screening of a sample solution. The invention allows simultaneous screenings for many different sequences in a single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3' LTR promoter region"
Immobilised on the solid support at one time and irradiation will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
1. 354
7.tag=
7.htag= pBR322 backbone contg. bacterial origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New vectors for gene therapy, partic for tumours - comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= e
note= "3' untranslated region of HLA-B7
                                                                                                                                                                                                                                                                                 Gaps: 0 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "SV40 polyA signal sequence" complement (1412, .1560)
                                                                                                                                                                                10 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= f
/note= "HLA-B7 open reading frame"
complement (2886. 3415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "SV40 small t intron"
complement (1561. .1794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= g
/note= "Rous sarcoma virus
                                                                                                                                                                                6
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (1795, .2880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nabel GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1410./*tag= c
                                                                                                                                                                                ე
ე
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy chain mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 GCACAGACTGACCGAGAGAACCTGCGG 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to reverse of: 051474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AlaGlnThrAspArgGluAsnLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lew D, Marquet M, Nabel EG, WPI; 95-036494/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID 075974 standard; cDNA; 4059
AC 075974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . .1170
                                                                                                                                                                                2 A;
                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-33 x Q51474/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seg_name: N_Geneseg_36:Q75974
                                                                                                                                                                                                                                                                                      Quality: 45.00
Ratio: 5.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNMI ) UNIV MICHIGAN. (VICA-) VICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     006069
                                                                                                                                                                                30 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-DEC-1994.
27-MAY-1994; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9429469-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3'utr
                                                                                                                                                          step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ltr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONTRACTOR OF THE PROPERTY OF 
888888888
```

```
genetic material encoding one or more cistron(s) which express immunogenic or therapeutic peptide(s)

(laim 9; Page 42-43; Sopp; English.

This HLA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resisitance gene. The eradication of two open reading frames encoding portions of SV40 viral proteins lowers the risk of tumourigenicity. The vector may also operate as a cassette into which cistrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest. The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain, derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3.3-Aug-1995 (first entry)
pHAA-B7/Deta-2 microglobulin expression vector.
expression vector; pHIA-B7/Deta-2 microglobulin; heavy human HIA-B7;
expression vector; pHIA-B7/Deta-2 microglobulin; heavy human HIA-B7;
Hight beta-2 microglobulin; class I major histocompatibility complex;
MHC; bicistronic mRNA; human leukocyte antigen; HLA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy chain mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region of a synthetic oligonucleotide which modifies this requiatory sequence to effect a higher level of expression of downstream sequences. The oligonucleotide removes a polyadenylation signal sequence originally found in the RSV DNA sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "tag= 1
note= "3' untranslated sequence of HLA-B7 heavy
                                                                                                                                                                                         Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "*tag- c
note- "HLA-B7 heavy chain open reading frame"
                                                                                                                                                                                         1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
/note= "Rous sarcoma virus LTR promoter do
for the Schmidt-Rupin strain nucleotides
8673-9146. This region also includes a 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- consensus_Kozak_signal_sequence
535. .1620
/*tag- c
                                                                                                                                                                                         1033 G;
                                                                                                                                                                                                                                                                                                                                                               4059
                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag* d
note= "encodes putative signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              putative HLA-B7
                                                                                                                                                                                                                                                                                                                                                               ::
2
                                                                                                                                                                                                                                                                                                                                                               Н
                                                                                                                                                                                         1051 C;
                                                                                                                                                                                                                                                                                                                                                               from:
                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-B7 heavy chain' 607. .1620
                                                                                                                                                                                                                                                                                                                                                                                           1 LysAlaGlnThrAspArgGluAsnLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    covalently closed circular DNA; ds Synthetic.
                                                                                                                                                                                                                                                                                                                                                             to reverse of: Q75974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e
"encodes p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q75973 standard; cDNA; 4965 BP.
                                                                                                                                                                                         975 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain mRNA"
1854. 1888
/*tag= g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1621. .1853
/*tag= f
                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-33 x Q75974/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . . 534
                                                                                                                                                                                                                                                 Ouality: 41.00
Ratio: 4.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note-
                                                                                                                                                                                         4059 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    075973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cds
```

1338 G;

ΰ

1293

```
1171 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID T05843 standard; DNA; 934 BP.
AC T05843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID N92449 standard; DNA; 534 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.00
3.545
73.333
                                                                                                                                                                                              Quality: 41.00
Ratio: 4.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:T05843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:N92449
                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-33 x Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-653-294-33 x T05843
                                          4965 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9531548-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
    in vivo.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMERGE
        ပ္ပင္တ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WITE STORAGE TO THE THE TOTAL TOTAL THEORY STORAGES TO THE THE THEORY TO THE THEORY TO THE THEORY TO THE THEORY TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note- "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence" 2979. 2984
/*tag= m 3112. 3151
                                                                                                                                                                                              /note- "murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nucleotides 255-843 of cloned EMCV genomic DNA. It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HLA-B7 stop codon on this biscistronic mRNA to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2480. .2839
/*tag= "encodes beta-2 microglobulin; this cDNA is deriv. from chimpanzee (differs to the human cDNA by only 4 bases)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4014. .4965
//ttag- p
//note= pp
/note= ppriss22 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"
/note- "multiple cloning site, forms a junction between the HIA-B7 sequence and the EMCV-CITE sequence, and is used to facilitate subcloning" 1889. .2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31127. 3151
/*tag= n
/note= "synthetic linker to facilitate cloning"
complement (3151. 3967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= j
/octe= "3' untranslated region of the beta-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note- "synthetic linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-DBC-1994: U06069.
07-MAY-1994: U06069.
07-UNN-1993: US-074344.
(UNMI ) UNIV MICHIGAN.
(VICA-) YICAL INC.
LEW D. MATQUET M. Nabel EG, Nabel GJ;
WPI; 95-036494/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 microglobulin mRNA"
2847. .2870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9429469-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3'utr
                                                                                                                               rbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cds
```

```
Claim 8; Page 134-155; 226pp; English.
Sequences encoding the 5' Hianking region of the capsular
Sequences encoding the 5' Hianking region of the capsular
polysaccharide gene (cps) of Streptococcus pneumoniae and which are
of sufficient length to allow hybridisation under standard
hybridisation conditions to a S. pneumoniae cps gene flanking region
may be used in methods to detect and serotype S. pneumoniae.
may also be used for the diagnosis and prevention of S. pneumoniae
infection. This sequence corresponds to the downstream region of
the 5' cps gene flanking region and is termed the "repeat region".
Sequence 934 BP; 311 A; 136 C; 220 G; 257 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used
fs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A3-APR-1996 (first entry)
Repeat sequence of cps gene locus operon of S.pneumoniae.
Capsular polysaccharide; cps; peptide; flanking region; detect serotype; diagnosis; prevention; Streptococcus pneumoniae; ss. Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAY-1995.
16-MAY-1995, U06119.
16-MAY-1994, US-243546.
(UABR-) UAB RES FOUND.
Dillard JP, Yother J;
WPI: 96-010934/01.
We Streptococcus pneumoniae capsular polysaccharide genes for detection, serotyping and for diagnosis and prevention pneumoniae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-MAY-1990 (first entry)
Sequence of carcinoembryonic antigen domain III.
Carcinoembryonic antigen; domain III; domain A; domain B.
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 AAAATCCAGACACCTAAAGCAGACAAAAGGGTTGCCATCAGGTAT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LysalaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: T05843 from: 1 to: 934
                                                                                                                                                                                                                                                                                                                                       1 LysalaGlnThrAspargGluAsnLeuArg 10
                                                                                                                                                                                                                                to: Q75973 from: 1
```

```
Carcinoembryonic antigen fragments - used in assays to determine the presence and amt. of the antigen in samples also contg. related antigens. Disclosure; page 4; 15pp; English.

CEA fragments can be used in assays to determine the presence and amt. of CEA in samples which also may contain related antigens including its normal cross-reacting antigen or the 128 kD antigen.

Sequence 534 Bp; 137 A; 172 C; 110 G; 115 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carcinoembryonic antigen (CEA) derivs - useful as reagents in immunoassay for diagnosis of neoplastic diseases claim 4; Page 18; 30pp; English.

(7)1567 is the DNA sequence which encodes carcinoembryonic antigen (CEA) R60619. CEA is free from cross-reactive CEA-like antigens, it is antigenically indistinguishable from the solution form of CEA shed from tumour cells, and it is devoid of ethanolamine. R60619 can be used in reagent composition for detecting neoplastic diseases in biological samples, or in an immunoassay process where it can specifically detect the presence of tumour cells in a biological sample e.g. blood.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-MAY-1995 (first entry)
Carcinoembryonic antigen DNA.
Carcinoembryonic antigen; CEA; neoplastic diseases; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: N92449 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AspargGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-1994.
15-MAR-1994; 103986.
25-MAR-1993; EP-810214.
(HOFF ) HOFFMANN LA ROCHE & CO AG F.
MACh J, Pelegrin A, Terskikh A;
WPI; 94-304461/38.
P-PSDB; R60619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
103. .2028
/*tag= a
             /*tag= a
1. .26
/*tag= b
/note="domain A"
268. .534
/*tag= c
/note="domain B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               071567 standard; DNA; 2031 BP 071567;
                                                                                                                                                                                                                                                                                                                                                                                                           38.00
4.222
81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-33 x N92449/rev
                                                                                                                                     29-NOV-1989, 305232, 24-MAY-1989, 305232, 25-MAY-1988, US-198289, (CITY) City of Hope. Shively JE; WPI; 89-349991/48, P-PSDB; P93499,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:Q71567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                               misc_feature
                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                         EP-343946-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP-618292-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mat_peptide
```

THIS PAGE BLANK (USPTS)

```
T24384 crs1519 lambdaZAPST R
D74882 CELK089FYF Yuj1 Kohar
AV202520 AV202520 Yuj1 Kohar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Depotation rest of (3), out-size (1990)

E 97044478

On May 8, 1995 this sequence version replaced gi:800234.

Contact: Wilson RX

Mashington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
Trace considered overall poor quality
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 1.

Location/Qualifiers

roe

1. .255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 255)
1 (bases 1 to 255)
1 (bases 2 to 255)
1 (bases 3 to 255)
1 (bases 4 to 255)
1 (bases 5. Dietrich, N., Dubuque, T., Favello, A., Gish, W., Haukins, M., Hultman, M., Rucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Trevaskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ~3' adaptor sequence: 5'
                                                                                                                                                                       seq_documentation_block:
LOCUS AA151891 255 bp mRNA
LOCUS AA151891 10-DEC-1996
DEFINITION 2001f06.r1 Stratagene colon (#937204) Homo sapiens cDNA clone
IMAGE:566435 5' similar to gb:M15497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lengrn: 14
Gaps: 0
Percent Identity: 92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       351
360
360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 255
   86.35
88.94
88.94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 g
135.65
135.42
135.42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AA151891 from: 1
                                                                                                                                                                                                                                                                                                                         sequence.
AA151891
AA151891.1 GI:1720754
   40.00
40.00
40.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.714
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-33 x AA151891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66.00
                                                                                                                      seq_name: gb_est10:AA151891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57
                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
gb_est1:T24384
gb_est5:D74882
gb_est36:AV202520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Documentation ...

AA151891 zoo1f06 .r.1 Stratagene A159260 qy27b07.xl NUI_CGAP_Br AA141715 zoo32406 .r.1 Stratagene AL03660 DKF2p56402463.rl 564 (R13904 yf62c03.rl Soares infant Co0345 Human heart CONA AA26138 PMY0534 Kluman heart CONA AA26138 PMY0534 Kluman pancred A169864 wc74hll.xl NUI_CGAP_PR A20518 PMY0534 Kluman pancred A169864 wc74hll.xl NUI_CGAP_PR A1007865 EST0215 Normalized r A007865 EST0216 Normalized r A003523 HS_2029_A2_D07_MR CIT A057265 ST04 Human pancred A4633981 acd3401.sl Stratagene A224339 HS_2029_A2_D07_MR CIT A057255 CIT-HSP-23983 TCTT CIT A057353 HS_203_B2_C07_T7 CIT A057333 HS_203_B2_C07_T7 CIT A057333 HS_203_B2_C07_T7 CIT A057333 HS_203_B2_C07_T7 CIT A057333 HS_203_B2_C07_SP6E RF A007633 EST02172 Adrenal gland Av065386 A0065386 Rice root Ory A006000 EST181593 Jurkat T-cel A066386 A0065386 Rice root Ory A0070735 AU070735 Rice conA from D25113 RCR1226A Rice root Ory A0080209 HS_502_B2_D07_T7 CIT A0828908 HS_4809_Al HU06_SP6E CI A05732 AU057732 CYCA A1731234 BNLGH189363 S1x-day Cot A173124 BNLGH189363 S1x-day Cot A173124 BNLGH18363 S1x-day Cot A173124 BNLGH18363 S1x-day Cot A173124 BNLGH18363 S1x-day Cot A17312993 BNLGH18363 S1x-day Cot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ٠,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C99613 C99613 Rice panicle
AQ328864 nbxb0043P20r CUGI |
AQ579309 nbxb0084M23r CUGI |
                                                                                                                                                                                                                          -MODEL-frame-plan.model -DEV-xlp

-0-/cgn1_1/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2

-0-/cgn1_1/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2

-DB-EST_-CRMT-fastap -SUFFIX-rst -GAPOP-12.000 -GAPEXT-4.000

-MINMATCH-0.100 -LOOPEXT-0.000 -LOOPEXT-0.000 -GAPOP-4.500

-GAPEXT-0.005 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000

-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000

-LIST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL

-OUTFWM-pfs -NORM-ext -MINLEN-0 -MAXIELEN-1000000 -USER-US08653294

-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EScore I
0.0003
0.0009
0.0052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.0297
0.0374
0.0374
0.0519
0.1160
0.9704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78.42
79.55
80.50
85.84
99.40
1113.43
121.04
129.53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.23
4.05
4.05
112.34
112.34
112.34
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
112.35
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253.00 ce 223.3.00 ce 223.00 ce 223.00
OM of: US-08-653-294-33 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
Query: US-08-653-294-33
Query length: 15
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 7600.090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ofig

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 000

0 0
                                                                                                                                                                                                        Command line parameters:
                                                         6:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est3:A154815
gb_est23:A1124815
gb_est6:D82189
gb_est2:R20954
gb_est22:A1007865
gb_gss8:AQ033523
gb_est6:D82177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
gb_est10:AA151891
gb_est26:A1359260
gb_est10:AA147151
gb_est28:AL036690
gb_est2:R13904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est12:AA319533
gb_est32:AV058574
gb_est33:AV104196
gb_est31:AU065386
gb_est32:AU070735
gb_est24:C99692
gb_est1:D25133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_gss3:B21407
gb_gss5:AQ753331
gb_est26:AA817822
gb_est37:A1943589
                                                         Date: Feb 8, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est8:C03945
gb_est11:AA263158
gb_est6:D82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_gss10:AQ224339
gb_gss14:AQ572652
gb_gss8:AQ056225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_gss4:AQ704919
gb_est9:C18310
gb_est26:AI008245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est32:AI730993
gb_est24:C99613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est12:AA310808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_gss6:AQ828908
gb_est30:AU057732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est17:AA633983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss9:AQ164696
gb_est32:AI731234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_gss11:AQ328864
gb_gss14:AQ579309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score_list:
```

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL COMMENT

```
AA147<u>151</u> 581 bp mRNA EST 05-DEC-1996 2032d06.rl Stratagene colon (#937204) Homo sapiens cDNA clone IMAGE:588587 5' similar to gb:M64740 HLA CLASS I HISTOCOMPATIBILITY ANTICEN, A-24(A-9) A*2402 ALPHA (HUMAN);, mRNA sequence.

AA147151. GI:1716526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DO Sep 12, 1996 this sequence version replaced gi:1393699.
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 272.
High quality sequence stop: 272.
                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to SB1)

11 (bases 1 to SB1)

11 (bases)

12 (bases)

13 (bases)

14 (bases)

15 (bases)

16 (bases)

17 (bases)

18 (bases)

18 (bases)

18 (bases)

19 (bases)

10 (bases)

11 (bases)

12 (bases)

13 (bases)

14 (bases)

15 (bases)

16 (bases)

17 (bases)

18 (bases)

18 (bases)

18 (bases)

19 (bases)

19 (bases)

10 (bases)

11 (bases)

11 (bases)

12 (bases)

13 (bases)

14 (bases)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   and Marra.M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AL036690 171 bp mRNA EST 27-SEP-1999
DEFINITION DKF2p564D2463_r1 564 (synonym: hfbr2) Homo sapiens cDNA clone
DKF2p564D2463_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 14
Gaps: 0
Percent Identity: 85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 AlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         162 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 62.00
Ratio: 4.429
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AA147151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-33 x AA147151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est38:AL036690
       seq_documentation_block:
                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134
                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                 KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                             LOCUS
DEFINITION
                                                                                                                     ACCESSION
VERSION
                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. con Library Arrayed by: Greg Lennon, Ph.D. con Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCL-GAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                               'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
                                            seq_documentation_block:

LOCUS
A1359260
618 bp mRNA
EST
15-FEB-1999
DEFINITION qy27b07.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2013205:
similar to qb:D32129 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
AW-66(A-10) A*6601 ALPHA (HUMAN);, mRNA sequence.

ACCESSION A1359260
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases) Primates; Catarrhini; Hominidae; Homo.

1 (bases) Primates; Catarrhini; Hominidae; Homo.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Unpublished (1998)

Contact: Robert_Strausberg@nih.gov

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 14
Gaps: 0
Percent Identity: 92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        www-bio.llni.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soares and M.Fatima Bonaldo."
171 c 182 g 137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 691 Std Error: 0.00 Seq primer: -400P from Gibco High quality sequence stop: 458. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: AI359260
                                                                                                                                                                                       AI359260.1 GI:4110881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-33 x AI359260/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio: 4.714
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.00
seq_name: gb_est26:AI359260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est10:AA147151
                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                           human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
```

source

FEATURES

BASE COUNT

ORIGIN

```
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C03945
C03945.1 GI:1467196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.538
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: R13904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-33 x R13904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est8:C03945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
                                                                                                                                                                                                                                                                                                                                            EST (Duesterhoeft, et al.)
Unpublished (1999)
Un Jul 7, 1999 this sequence version replaced gi:5866258.
Contact: Duesterhoeft A MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemannédkfz-heidelberg.de;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Genome Project.

No sl sequence available.

This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
Locus

                                                                                                                                                                          Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 17)
Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 459)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pAMP1; Site_1: NotI; Site_2: SalI" 53 c 60 g 22 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LysAlaGlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Dkr2p56402463"
/clone=lib="564 (synonym: hfbr2)"
/tissue_type="brain"
/dev_stage="fetal"
/lab_host="X1-2blue"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 15
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
   AL036690
AL036690.3 GI:5927859
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
R13904
R13904.1 GI:766980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.00
4.538
86.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AL036690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-653-294-33 x AL036690
                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est2:R13904
                                                                                                                                                                                                                                                                                                               Wiemann, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

The state of the s

```
15
                                                                                                                                                                                                                                                                                                                                                                                                   3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 272-20-8856
Fax: 272-20-8896
Email: jtaked@8b.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  ;
ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;;
                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D82221.1 GI:1183739
                                                                                                                                                                                                                               56.00
4.667
92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.667
                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AA263158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.00
                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-33 x AA263158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: D82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block: .
US-08-653-294-33 x D82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS D82221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est6:D82221
                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75
                                                                                                                                                                                                                                                      Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . uman
                                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA263158 283 bp mRNA EST 02-JUL-1998
PMY0534 KG1-a Lambda Zap Express CDNA library Homo sapiens CDNA 5',
mRNA sequence.
                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon.9606"
/db_xref="taxon.9606"
/clone="3NHC2454"
/clone_11b="Human heart cDNA (YNakamura)"
/dev_stage="adult"
/note="Organ: heart; normalized directionally cloned cDNA from adult heart; normalized directionally cloned cDNA from adult heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 283)
Claudio,J.O., Liew,C.C., Dempsey, A.A., Cukerman, E., Stewart, A.K.,
Na, E., Atkins, H.I., Iscove, N.N. and Hawley, R.G.
Identification of sequence-tagged transcripts differentially
expressed within the human hematopoietic hierarchy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Tel: 416 3403834
Fax: 416 3403833
Email: r.hawley@utoronto.ca
Similar to M58636 MHC class I HLA-Bw gene. Clone was randomly
picked from KGla primary library.
Seq primer: 5' GAATAAACCTCAATAAAGGG 3'
High quality sequence stop: 283.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="KG1-a Lambda Zap Express cDNA library"
/cell_type="promyeloblast"
On Oct 24, 1995 this sequence version replaced gi:1040105.
Contact: Yusuke Nakamura
Institute of Medical Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        On May 5, 1995 this sequence version replaced gi:797810.
Contact: Hawley RG
Oncology Research Laboratories
                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 13
Gaps: 0
Percent Identity: 92.308
                                                    University of Tokyo
4-6-1, Shirokanedal, Minato-ku, Tokyo 108,
Tel: 81-3-5449-5372
Fax: 81-3-5449-5433
Email: yusuke@ims.u-tokyo.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 50 (1), 44-52 (1998) 98292493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: C03945 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA263158.1 GI:1898964
                                                                                                                                                                                                                                                                                                                                                                                                                   56.00
4.667
92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est11:AA263158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-33 x C03945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AA263158
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
   COMMENT
```

```
/cell_line="KG1-a"
/note="Vector: Lambda Zap Express (Stratagene); Site_1:
ECORI; Site_2: XhoI; Unidirectional cloning sites:
ECORI.4XhoI. mRNA was purified from KG1-a cell line, CDNA
was synthesized using an XhoI-OligodT linker primer. ECORI
adaptors were ligated, followed by digestion with XhoI for
directional cloning into predigested Lambda Zap Express"

91 c 88 g 40 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_llb="Human pancreatic islet"
/clone_llb="Human pancreatic islet"
/note="Vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D82221 375 bp mRNA EST 09-FEB-1996
HUMHBC4626 Human pancreatic islet Homo sapiens cDNA similar to
HLA-B, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 375)
Takoda,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785255.
Contact: Jun Takeda
                                                                                                                                                                                                                                                                                                                                                                                             Length: 13
Gaps: 0
Percent Identity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 13
Gaps: 0
Percent Identity: 92.308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGCTAC 149
```

The second

から 素味

```
AI124815
AI124815.1 GI:3593329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EST.
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index.
Tumor Gene Index.
Unpublished (1997)
On Mar 16, 1998 this sequence version replaced gi:2961758.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@hih.gov
Contact: Robert_Strausberg@hih.gov
Email: Robert_Strausberg.
Contact: Robert Strausberg.
Email: Rob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.72 kb. Life Technologies catalog #:
                                                                                                                                                                                                 seq_documentation_block:

LOCUS A1696864 748 bp mRNA EST 03-JUN-1999

DEFINITION wc74h11.x1 NCI_CGAP_Pan1 Homo sapiens CDNA clone IMAGE:2324421 3'

Similar to gb:M28205 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,

B-51(B-5) B*5101 ALPHA (HUMAN);, mRNA sequence.

ACCESSION A1696864

WERSION A1696864.1 GI:4984764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 748)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NAI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS
AI124815
AI124815
DEFINITION am56e06.X1 Johnston frontal cortex Homo sapiens cDNa clone
DEFINITION am56e06.X3 Johnston frontal cortex Homo sapiens cDNa clone
IMAGE:1539586 3' similar to 9b:M24038_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, BW-44(B-12) B*4402 (HUMAN); contains
MER22.t3 TAR1 repetitive element ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 92.308
                                       297 CAGACTTACCGAGAGAACCTGCGGATCGCGCTCCGNTAC 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.748
/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2324421"
/clone=lib="NOI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlnThrAspArgGluAsnLeuArgIleAlaLeuArgTyr 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: -400P from Gibco
High quality sequence stop: 424.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    237 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11548-013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: AI696864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-33 x AI696864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est23:A1124815
                                                                                                                                    seq_name: gb_est31:A1696864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
```

```
A1007865 325 bp mRNA EST 25-JAN-1999 EST202316 Normalized rat brain, Bento Soares Rattus sp. cDNA clone RBRAV89 3' end, mRNA sequence. A1007865 A1007865.1 GI:3221697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 325) Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D. Rat Genome Project: Generation of a Rat EST (REST) Catalog & Bene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
On Jan 17, 1998 this sequence version replaced gi:1900396.
Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Normalized rat brain, Bento Soares"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20850,
                                                                  /organism="Homo sapiens"
/db_xref="GDB:403812"
/db_xref="taxon:9606"
/clone="IMAGE:31465"
/clone_llb="Soares infant brain INIB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 12
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD
1971, Medical Center Drive, Rockville, MD
1971, 1931, 1938-1920
Email: nhlee@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Rattus sp."
/db_xref="ATCC (inhost):2016137"
/db_xref="taxon:10118"
/clone="RBRAV89"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 TCACAGACTGACCGAGAGACCTGCGGNTCGCGCTT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AlaGlnThrAspArgGluAsnLeuArgIleAlaLeu 13
  High quality sequence stop: 345.
Location/Qualifiers
1..567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: R20954 from: 1
                                                                                                                                                                                 /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49.00
4.455
91.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est22:AI007865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-33 x R20954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AI007865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus sp.
Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/do_xref="taxon:9606"
/do_xref="taxon:9606"
/clone_lib="Human pancreatic islet"
/note="vector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I: mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences clone
134 c 133 g 61 t 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L Unpublished (1995)
Contact: Wilson Red (1996)
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est Waterson.wustl.edu
Insert Size: 1653
High quality sequence stops: 345 Source: IMAGE Consortium, LLNL
This clone is available royalty/free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: MI3RP1
Seq primer: MI3RP1
                Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785206.
Contact: Jun Takeda
Institute for Molecular and Cellular Regulation, Gunma University
3-9-15 Showa-machi, Maebashi Gunma 371, Japan
Fax: 272-20-8896
Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases I to 567)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    yg06c01.rl Soares infant brain lNIB Homo saplens cDNA clone
IMAGE:31465 5' similar to gb:M15497_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, A-24(A-9) A*2401 (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.00 Length: 13
4.545 Gaps: 0
84.615 Percent Identity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 415
                                                                                                                                                                                                   Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: D82189 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      567 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R20954.1 GI:775735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-653-294-33 x D82189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est2:R20954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R20954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
```

6 Rat

```
Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 410)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:

LOCUS AQ033523 410 bp DNA GSS 02-JUL-1998

DEFINITION HS_2229_A2_D07_MR CIT Approved Human Genomic Sperm Library D Homo Sapiens genomic clone Plate=2229 Col=14 Row-G, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606" /clone="Plate=2229 Col-14 Row=G" /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2229 row: G column: 14
Class: BAC ends
High quality sequence stop: 410.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
                                                                                                                                    Length: 11
Gaps: 0
Percent Identity: 72.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.00 Length: 15
3.214 Gaps: 0
93.333 Percent Identity: 53.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 t
                                                                                                                                                                                                                                                                                                                                 204 GACAGGAAGAATGTACGGTTGGCATTGAGATAC 236
                                                                                                                                                                                                                                                                        to: 325
                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .410
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                           5 AspArgGluAsnLeuArgIleAlaLeuArgTyr
                                        76 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 g
                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ033523.1 GI:3285641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-33 x AQ033523/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 C
                                                                                                                                                          Ratio: 4.182
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                      Align seg 1/1 to: AI007865
                                                                                                                                      46.00
                                                                                                                                                                                                                alignment_block:
US-08-653-294-33 x AI007865
                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_gss8:AQ033523
                                          ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                        107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human.
                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
```

```
Institute for Molecular and Cellular Regulation, Gunma University
33-15 Showa-machi, Maebashi Gunma 371, Japan
Tel: 272-20-8856
Fax: 272-20-8896
                                                                                                                  D82177 330 bp mRNA EST 09-FEB-1996
HUMHBC4504 Human pancreatic islet Homo sapiens cDNA similar to
D82177
                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 330)
Takeda,J.
                                                                                                                                                                                                                                                                                                                                       Human pancreatic islet ESTs
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:785191.
Contact: Jun Takeda
                              1 LysalaGlnThraspArgGluAsnLeuArgIleAlaLeuArgTyr 15 || || || :::|||:::|||||||||| 218 AAGAAGAAGAACAAGAATCTTAAAATAGTTTTGAGGTAT 174
Align seg 1/1 to reverse of: AQ033523 from: 1 to: 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 11
Gaps: 0
Percent Identity: 90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                          D82177.1 GI:1183645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: D82177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-33 x D82177
                                                                                                                            seq_documentation_block:
Locus D82177
                                                                                            seq_name: gb_est6:D82177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio
Percent Similarity
                                                                                                                                                                                                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
```

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 1.773 Million cell updates/sec Run on:

US-08-653-294-34 51 1 RESLRNLRGY 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. A\_Geneseq\_36:\* Database :

## SUMMARIES

		į į	HLA-B/ CTL modulat	Peptide B7.75-84 t	Peptide B7.75-84 t	TL m	4-75-	B7.84		fragm	CTL	ပ္ပ	2.60-84	HLA-B35 antigen. H	Peptide fragment o	HLA-Bw46 CTL modul	3	HLA-C exon Cb-1. H	HLA-C exon Cb-2. H	Breast cancer asso	Consensus sednence	lating		HLA-alpha-1. Use o	oue.	SABP encoded by pC	Tobacco salicylic	Avenacinase-like p	. thermophil	U	გ	HΙV	u	Glucoamylase from
SUMMAKIES	ID	R41209	R83061	W33786	W33796	R92913	R95415	W33790	W33797	R41207	R83073	R95431	R95419	R12464	R41206	R83072	R95418	R12465	R12466	X07033	P80911	W07518	R44112	R71629	R47268	R74305	W04316	R85199	W57445	W05178	W90345	R42577	R11329	R77674
	DB	μ,	٦.	-	H	-	П	-	-	~	-	Н	-	Н	Н	-	Н	Н	Н	-1	-1	н.		н.	н.	Н	~	-	-	-		-	Н	7
	Length	:	0 5	10	10	20	50	20	20	25	25	25	25	362	25	25	25	366	366	366	274	10	22	4	ω,	œ	489	g	82	1130	20	σ	425	Ò
de	Ouery Match	. 00	0.00	38	00	80	00	8	9	8	8	8	9	100.0				86.3						9.89						64.7	64.7	62.7	62.7	62.7
	Score	ינהו י	2,1	21	51	51	51	51	51	51	51	51	51	51	44	44	44	44	44	44	41	37	32	35	32	35	35	33	33	33	33	32	32	32
	Result No.	i	7 ~	<b>4</b>	2	9	7	ω.	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34

rizzled interfe la-zost enase. poxygen la-zost fragme modulat N-termi	Banana bunchy top
W31274 R04907 P70347 R230570 R2215 R41211 W07521 W30133	W54071
аннаннана.	-
788 785 865 865 10 10 12 12	286
6600.8 602.77.77.77.77.77.77.77.77.77.77.77.77.77	8.09
	31
888 4444 988 84444 988 97 87 87 87 87 87 87 87 87 87 87 87 87 87	45

## ALIGNMENTS

ö

X83061 standard; peptide; 10 AA.

XG 783061, The MAY-1996 (first entry)

XG 15-MAY-1996 (first entry)

XG 15-MAY-1996 (first entry)

XG 47.15-84).

XG 7.15-84).

XG 7.15-87.

XG 7. 

```
M3786;
19-JUN-1998 (first entry)
19-JUN-1998 (first entry)
Peptide B7.75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
Immunomodulation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beulow R, Clayberger C, Krensky AM; WPI; 98-086530/08.
                                                                                                                                                                                           W33786 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-1997.
22-MAY-1997; U08689.
                             1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hômo sapiens.
WO9744351-Al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
W33796
                                                                                                                                                                                                                            NAME OF THE PROPERTY OF THE PR
                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 major instruction.

Tractment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating T cell mediated attack on target cells

Claim 7: Page 20: 24pp; English.

W07512-W07518 represent T-cell modulating peptides that can be used in the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the major histocompatability complex (MFC) class I antigem (see W07510). The method is for affecting the course of an autoimmune disease involving T-cell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes mellitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are mulitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are mulitus, preferably being administered during the pre-clinical stage to gravis, etc. The peptides modulate T-cell mediated attack on autologous carvickines, perferins, and may also reduce inflammation, swelling, and release of cytokines, perferins, granzymes etc. associated with T cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                              Claim 13; Page 66; 80pp; English.

This sequence represents a fragment of a class I major histocompatibility complex (MHC) antigen. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B7. This sequence, and the peptide fragments represented by R83062-R83085, R83090-R83096 and P82907-R82913 can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subcherapeutic amount of period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or linhbit) the activity of the cytotoxic I lymphocytes (CILs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-AUG-1997 (first entry)
T-cell modulating peptide #4.
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
T-cell modulator; autoimmune disease; tissue destruction; alphal-domain;
mammal; major histocompatability complex; MHC class I; antigen; perforin;
insulin-dependent diabetes mellitus; multiple sclerosis; inflammation;
rheumatoid arthritis; psoriasis; pemphigus vulgaris; Sjogren's disease;
thyroid disease; Hashimnto's thyroiditis; myasthenia gravis; granzyme;
autologous target cell; cytokine release; T cell activation; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps

    using Class I B75-84 MHC antigen of the recipient

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 1; Length 10; 100.0%; Pred. No. 0.00074; Ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 100.0%; Score 51; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00074; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W07515 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-787-1996; U04710,
12-MAY-1995; US-440504,
(SANG-) SANGSTAT MEDICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 96-518410/51.
donor hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
ó
```

```
Will solutions of the peptide (s) - based on a class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autofimmune diseases.

PT treating autofimmune diseases.

Example 1; Page 19; 41pp; English.

CC Peptides Wi3784-98 and Wi33778-9 were assayed for their immunomodulating cativity. A peptide-type compound or variant is claimed which has cit immunomodulating activity, including the N-terminal acylated and/or creminal anidated or esterified forms of up to 60 anino acids, where the peptide-type compound comprises the formula; A-B, where A, B = CC (R ani - T) (ani - Page) (ani - T) 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1998 (first entry)
Peptide B7.75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoAmmune disease; Class I HIA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 51; DB 1; Length 10; 100.0%; Pred. No. 0.00074; Pred. No. 0.00074; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-NOV-1997.
22-MAX-1997; U08689.
24-MAX-1996; US-653294.
GSTR ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used for detection and diagnosis.
Sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W33796 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
WO9744351-Al.
```

Gaps

ö

1 RESLRNLRGY 10

ò

```
Beulow R, Clayberger C, Krensky AM;
WPI: 98-086530/08.

New immunomedulating dimer peptide(s) - based on a class I HiA-B in municulating dimer peptide(s) - based on a class I HiA-B in the immunomedulating discretion of transplants or treating autoimmune diseases

Example 1; Page 19; 41pp; English.

Example 2; 41pp; English.

Example 3; 41pp; English.

Example 3; 41pp; English.

Example 4; 41pp; English.

Example 4; 41pp; English.

Example 4; 41pp; English.

Example 5; 41pp; English.

Example 6; 41pp; 41pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92207-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparate to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CLLs)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-MXY-1996 (first entry)
HLA-B7 CTL modulating peptide (B7.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 51; DB 1; Length 10; Best Local Similarity 100.0%; Pred. No. 0.00074; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-APR-1994; US-222851.
(STRD.) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R92913 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-1995.
05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayberger C, Krer
WPI: 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
R92913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

```
Parapers comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example, Page 18: 29pp; English.

Example, Page 18: 20pp; English.

Example, Page 18: 20pp; English.

Example, Page 18: 20p; English.

Example, Page 18: 20p; English.

Example, Page 18: 20p; English English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                    ö
                                                                                                                                                                                                                                                                                                12-NOV-1996 (first entry)
HIA-B7.84-75-84 Palindrome.
HIA-B7.84-75-84 Palindrome.
HIA-B7.84-75-84 Palindrome.
HIA-P7-84 Indept. Numan-leucocyte-associated antigen; inhibitor;
HIA-P7-84 Indept. Numan-leucocyte-associated antigen; Hac70; APC;
T-cell lysate; membrane protein; mammal; heat shock protein; Hac70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1998 (first entry)
Peptide B7.84-7575-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CIL activation; transplantation; autoAnmune disease; Class I MLA-B alpha-1 domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 1; Length 20; illarity 100.0%; Pred; No. 0.0015; Conservative 0; Mismatches 0; Indels
                                    Indels
Pred. No. 0.0015; wismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                            Ą.
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W33790 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                       R95415 standard; peptide; 20
R95415;
       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krensky AM;
                                 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1994; U12985
     Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                  1 RESLRNLRGY 10
                                                                                                              1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clayberger C, Kre
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
WO9744351-Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33790;
                                                                                                                                                                                                           ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ထ
                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
                                                                                                                                                                                                                                                            DOS WWW END
                                                                                       ò
                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
```

```
RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41207
                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
  888888888888
                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAT WELL'S PS-003230/00.

WITH TABLE TO COMMENT TO PROBLEM SECTION OF TRANSPLANTS OF TREATMENT OF THE TREATMENT OF THE TREATMENT OF TREATMENT OF TREATMENT OF TREATMENT OF TREATMENT OF THE TRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New; 38 000330,000

New; 38 000330,000

alpha-1 domain, used for preventing rejection of transplants or

treating autoimmune diseases

Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating

activity. A peptide-type compound or variant is claimed which has

immunomodulating activity, including the N-terminal acylated and/or

C-terminal anidated or esterilied forms of up to 60 amino acids, where

the peptide-type compound comprises the formula; A-B, where A, B =

C, S or N; aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 =

D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or

small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino

acid. The sequence in the brackets may optionally be absent or truncated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at any peptide type bond within the brackets. The compounds comprise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W33797;
19-JUN-1998 (first entry)
19-JUN-1998 (first entry)
Peptide B7.84-75/75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 51; DB 1; Length 20; 100.0%; Pred. No. 0.0015; ive 0; Mismatches 0; Indels
27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM; WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W33797 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1997.
22-MAY-1997; U08689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33797
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Market of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-BW62 CTL modulating peptide (Bw62.60-84).
Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; imminosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-Bw62.
    (positions
amino acid sequences related to a class I HLA-B alphal domain (position 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of I cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autolmmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic T lymphocyte; modulation.
Synthetic.
W09317699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 1; Length 20
100.0%; Pred. No. 0.0015;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 51; DB 1; 100.0%; Pred, No. 0.0019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R41207 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R83073 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity
Matches 10; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-1995.
05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 RESLRNLRGY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R83073;
16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
```

```
Clayberger C, Kr
WPI; 95-194027/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-B35 antigen.
                                                                                                                                                                                                                                    16 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAY-1995
                                                                                Best Local Sin
Matches 10;
                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                RESULT
RESULT
R95419
R95419
R95419
R95519
RWW
HLLA
RWW
HLA
RWW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R12464
                                                                                                                                                                                                                                                                    원
                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  а
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              While Stringers of the comperison of surface membrane proteins - which may limibit cytolytic activity and differentiation of CTLs.

Example 12, 20pp; English.

Example 12, 20pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the Frotein P74 is a T-cell surface membrane protein p74 is a T-cell surface membrane protein p74 is a T-cell surface membrane protein p74 is a sociated with T-cell activation in mammalian T-cells, and is also associated with T-cell activation in mammalian T-cells, and is also and Induced number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an containing a covalently bound HLA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60 eW (see R95446), induces calcium influx, and inhibits cytocoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of determining the amount of binding between the candidate composition or CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                            Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-BW62. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1996 (first entry)
HLA-B7.60-84.
HLA-P7.60-84.
HLA-P7.60-84.
The p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                    Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 51; DB 1; Length 25; 100.0%; Pred. No. 0.0019; ive 0; Mismatches 0; Indels
                                                                            Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R95431 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clayberger C, Krensky AM; WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 100.
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1994; U12985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111111111
16 RESLRNLRGY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9513288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R95431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R95431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME OF THE PROPERTY OF THE PR
    ò
```

```
R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-Bw62.60-84. These sequences can be used to isolate the protein p74 crown a T-cell lysate. P74 is a T-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. P74 is found in a limited number of cell types, but is particularly expressed on and T cells. P74 can be isolated by lysis of a suitable cell with an amphoreric detergent, and then passed through an affinity column containing a comprising the extracellular fragment of p74 combined with HLA-B7702.60-84 (see R95416), induces calcium influx, and inhibits compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of containing the amount of binding between the candidate composition containing the amount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-Bw62.60-84.

HLA: p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Compsns. comprising lymphoid surface membrane proteins - which may hibbli toytolytic activity and differentiation of CTLs. Example: Page 9: 29pp: English. R95413, and R95415-R95431 represent palindromes and fragments of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;;
0
                                                               ;
0
100.0%; Score 51; DB 1; Length 25; 100.0%; Pred. No. 0.0019; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 51; DB 1; Length 25; 100.0%; Pred. No. 0.0019; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAI-1994; U12985.
10-NOV-1994; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytolysis; antigen presenting cell. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R12464 standard; Protein; 362 AA.
R12464;
                                                                                                                                                                                                                                                                                                                                               Å.
                                                                                                                                                                                                                                                                                                                                         R95419 standard; peptide; 25
R95419;
                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                            Conservative
                                                                                                                         1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
J03112486-A.
```

```
ö
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mew peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets claim 9; Rage 53; 61pp; Engilsh.

The peptide (or a fragment of at least 10 amino acids, joined at at The peptide (or a fragment of at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which beind to it and removing subsets of CTLs from a T-cell composition.
                                                                                           HAP-B15 (12115.)
HAP-B15 gene - used in DNA probe and transformant cells for immunising animals, for developing monoclonal antibody.
Claim 1: Page 1: 11pp: Japanese.
Probes comprising part of the sequence encoding this sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-B35 antigen. See also J03112485 and J03112487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen; HLA; peptide; transplantation; neoplasia;
parassitic disease; cytotoxic T lymphocyte; modulation.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                     Ouery Match 100.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 0.031; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86.3%; Score 44; DB 1; Length 25; 90.0%; Pred. No. 0.04; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R41206 standard; peptide; 25 AA.
                                       22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           99 RESLRNLRGY 108
                  22-SEP-1989; 247697
22-SEP-1989; JP-247
                                                                                                                                                                                                                                                                                                                                                                                                  1 RESLRNLRGY 10
                                                                            WPI; 91-182991/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9317699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
R41206
                                                                                                                                                                                                                                                                                                                                                                                                                                   g
ô
```

Gaps

; 0

Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

1 RESLRNLRGY 10 

õ

9 08:50:33 2000

Wed Feb

j

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 7, 2000, 18:04:41; Search time 111.22 Seconds (without alignments) 4.241 Million cell updates/sec Run on:

US-08-653-294-34 51 1 RESLRNLRGY 10 score: Title: Perfect so Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 segs, 47169319 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_62:\* Database :

pir1:\* pir2:\* pir3:\* pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	MHC class I antige	class I	MHC class I antige	H	cell sur	MHC class I histoc	MHC HLA-B39 chain	m	cell surface antig	뒴	cla	MHC HLA B71 - huma	Н	H	н	н	н	I S	н	class I	class I	class I	ss I hist	class I	class I	class I	class I		HLA-B*5602 - human	lymphocyte antigen
SUMMARIES	ΩI	I38875	I38876	I38860	I38874	159188	HLHU40	168774	S24439	168701	I36956	168747	I54308	S24436	S24437	S24438	S24440	S24433	803538	154418	HLHUB7	S77966	G01230	S16789	45	37	137520	37	844	172755	I84488
	DB	7	~	7	7	7	Н	7	7	7	7	7	~	~	7	7	N	7	7	7	-	~	N	N	N	N	7	7	~	~	N
	& Query Match Length	137	137	137	137	181	270	274	274	300	308	350	350	354	354	354	354	354	358	361	362	362	362	362	362	362	362	362	362	362	362
•	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	21	51	51	51	51	51	51	51	51	51	51	51	51
	Result No.	:	7	٣	4	ស	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

HIA-B*5501 - human HIA-B*5502 - human HIA-B*5501 - human MAC class I histoc HIA-B alpha-chain lymphocyte antigen HIA-B*5401 - human MAC class I proted HIA-B*5401 - human MAC class I proted Ilymphocyte antigen lymphocyte antigen lymphocyte antigen MAC HIA-B*42, HIA- MAC HIA-B*14 chain	
172752 172754 172754 172754 137492 156130 156149 156149 159651 151865 161859	
00000000000000	
22222222222222222222222222222222222222	
000000000000000000000000000000000000000	
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	

## ALIGNMENTS

```
Rigarber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stef Immunogenetics 42, 19-27, 1995
A; Title: HIA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A; Reference number: 138860; MUID:95317819
A; Accession: 138875
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-137 < RES>
A; Residues: 1-137 < RES>
A; Cross-references: EMBL:015639; NID:9930332; PIDN:AAA74046.1; PID:9930333
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
MHC class I antigen - human (fragment)
C;Species: Homo saplens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                   C; Accession: I3887
```

ö Gaps ö Length 137; 100.0%; Score 51; DB 2; Length 13 100.0%; Pred. No. 0.0045; ive 0; Mismatches 0; Indels Query Match Best Local Similarity 100.0 Matches 10; Conservative

1 RESLRNLRGY 10 ò

g

MHC class I antigen - human (fragment)

Gaps ö Length 137; Query Match 100.0%; Score 51; DB 2; Length 13 Best Local Similarity 100.0%; Pred. No. 0.0045; Matches 10; Conservative 0; Mismatches 0; Indels

; 0

1 RESLRNLRGY 10 ò g

40 RESLRNLRGY 49

Mary many day on the

Gaps

ö

```
A,Molecule type: protein A,Residues: 1.270 LCD>
C,Comment: Comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2 c).Comment: comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2 y restricted to the alpha-1 and alpha-2 domains. The most conspicuous clustering of vossible alloantigenic determinants of these antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication: glycoprotein; heterodimer; membrane protein; transplantation
F;1-90/Domain: alpha-1 <EXI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MECCLASS I histocompatibility antigen HLA-B40 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: 18-30186: #sequence_revision 28-Aug-1985 #text_change 02-Sep-1997
C;Accession: A02186: #sequence_revision 28-Aug-1985 #text_change 02-Sep-1997
C;Accession: A02186: Bragado, R.; Strong, D.M.; Strominger, J.L.
Blochemistry 22, 3961-3969, 1983
A;Tille: Primary structure of papain-solubilized human histocompatibility antigen HLA
A;Reference number: A02186; MUID:84000412
A;Map position: 6p21.3-6p21.3
A;Introns: 90/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: 9lycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;91-181/Domain: alpha-2 <EX2>
F;95-186/Domain: lmmunoglobulin homology <IMM>
F;195-260/Domain: lmmunoglobulin homology <IMM>
F;86/Binding site: carbohydrate (Asn) (covalent) *status experimental F;86/Binding site: carbohydrate (Asn) (covalent) *status experimental F;101-163,202-258/Disulfide bonds: *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 51; DB 1; Length 270; Best Local Similarity 100.0%; Pred. No. 0.0093; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 274;
                                                                                                                                                                                                Length 181;
                                                                                                                                                                                                Query Match 100.0%; Score 51; DB 2; Length 18
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 2;
Pred. No. 0.0095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC HLA-B39 chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                1 RESLRNLRGY 10 >
                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                 111111111
74 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A02186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: GDB:HLA-B
                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                 MHC class I antigen - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: O7-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 138860
R;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefanc R;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefanc A;Tille: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A;Reference number: 138860; MUID:95317819
A;Accession: 138860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC cell surface glycoprotein - human (fragment)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 0.2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Accession: 159188
R; Bronson, S. K.; Pei, J.; Taillon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, D. Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A; Title: Isolation and characterization of yeast artificial chromosome clones linking the A; Reference number: 159188; MUID:91156671
A; Accession: 159188
A; Molecule rype: DNA
A; Molecule type: DNA
A; Residues: 1-181 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefand Immunogenetics 42, 19-27, 1995
A;Title: HIA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A;Reference number: I38860; MUID:95317819
A;Accession: I38874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
Species: Homo sapiens (man)
Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                         A;Status: prelininary; translated from GB/EMBL/DDBJ
A;Status: prelininary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosidues: 1-137 < RES.
A;Residues: 1-137 < RES.
A;Cross-references: EMBL:U14756; NID:9930328; PIDN:AAC50171.1; PID:9930329
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Mossidues: 1-137 < RES.
A; Cross-references: EMBL:U15638; NID:9930330; PIDN:AAA74045.1; PID:9930331
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross_references: GB:M59841; NID:g187697; PIDN:AAA59623.1; PID:g187698 C:Genetics: A:Gene: GDB:HLA-B A:Cross_references: GDB:120048; OMIM:142830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 51; DB 2; Length 137; 100.0%; Pred. No. 0.0045; O. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 51; DB 2; Length 137; 100.0%; Pred. No. 0.0045; Pred. O. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHC class I antigen - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 RESLRNLRGY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESLRNLRGY 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Homo sapi
C; Date: 07-Jun-1996
C; Accession: I38874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
```

ö

Gaps

ö

```
C;Species: Homo sapiens (mai)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Date: 107-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 168747
R;Pohla, H; Kuon, W; Tabaczewski, P; Doerner, C; Weiss, E.H.
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the HLA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 02-011-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: 154308
R;Rodriguez, S.G.; Johnson, A.H.; Hurley, C.K.
Hum. Immunol. 37, 192-194, 1993
A;Title: Wolecular characterization of HLA-B71 from an African American individual.
A;Reference number: 154308; MUID:94064392
A;Reference number: 154308
A;Reference pumber: translated from GB/EMBL/DDBJ
A;Reference pumber: A;Reference number: 1-350 <RES>
  02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                              A; Residues: 11308 <RES>
A;Cross-references: GB:M24044; NID:g176812; PIDN:AAA35423.1; PID:g176813
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:M28204; NID:9576472; PIDN:AAA53257.1; PID:9576473 C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:L07950; NID:g307236; PIDN:AAA59683.1; PID:g307237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 51; DB 2; Length 308; llarity 100.0%; Pred. No. 0.011; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 2; Length 35-
100.0%; Pred. No. 0.012; Undels
                       C; Accession: 136956
R; Parhlam, P., Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A; Title: Diversity and diversification of HLA-A,B,C alleles. A; Reference number: 136956; MUID:89235215
A; Accession: 136956; MuiD:89235215
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: 154457; WUID:89233295
A;Accession: 16847
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
168747
MHC class I lymphocyte antigen - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GDB:120048; OMIM:142830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154308
MHC HLA B71 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Residues: 1-350 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A: Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                C;Accession: S24439
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992
Nature 357, 329-333, 1992
Nature 357, Number HLA-B alleles in a tribe of South American Amerindians indicate A;Reference number: S24027; MUID:92269956
A;Accession: S24439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-B-3901 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Accession: 168701
R; Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.
Immunospenetics 20, 237-252, 1984
A; Title: Inter-locus and intra-allelic polymorphisms of HLA class I antigen gene mRNA.
A; Reference number: 154412; MUID:84287690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                            class I histocompatibility antigen HLA-B-3901 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Molecule type: mRNA
A.Residues: 1-300 <RES>
A.Cross-references: GB:MJ7540; NID:g187733; PIDN:AAA59638.1; PID:g386890
C.Superfamily: class I histocompatibility antigen; immunoglobulin homology
C.Keywords: surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C.Superfamily: Class I histocompatibility antigen; immunoglobulin homology C.Sepwords: glycoprotein F:1-74/Product: class I histocompatibility antigen HIA-B-3901 #status pref: F:1-90/Domain: alpha-1 #status predicted <EX1>F:1-182/Domain: alpha-2 #status predicted <EX1>F:91-182/Domain: alpha-2 #status predicted <EX2>F:96-261/Domain: immunoglobulin homology <IMM>F:96/Shinding site: carbohydrate (Asn) (covalent) #status predicted F:101-164,203-259/Disulfide bonds: #status predicted
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 51; DB 2; Length 300; 100.0%; Pred. No. 0.01;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 2; I
100.0%; Pred. No. 0.0095;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Accession: 168701
A, Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell surface antigen - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC ChlA chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
  Conservative
                                                    1 RESLRNLRGY 10
                                                                                    FESTRNINGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-274 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: HLA-B-3901
C;Superfamily: cla
10;
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
136956
                                                                                                        75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                        g
                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
```

ö

Gaps

```
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C;Accession: S244838
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Ga Nature 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians Indic A; Accession: S24438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ajdene: HLA-B-4801
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Seywords: glycoprotedn; transmembrane protein
F;1-1/7bomain: signal sequence #status predicted <SIG>
F;17-294/Domain: extracellular #status predicted <EXT>
F;17-299/Domain: extracellular #status predicted <EXT>
F;07-198/Domain: alpha-2 #status predicted <EXZ>
F;212-277/Domain: immunoglobulin homology <Imm>
                                                                                                                                                                                                                                                                                                                                                       class I histocompatibility antigen HLA-B-4801 precursor - human (fragment)
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F:300-323/Domain: transmembrane #status predicted <TWM>
7:304-354/Domain: intracellular #status predicted <INT>
F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:117-180,219-275/Disulfide bonds: #status predicted
Score 51; DB 2; Length 354;
Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 51; DB 2;
Pred. No. 0.012;
                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7, 2000, 18:04:41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                             Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: February
Job time: 22207 sec
                                                                                                                                                                 1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA
Residues: 1-354 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RESLRNLRGY 10
      Query Match
                                                                                                                                ö
                                                                                                                                                                                     ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      윱
                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: S24436
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe
Rswatkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe
Rsture 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate
A;Reference number: S24027; MUID:92269956
A;Accession: S24436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: S24437
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate A;Reference number: S24027; MUID:92269956
A;Reference number: B24437
A;Roclecule type: mRNA
A;Roclecule type: mRNA
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C. Superfamily: class I histocompatibility antigen; immunoglobulin homology
C. Keywords: glycoprotein; transmembrane protein
C. Keywords: glycoprotein; transmembrane protein
F.1-17/Domain: slgnal sequence #status predicted <SIG>
F.17-299/Domain: alpha-2 #status predicted <EXT>
F.17-299/Domain: alpha-2 #status predicted <EXT>
F.107-198/Domain: alpha-2 #status predicted <EXT>
F.207-277/Domain: alpha-2 #status predicted <IMM>
F.307-353/Domain: immunoglobulin homology <IMM>
F.307-353/Domain: intransmembrane #status predicted <IMM>
F.307-353/Domain: intracellular #status predicted <INT>
F.102/Binding site: carbohydrate (Asn) (covalent) #status predicted
F.117-180,219-275/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: class I histocompatibility antigen; immunoglobulin homology C; Keywords: glycoprotein; transmembrane protein C; Keywords: glycoprotein; transmembrane protein C; Keywords: glycoprotein; transmembrane protein E;1-17/Domain: signal sequence #status predicted <SIG> F:17-299/Domain: stracellular #status predicted <EXT> F:17-299/Domain: alpha-2 #status predicted <EXT> F:107-199/Domain: alpha-2 #status predicted <EXT> F:12-277/Domain: immunoglobulin homology <IRMN> F:312-337/Domain: inmunoglobulin homology <IRMN> F:324-347/Domain: inransmembrane #status predicted <IRM> F:102/Binding site: carbohydrate (Asn) (covalent) #status predicted F:117-180,219-275/Disulfide bonds: #status predicted
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                   class I histocompatibility antigen HLA-B-3504 precursor - human (fragment) C:Species: Homo sapiens (man) C:Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          class I histocompatibility antigen HLA-B-4802 precursor - human (fragment)
                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 2; Length 354; 11arity 100.0%; Pred. No. 0.012; Conservative 0; Mismatches 0: Indele
                                    Indels
                             ö
0.012;
   Pred. No. 0.0
Mismatches
                                 ö
Best Local Similarity 100.0%;
Matches 10; Conservative (
                                                                                                                                Ouery Match
Best Local Similarity
Matches 10; Conserv
                                                                                               1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-354 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: HLA-B-4802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: HLA-B-3504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                               ò
                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ò
```

ô

Gaps

homo sapien homo sapien homo sapien homo sapien pan troglod homo sapien homo sapien homo sapien homo sapien homo sapien homo sapien

029631 P30505 P30506 P30503

P30498 P10321 P30484 P30499 P30686 P30500

J

score:

Title: Perfect sc Sequence:

protein

Run on:

Scoring table:

Searched:

```
1B33_HUMAN STANDARD; PRT; 270 AA.
P01890;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-60(B-40) B*4001 ALPHA CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                             MEDINE; 84000412.

MEDINE; 84000412.

MEDINE; 84000412.

"Primary Structure of papain-solubilized human histocompatibility antigen His-B40 (-Baw6). An outline of alloantigenic determinants."; antigen His-B40 (-Baw6). An outline of alloantigenic determinants."; elochemistry 22:3961-3969(1983).

-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-I- SUBJUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 51; DB 1; Length 270; 100.0%; Pred. No. 0.0048; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .n.

181

32 >>70 EX.

86 86

101 163

202 258

70 270

. 31205 MW; BFE44EFF CRC32;

Score 51, DB .

ed. No. 0.0'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    354 AA
                                                                                                                                           ALIGNMENTS
          1CXX_HUMAN
1B44_HUMAN
1C01_HUMAN
1C01_PANTR
1C02_HUMAN
1C02_HUMAN
                                                                        1C06_HUMAN
1C11_HUMAN
1C12_HUMAN
1C13_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A02186; HLHU40.
HSSP: P30466: LAGB.
MIM: 142830.
PROSITE: PS00290; IG_MHC; 1.
PFAM: PF00047; 1g; 1.
MHC I: Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 25,
(Rel. 25,
(Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91
182
86
86
101
202
270
270 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111111111
75 RESLRNLRGY 84
100.0
866.3
866.3
866.3
866.3
866.3
866.3
866.3
                                                                                                                                                                                                                                                                          HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
1B24_HUMAN
1D 1B24, HUMAN
AC P30470;
DT 01-APR-1993 (C
DT 15-JUL-1999 (C
 CARBOHYD
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                         RESULT 1
1B33_HUMAN
 ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           å
                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapien
                                                                                                                                                                                                                                                                                                                                                                                                                              P01890 homo sapien
                                                                                    (without alignments)
4.352 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                          ; Search time 68.63 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P30480
P30483
P30486
P30486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P30492 |
P30493 |
P30494 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P30475
P30476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              004826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P30469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P30473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P30478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P30479
                                                                                                                                                                                                                    82229
           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                              82229 seqs, 29864866 residues
                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                        February 8, 2000, 01:26:01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1808_HUMAN
1810_HUMAN
1811_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                              1B33_HUMAN
1B24_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1A02_PANTR
1B02_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B13_HUMAN
1B21_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1827_HUMAN
1828_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B43_HUMAN
1B46_HUMAN
1B48_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1B02_PANTR
1B04_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B32_HUMAN
1B34_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1B35_HUMAN
1B36_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B55_HUMAN
1B56_HUMAN
                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IB12_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1B25_HUMAN
1B26_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1B31_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBO7_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B22_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B23_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LB38_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LB39_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _HUMAN

    protein search, using sw model

                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                   US-08-653-294-34
51
1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                        Length DB
                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                         SwissProt_38:*
                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
```

Score

Result Š

Database :

ö

Gaps

ö

```
LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.; "Comparison of class I MHC alleles in humans and apes."; Immunol. Rev. 113:147-188(1990).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                        THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
 MEDLINE; 90201944
                                                                                                                                                                                                                                                                       25
                                                                                                                                                                                                                                                                                            25
207
207
209
309
333
333
227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-B OR HLAB.
                                                                                                                                                                                                     HSSP; P30685;
PROSITE; PS002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B02_HUMAN
P01889;
                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1B02_HUMAN
 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 엄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1A02_PANTR STANDARD; PRT; 362 AA.
P16210;
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                   -:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-:- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                             SEQUENCE FROM N.A.
MEDLINE; 92269956.
WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HLA-B alleles in a tribe of South American
                                                                                                                                              Amerindians indicate rapid evolution of MHC class I loc1."; Nature 357:329-333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 1; Length 35
100.0%; Pred. No. 0.0065; Viennitches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 6564795A CRC32;
                                                                                                                                                                                                                                                                                                                                    MIN: 12830; -PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                   EMBL; M86403; -; NOT_ANNOTATED_CDS. HSSP; P30685; 1A1N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39617 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                      MHC I; Transmembrane;

NON_TER 1 16
SIGNAL <1 16
CHAIN 17 354
                                                                                                                                                                                                      MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
291
301
325
                        HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1A02_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D., KRENSKY A.M., LAWLOR D.A., LITTMAN D.R., NORMENT A.M., ORR H.T., SALTER R.D., ZEMMOUR J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-FED-1991 (Rel. 17, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HLA CLASS 1 HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
PRECURSOR (B7.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 0.0066; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A-5 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
97E6CE8A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 AA.
                                                                                                                                                                                                                                                                                                                                              PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40487 MW;
                                                                                                                                                                                                                                                        EMBL; M30679; AAA87971.1; -.
                                                                                                                                                                                                                                                                                                                 PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                        IAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE; 90315860.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 90207291
```

362 AA.

PRT;

STANDARD;

```
"Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
                                                               01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
                                                                                                             Pan troglodytes (Chimpanzee).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                      MEDLINE; 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
                                                                                                                                                           SEQUENCE FROM N.A.
                                            1802_PANTR
P13751;
                                                                                                                                                                                                                                                 REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                               MAYER W.
                                                                                                                                                                                            KLEIN J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                       RESULT 5
1B02_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                         ò
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                      MEDLINE; 85287366.
SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
DUCEMAN B.W., WEISSMAN S.M.;
"Structure and polymorphism of class I MHC antigen mRNA.";
Immunogenetics 22:101-121(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                      ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
"Complete amino acid sequence of a papain-solubilized human
histocompatibility antigen, HLA-B7. 2. Sequence determination and
search for homologies."
Biochemistry 18:5711-5720(1979).
"Diversity of class I HLA molecules: functional and evolutionary interactions with T cells."; Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989).
                                                                                                                                                                                                                                                           THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 100.0%; Score 51; DB 1; Length 362; I Similarity 100.0%; Pred. No. 0.0066; 10; Conservative 0; Mismatches 0; Indels
                                                                                                                        SEQUENCE FROM N.A. ELLEXSON M.E., ZHANG L., HILDEBRAND W.H.; Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AALA -> GPW (IN REF. 3).

Q -> E (IN REF. 5).

W -> S (IN REF. 3).

R -> G (IN REF. 3).

GL -> RP (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M32317; AAA36230.1; -.
EMBL; M16102; AAA59622.1; ALT_SEQ.
EMBL; U29057; AAA91229.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A02185; HLHUB7.
PIR; B35997; B35997.
HSSP, P30460; 1AGB.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                  MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
207
209
310
310
110
125
227
227
227
3297
36
36
36
37
36
37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                     SEQUENCE OF 25-295
MEDLINE; 80088278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                        CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN.
B-2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                    THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 1; Length 36
100.0%; Pred. No. 0.0066;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 4BF65A6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AA
                                                                                                                                                                                                                                                                                                                                        PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ğ.
                                                                                                                                                                                                                                                                      EMBL; X13116; CAA31508.1; -.
                                                                                                                                                                                                                                                                                                                            PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1114
2006
2008
3308
332
362
1108
1100
                                                                                                                                                                                                                                                                                          PIR; S03538; S03538.
HSSP; P30685; 1AlN.
PROSITE; PS00290; IG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1B04_HUMAN
P30460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
1B04_HUMAN
ID 1B04_HI
AC P30460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
```

ö

Gaps

ö

g ò

1 RESLRNLRGY 10

Matches

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-APR-1993 (Rel. 25, 'Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARHAM F., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                             01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HIA-B OR HIAB.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.0066; Pred. O. Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9BED8199 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362 AA.
362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_1; 1.
MHC_1; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M24040; AAA59661.1; -. HSSP; P30466; IAGB. MIM: 142830; -. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
115
207
299
310
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 89235215
                                                                                                                                                                                                                                                   HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1808_HUMAN
AC 01-APR-1993
DT 01-APR-1993
DT 01-APR-1993
DT 01-APR-1993
DT 01-APR-1993
DT 01-APR-1993
CM HIA-B OR HIA-B OR HIA-B OR HIA-B OR HIA-B OC EUKATYOLA; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
   STATE THE TENT TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            원
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Antagonist HIV-1 Gag peptides induce structural changes in HLA B8."; J. Exp. Med. 184:2279-2286(1996).
-!- FUNCITON: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBJUNT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REID S.W., MCADAM S., SMITH K.J., KLENERMAN P., O'CALLAGHAN C.A., HARLOS K., JAKOBSEN B.K., MCMICHAEL A.J., BELL J.I., STUART D.I.,
   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                              HLA-B OR HLAB.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.0066; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                               SECUENCE FROM N.A.
MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA CLASS I HISTOCOMPATI)
B-8 B*0801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 1467B8EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M24036; AAA52662.1; --
PDB; 1AGB; 16-JUN-97.
PDB; 1AGC; 16-JUN-97.
PDB; 1AGD; 16-JUN-97.
PDB; 1AGF; 16-JUN-97.
PDB; 1AGF; 16-JUN-97.
PPB; 1AGF; 1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC I; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
115
207
299
310
334
110
125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 97130420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
SEQUENCE
```

SIGNAL

CHAIN

DOMAIN DOMAIN DOMAIN RESULT 7 1B07\_HUMAN

66

qq

δ

ö

Gaps

ő

```
IISSUE-BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B11_HUMAN
P30465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B11_HUMAN
  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ID DATE OF THE STANDARD OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                          FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BW-65(B-14) B*1402 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LITILE A. M., PARHAM P., "The HLA-BW75 subtype of B15: molecular characterization and comparison with crossreacting antigens."; Tissue Antigens 38:186-190(1991).
                                                                                                                                                                                                                                                 DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.0066; Live 0; Mismatches 0; Indels
                                                                                                          PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.; "Diversity and diversification of HLA-A,B,C alleles."; J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
Sutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE68AC9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P30460; 1AGB.
MIM: 142830; -
PROSTTE; PS00290; 1G_MHC; 1.
PFAM: PF00047; 1g; 1.
PFAM: PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M24032; AAA59664.1; -. HSSP; P30460; 1AGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1B10_HUMAN
ID 1B10_HUMAN STANDARD;
AC P30464;
                                                                                                                                                                                                                                                 SUBUNIT: DIMER C MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25
115
207
209
310
334
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 92196792.
                                                   SEQUENCE FROM N.A. MEDLINE; 89235215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
  SOTETTTTT THE TEST THE SOLUTION OF THE STANCE OF THE SOLUTION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 93056508.
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOIT E.D., PARHAM P.;
"Distinctive HiA-A,B antigens of black populations formed by
interallelic conversion.";
                                                                                                                                                        Tissue Antigens 47:265-274(1996).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin!; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 51; DB 1; Length 362; Llarity 100.0%; Pred. No. 0.0066; Conservative 0; Mismatches 0; Indels
MEDLINE; 96369309.
LIN L., TOKUNAGA K., TANAKA H., NAKAJIMA F., IMANISHI T.,
KASHIWASE K., BANNAI M., MIZUNO S., AKAZA T., TADOKORO K.,
SHIBATA Y., JUJI T.;
"Further molecular diversity in the HLA-B15 group.";
Tissue Antigens 47:265-274(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
i, 8CF9BCDO CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M75138; AAA59630.1; -.
EMBL; D50293; BAA08824.1; -.
HSSP; P30685; IAIN.
MIM; 142830; -.
PROSITE; P500290; IG_MRC; 1.
PFAM; PF00147; 14; 1.
MRC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                          MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RESLRNLRGY 10
```

```
FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
                 THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-B OR HLAB
                                         -i- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1813_HUMAN
P30466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
1B13_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B1503 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
   J. Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR'1993 (Rel. 25, Created)
01-FBB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
PRECURSOR.
HLA-B OR HLAB.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILIRE, 92569956.
WATKINS D.1., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GARBER T.L., DOGON A.L., LOND C.I., GHIM S.H.,
TROUP G.M., HUGHES A.L., LETVIN N.L.;
New recombinant HIA-B alleles in a tribe of South American
Amerindians indicate rapid evolution of MHC class I loci.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 100.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 0.0066; Matches 10; Conservative 0; Mismatches 0; Indels
                                                           -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RAMOS M., BARBER D.F., LAYRISSE 2., DE CASTRO J.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99D70546 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY
                                                                                                                                                                                                                                                                 EMBL; X61709; CAA43878.1; -. PIR; S16789; S16789. HSSP; P30665; IAIN. MIM; 142800; -. PROSITE; PS00290; IG_MHC; 1. PFAM; PF00047; 19; 1. MPC I; Transmembrane; Glycoprot SIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40387 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 357:329-333(1992)
                                     THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
115
207
299
310
334
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1B12_HUMAN
ID 1B12_HUMAN
AC P30513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCOORDING TO A STANDARD ACCOORDING TO A STAND
   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EWBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PARRAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 51; DB 1; 100.0%; Pred. No. 0.0066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Y SIMILARITY.
E80FC24C CRC32;
                                                                                                                                                                                                                                                                                    EMBL; M84382; AAA59632.1; --
EMBL; U70528; AAB16918.1; --
PIR; S24433; S24433.
HSSP; P30685; IAIN.
MIM; 142830; --
PROSTIE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF01029; MHC_1; 1.
MHC_1; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
115
207
209
310
334
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 RESLRNLRGY 108
                           MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 89235215.
```

```
EMBL, M28115; AAA59617.1; EMBL, M28109; AAA59617.1; EMBL, M28110; AAA59617.1; JOINED. EMBL; M28111; AAA59617.1; JOINED. EMBL; M28111; AAA59617.1; JOINED. EMBL; M28112; AAA59617.1; JOINED. EMBL; M28114; AAA59617.1; JOINED. PIR; A45880; A45880. PDB; IAN; 08-APR-98. PDB; IAN; 08-APR-98. PDB; IA9B; 18-NOV-98. PDB; IA9B; 18-NOV-98. MM; 142830; ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1114
2206
2298
3308
332
362
1110
288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 RESLRNLRGY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
115
207
209
339
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1B22_HUMAN
P30468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
1B22_HUMAN
            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "An altered position of the alpha 2 helix of MHC class I is revealed by the crystal structure of HLA-B*3501."; Immunity 4:203-214(1996).
                                                                                                                                                                                                                                                              HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE: 89339610.
OOBA T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
"The structure of HLA-B35 suggests that it is derived from HLA-Bw58
by two genetic mechanisms.";
Immunogenetics 30:76-80(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ဥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1B21_HUMAN STANDARD; PRT; 362 AA.
P30683.
01-ARR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
115-DEC-1998 (Rel. 37, Last annotation update)
116-DEC-1898 (Rel. 37, Last annotation update)
PRECURSOR I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 25-300.
MEDLINE; 96209671.
SMITH K.J., REID S.W., STUART D.I., MCMICHAEL A.J., JONES E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
MENSERN R., ORTH P., ZIEGLER A., SAENGER W.;
Submitted (APR-1998) to the PDB data bank.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.0066; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                               Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
038EC3FC CRC32;
                                                                                                                                  HDS., ...
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40275 MW;
                                                                                                       EMBL; M24039; AAA59662.1;
HSSP; P30460; 1AGB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                        MHC I; Transmembrane;
SIGNAL 1 2
CHAIN 25 36;
                                                                                                                                                                                                                                                                                                                                                                                                                         110
125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BELL J.I.;
                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
        STITE TETTER SO SET TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  유
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the EMBL outstation the European Bloinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseelab-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDLINE; 91365651.

CHERTKOFF L.P., HERRERA M., FAINBOIM L., SATZ M.L.;

COMPLETE nucleotide sequence of a genomic clone encoding HLA-B35
isolated from a Caucasian individual of Hispanic origin.

Identification of a new variant of HLA-B35.",

Hum. Immunol. 31:153-158(1991).

- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO

THE IMMUNE SYSTEM.

THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.0066; Pred. No. 0.1006; o. Indels 1. 100.0%; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B-35 B*3501 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC TAIL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40455 MW; AECIC675 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 AA
```

SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN)

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN. EXTRACELLUIAR ALPHA-1. EXTRACELLUIAR ALPHA-2. EXTRACELLUIAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 92176661.
ZEMMOUR J., LITILE A.M., SCHENDEL D.J., PARHAM P.;
"The HLA-A,B 'negative' mutant cell line C1R expresses a novel
HLA-B35 allele, which also has a point mutation in the translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1B23_HUMAN STANDARD; PRT; 362 AA.
P30469;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 51; DB 1; Length 362; illarity 100.0%; Pred. No. 0.0066; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                       CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                  D7B5C2C9 CRC32;
                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                             SIMILARITY.
SIMILARITY.
                                                                                                                                                                 PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Immunol. 148:1941-1948(1992).
                                                                                                                                                                                                                                                                                                                                                                    Ξ.
                                                                                                                              HSSP; P30685; 1A1N.
MIM; 142830; -.
PROSITE; PS0<u>0</u>290; IG_MHC; 1.
                                                                                                               EMBL; M63454; AAA59682.1; -. HSSP; P30685; 1AlN.
                                                                                                                                                                                                                                                                                                                                                                    40564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B23_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
ô
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                            HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
B-35 B*3503 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 100.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 0.0066; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                  CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
;; 4222D30A CRC32;
                                                                                                                                                 EMBL; M81798; AAA59684.1; -.
EMBL; D5029; BAA08828.1; -.
HSSP, P30685; 1AlN.
MIN; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PRAM; PF0047; 14; 1.
PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8, 2000, 01:26:01
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                  40515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: February
Job time: 1561 sec
                                                                                                                                                                                                                                                                                                                                                                          333
110
125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                   MHC I;
SIGNAL
                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Database

```
sapien sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                           homo
homo
homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
0078174
0019638
0019557
0019576
0019576
0019581
0019581
0019581
0019581
0019581
0019581
0019581
0019581
0019581
0019581
0019781
0019776
0019776
0019776
0019776
0019776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D., RUNGKOUNG B., BEJCHANDRA S., SUDMAKOUNG B., BEJCHANDRA S., SUDMAILTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AFO14769; AAB67807.1; -. PFRAM; PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Match 100.0%; Score 51; DB 7; Length 81; Local Similarity 100.0%; Pred. No. 0.013; les 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               019525 PRELIMINARY; PRT; 81 AA.
019525; 01-JAN-1998 (TYEMBLrel. 05, Created)
01-JAN-1998 (TYEMBLrel. 05, Last sequence update)
01-NOV-1998 (TYEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HIA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 1
81 81
81 AA, 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
0078174
019563
019567
019575
019575
019577
019581
029667
029665
029665
029665
029666
029667
029667
029666
029666
029666
029666
029666
029666
029666
029666
029666
029666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RESLRNLRGY 10
  NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    019523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
  RESULT
019525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SETT REPORTED TO SET THE SET T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3844488
8644481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapien
                                                                                                                                 Search time 176.54 Seconds (without alignments)
3.927 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  уошо
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     019523
019525
019525
019529
019533
019533
019533
019534
019548
019548
019548
019550
019550
019550
                                       Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                  GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                                       225878 seqs, 69334122 residues
                                                                                                                                   8, 2000, 19:16:17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       019523
019525
019527
019529
019531
019531
019531
019531
019543
019545
019548
019550
019551
019550
019550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0% Listing first 45
                                                                                                                                                                                                       US-08-653-294-34
51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                                                                                    1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BB
                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_mhc:*
                                                                                                                                     February
```

Score

Result No.

2008497008497008497008497

ö

Gaps

ö

NON\_TER NON\_TER SEQUENCE

019527

RESULT 019527

g

õ

Wed Feb

```
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D., RUNGROUNG E., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AFOL1775; ARBG7813.1; -- PFAM: PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
SUBMILLEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AFO14777; ABGF815.1; -.
PFAM: PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 51; DB 7; Length 81; 100.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
SUBMILTGE (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO14779; ARBG/B17.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                          Length 81;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
MIC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          019533;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HIA-B (FRAGMENT).
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                        100.0%; Score 51; DB 7; 100.0%; Pred. No. 0.013;
                                                                                                                        1 1
81 81
81. AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                             66 RESLRNIRGY 75
                                                                                                                                                                                                                                                                                                      1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                  NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                       019531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            019533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
019531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
019533
    SFTWRRA
                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                            SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
SUNDHITCHG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014771; AAB67809.1; -.
PFAM; PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014773; AAB67811.1; -.
PFRAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 51; DB 7; Length 81; 100.0%; Pred. No. 0.013; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Score 51; DB 7; Length 81;
Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
                                                                                                                                                                                                                        1 1
81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AA
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequ 01-NOV-1998 (TrEMBLrel. 08, Last annumHC CLASS I ANTIGEN HLA-B (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC CLASS I ANTIGEN HLA-B (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                       100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 05, (TrEMBLrel. 05, ) (TrEMBLrel. 08, )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 1
81 81
81 AA; 9405 MW;
                                                                                                                                                                                                                                                                                                                       Ouery Match 100.

Best Local Similarity 100.

Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.

Best Local Similarity 100.

Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                           1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1998
01-JAN-1998
01-NOV-1998
```

ö

Gaps

ö

NON\_TER SEQUENCE

019529

11D 019529 OD DT 0019529 OD DT 0019529 OD DT 0019529 OD DT 0019529 OD DT 0019529

RESULT

a

ö

NON\_TER

ö

```
Gaps
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                               ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. CHANDANAYINGYONG D., SIRIKONG M., LUANGIRAKOOL K., SRINAK D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 51; DB 7; Length 83; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
Submitted (Jul-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014785; AAB67823.1;
PFAM; PF00129; MHC_L; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 83;
              Query Match 100.0%; Score 51; DB 7; Length 81 Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AFO14787; AAB67825.1; -.
PFAM: PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                            01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-INOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05, Last sequence update)
08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 51; DB 7; 100.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1
83 83
83 AA; 9731 MW; 24B8D666 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 1
83 83
83 AA; 9731 MW; 24B8D666 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
MHC CLASS I ANTIGEN HLA-B (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                            1 RESLRNLRGY 10
                                                                                                                                   1 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          019541
                                                                                                                                                                                                                                                                  019539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
19541
10 19541
10 019541
10 019541
10 019541
10 019541
10 01-0AN-
1
                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                           ö
                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100.0%; Score 51; DB 7; Length 81;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                            Query Match 100.0%; Score 51; DB 7; Length 81; Best Local Similarity 100.0%; Pred. No. 0.013; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK RUNGROUNG E., BEJCHANDRA S.; Submitted d. (Jul.-1997) to the EMBL/Genbank/DDBJ databases. EMBL; AR014781; AR67819.1; -. PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
SUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014783; AAB67821.1;
FFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last Sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1
81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                               073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                   Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AA; 9405 MW; 073087CE CRC32;
                  1 1
81 81
81 AA; 9405 MW;
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                        1 RESLRNLRGY 10
                                                                                                                                                                                                                                               1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
              NON_TER.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                              019535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           019537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     019537
                                                                                                                                                                                                                                                                                                                                    RESULT
019535
SFFW
                                                                                                                                                                                                                                                                                                                                                                                õ
```

ö

ö

RESULT 019543

ò a

```
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 08, Last sequence update)
MHC. CLASS I HLA-B (FRAGMENT).
HOMO Saplens (Human).
Elwaryota, Metazoa, Chordata; Cranlata; Vertebrata; Mammalla;
Eutharyota, Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 51; DB 7; Length 89; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 51; DB 7; Length 89; 100.0%; Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                        CHOPEK M., CAO K., ZHANG G.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; U88249; AAB44893.1; -.
PFAM: PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. CHOPEN W.A. CHOPEN M., CAO N., ZHANG G.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases. EMBL, 188254; AAB484891.;
PFAM; PFO0129; MHC_I: 1.
                               01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Last sequence update)
, Last annotation update)
                                                                                                                                                                                                                                                                                                               89 AA; 10489 MW; A7D3DF93 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FA3EFCDC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                     0: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
MHC CLASS I ANTIGEN (FRAGMENT).
HLA-B.
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 AA; 10501 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 RESLRNLRGY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 68
                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P79620
P79620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 019548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
019548
AC 019548
AC 019548
DT 01-7AN
DT 01-NOV
DE MHC CL
GN HIA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
P79620
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014789; AAB67827.1; -.
PFAM; PF00129; MHC_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 51; DB 4; Length 89; 100.0%; Pred. No. 0.014; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARTER V., DUNN P.P.;
"Identification of a novel HLA-B*07 allele.";
Submitted (PRR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ237594; CAB40714.1; -.
                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 51; DB 7; 100.0%; Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 89
89 AA; 10609 MW; 659B735B CRC32
                                                                                                                        83 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 1
83 83
83 AA; 9731 MW; 24B8D666 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequ
01-NOV-1998 (TrEMBLrel. 08, Last anno
HAA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last seq 01-NOV-1999 (TrEMBLrel. 12, Last ann UUMAN LEUCOCYTE ANTIGEN B (FRAGMEN)
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                  1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9Y452
Q9Y452;
                                                                                                                     019543
```

ö g ö

Gaps ö

RESULT P79615

ò g

ö

ö

;

```
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RN [1]
RA CAO K., BURDETT L., ZHANG H., FERNANDEZ-VINA M.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF016299; AAB69444.1; -.
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10550 MW; 11452E40 CRC32;
```

Query Match 100.0%; Score 51; DB 7; Length 89; Best Local Similarity 100.0%; Pred. No. 0.014; Matches 10; Conservative 0; Mismatches 0; Indels Qy 1 RESLRNLRGY 10 111111111 Db 74 RESLRNLRGY 83

Search completed: February 8, 2000, 19:16:17 Job time: 21504 sec

THIS PAGE BLANK (USPTO)

```
! U52177 Human MHC class I ant
! U88249 Human MHC class I HLA
! AF181842 Homo saplens MHC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

1 (bases 1 to 243)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K., Rungroung, E. and Bechandra, S.
Bl5 alleles (B*1521)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K., Rungroung, E. and Bechandra, S.
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSHLABM1 243 bp DNA PRI 26-MAR-1997 Human cell line THAI DCH023 MHC class I HLA-B gene (allele HLA-B*1525), exon 2.
                                                                                                                                                                    seq_documentation_block:
LOCUS HSHLABK1 243 bp DNA PRI 26-MAR-1997
DEFINITION Human cell line THAI DCH022 MHC class I HLA-B gene (allele HLA-B*1521), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Corporation - The corporatio
     0.0613
0.0613
0.0613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: HSHLABK1 from: 1 to: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 CGAGAGCCTGCGGAACCTGCGCGCTAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
  178.85
178.85
178.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U91334.1 GI:1906675
                                                                                                                                                                                                                                                                                          U91332
U91332.1 GI:1906671
        51.00
51.00
51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-34 x HSHLABK1
                                                                                                                     seq_name: gb_pr2:HSHLABK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr2:HSHLABM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS HSHLABM1
DEFINITION Human cell l1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                       1 of 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 of 2
                                                                                                                                                                                                                                                                                                                                                                                                             human.
gb_pr2:HSHYUNA1
gb_pr2:HSU88249
gb_pr4:HUM31HLA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ехоп
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Documentation ...
1 U91332 Human cell line THAI DCH
2 U91334 Human cell line THAI DCH
3 U91335 Human cell line THAI DCH
3 U91336 Human cell line THAI DCH
4 MF01476 Homo sapiens MHC class
5 AF01477 Homo sapiens MHC class
5 AF01477 Homo sapiens MHC class
6 AF01477 Homo sapiens MHC class
7 AF01478 Homo sapiens MHC class
8 AF01478 Homo sapiens MHC class
1 AF01478 Homo sapiens HLA-B gen
1 AJ131852 Homo sapiens MHC class
1 AF01629 Homo sapiens HLA-B gen
1 AJ23794 Homo sapiens MHC class
1 AF01708 Homo sapiens MHC class
1 AF0130 Human HLA-B gene, allele
1 U76396 Human HLA-B gene, allele
1 U76394 Human HLA-B gene, allele
1 U76394 Human HLA-B gene, allele
1 U76395 Human HLA-B gene, allele
1 U76395 Human HLA-B gene, allele
1 U76396 Human HLA-B gene, allele
1 U76396 Human MHC class I antige
1 U76394 Human MHC class I antige
1 U76394 Human MHC class I antige
1 U76394 Human MHC class I antige
1 U76395 Human MHC class I antige
1 U76306 Human MHC class I antige
1 U56008 Human MHC Class I antige
                                                                                                                                                                                                                               -MODEL-frame+_p2n.model -DEV-x1p
-Q-Cqqn1_L1/USPTO-2pool.V1080865329f/runat_04022000_160701_15779/app_query.fasta.2
-DB-GenEmbl -OFWT-fastap -SUFFIX--rge -GAPOP-12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -QGAPOP-4.500
-GAPEXT-6.050 -XGAPOP-10.000 -XGAPEXT-0.500 -FGAPOP-6.000
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cd1
-LST-45 -DOCALIGN-200 -THR_SCORE-pct -ALIGN-15 -WODE-LOCAL
-OUTPMT-pfs -NORM-ext -MINIEN-0 -MAXEN-1000000 -USER-US08653294
-NCPU-6 -ICPU-3 -NO_XLPXY -WAIT -THREADS-1
                                                                                                                     About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
        out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .0613
        OM of: US-08-653-294-34 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
Query: 05-08-653-294-34
Query: 05-08-653-294-34
Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176.920000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Date: Feb 8, 2000 10:25 PM
                                                                                                                                                                                                     Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9bpr2: AF014773

9bpr2: AF014773

9bpr2: AF014779

9bpr2: AF014779

9bpr2: AF014781

9bpr2: AF014785

9bpr2: AF014789

9bpr2: AF014789

9bpr2: AF014789

9bpr1: HSA7603

9bpr1: HSA7603

9bpr1: HSA7603

9bpr2: HS0130081

9bpr2: HS0130081

9bpr2: HS0130081

9bpr2: HS0130081

9bpr2: HS013091

9bpr2: HS013773

9bpr2: HS019191

9bpr2: HS019191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           score_list:
Sequence
gb_pr2:HSHLABK1
gb_pr2:HSHLABM1
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 246)

1 (Dases 1 to 246)

2 (Dases 1 to 246)

3 (Dases 1 to 246)

4 (Dases 1 to 246)

5 (Dases 1 to 246)

5 (Dases 1 to 246)

6 (Dases 1 to 246)

7 (Dases 1 to 246)

8 (Dases 1 to 246)

8 (Dases 1 to 246)

9 (Dandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

8 (Dandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

8 (Direct Submission

8 (18 - 197) Transfusion Medicine, Faculty of Medicine, Sirital, Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF014769 246 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
AF014769
                                                                                                                                                                                                                                          /note="Allele: HLA-B*1525; similar to exon 2 of B*1501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=3
/product="MHC class I antigen HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                     Lengin: 10 Gaps: 0 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                             ų
                                                                                                               /cell_line="THAI DCH012"
/cell_type="Iymphoblastoid"
1. 243
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="6p21"
/cell_type="lymphoblastoid"
<1. .>246
/gene="HIA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH4060"
/chromosome="6"
                                                                                                                                                                                                                                                                                           28
                             /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        195 CGAGAGAGCCTGCGGAACCTGCGGGGGTAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                   /db_xref="taxon:9606"
/chromosome="6"
/map="6p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /allele="HLA-B*1502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                             84 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF014769.1 GI:2345103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="HLA-B"
                                                                                                                                                                                                                                                                     /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: HSHLABO1
  1. .243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-34 x HSHLABO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr2:AF014769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AF014769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thailand
                                                                                                                                                                                                                                                                                             22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                   Chandanayingyog, D., Strikong, M., Srinak, D., Longta, K.,
Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and
Grosse-Wille, H.
2 (bases) I to 243
Chases I to 243
Chase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and
Cosse-Wilde, H.
Direct Submission
Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 243)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K., Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and Grosse-Wilde, H.
                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo saplens"
/organism="Homo saplens"
/chromosome="6"
/map="6p21"
/map="6p21"
/cell_type="lymphoblastoid"
/cell_line="THAI DCH023"
/ gene="HAI B"
/note="similar to exon 2 of B*1501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U91336.1 GI:1906679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B15 alleles (B*1525)
Unpublished
     (bases 1 to 243)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: HSHLABM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-34 x HSHLABM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pr2:HSHLAB01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                 Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l of 2
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
SEGMENT
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
REFERENCE
AUTHORS
                                                                                                       TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                       FEATURES
```

```
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="2"
/number=2
                                        Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                           alignment_block:
US-08-653-294-34 x AF014771
                                                                                                                                                              to: AF014771
                                                                                                                                                                                                                                                                       seq_name: gb_pr2:AF014773
                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AF014773
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rhailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                           alignment_scores
                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="MHC class I antigen HLA-B"
/protein_id="AAB67809.1"
/protein_id="AAB67809.1"
//db_xref="C0::2345108"
//tanslation="TAMSRPGREPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPHIE
//tanslation="TAMSRPGRESLRHRGYYNQSEA"
// R2 9 28 t
/protein_id="AAB67807.1"
/db_xref="G1:2345104"
/translation="TAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPWIE
QEGPEWWDRNTQISKINTQTYRESLRNLRGYYNQSEA"
81 c 82 g 28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:

LOCUS AF014771 246 bp DNA PRI 27-AUG-1997

DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.

ACCESSION AF014771

VERSION AF014771 GI:2345107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotzi Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
Chases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Bl5 alleles (B*1502)
Unpublished
2 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Direct Submission
                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /cell_type="lymphoblastoid"
<1. .>246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9606"
/cell_line="Thai DCH4061"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .246
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                        1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'allele="HLA-B*1502"
                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <1. .>246
/gene="HLA-B"
/codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene-"HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /map="6p21"
                                                                                                                                                              Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="2
                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-34 x AF014769
                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AF014769
                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_pr2:AF014771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                            ๙
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                alignment_scores:
                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
```

```
Percent Smilarity: 51.00 Gaps: 10

Ratio: 5.100 Opercent Identity: 100.000

Jugnment_Dio.000

Jugnment
```

alignment\_block:

SOURCE ORGANISM

TITLE JOURNAL REFERENCE AUTHORS

TITLE JOURNAL

REFERENCE AUTHORS

DEFINITION

ACCESSION

VERSION KEYWORDS

```
/gene- na...
/gene- na...
/codon_start=3
/codon_start=3
/product="MHC class I antigen HLA-B"
/protein_id="AAB67815.1"
/db_xref="G1:2345120"
/translation="TAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRWAPRAPWIE
QEGPEYWDRNTQ1SRNTQTYRESLRULRGYYNQSEA"
82 q 28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2. (bases 1 to 246)
ChandanayIngyong, D., Strikong, M., Luangtrakool, K., Srinak, D.,
ChandanayIngyong, D. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), excon 2 and partial cds.
AF014777 GI:2345119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS
LOCUS
AF014779 246 bp DNA PRI 27-AUG-1997
DEFINITION Homo saptens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., B15 alleles (B*1502)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laugin: 10
Gaps: 0
Gaps: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="lymphoblastoid"<11..>246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH017"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 CGAGAGACCTGCGGGAACCTGCGGGGTAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /allele="HLA-B*1502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene-"HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l. .246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene-"HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map-"6p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AF014777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-34 x AF014777
                                          seq_name: gb_pr2:AF014777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_pr2:AF014779
                                                                                                                          seq_documentation_block:
LOCUS AF014777
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Marazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)

2 (bases 1 to 246)

3 (bases 1 to 246)

4 (bases 1 to 246)

5 Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

8 (bases 1 to 246)

8 (bases 1 to 246)

8 (bases 1 to 246)

9 (bases 1 to 246)

10 (bases 1 to 246)

11 (bases 1 to 246)

12 (bases 1 to 246)

13 (bases 1 to 246)

14 (bases 1 to 246)

15 (bases 1 to 246)

16 (bases 1 to 246)

17 (bases 1 to 246)

18 (bases 1 to 246)

18 (bases 1 to 246)

19 (bases 1 to 246)

10 (bases 1 to 246)

2 (bases 1 to 246)

2 (bases 1 to 246)

3 (bases 1 to 246)

3 (bases 1 to 246)

4 (bases 1 to 246)

5 (bases 1 to 246)

5 (bases 1 to 246)

6 (bases 1 to 246)

8 (bandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungtroung, E. Suhitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Medicine, Faculty of Medicine, Medicine, Medicine, Medicine, Medicine, Faculty of Medicine, Med
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"MHC class I antigen HLA-B".
/protein_id="AAB67813.1"
/protein_id="AAB67813.1"
/db_xref="GI:2345116"
//db_xref="GI:2345116"
/db_xref="GI:2345116"
                                                                                                                                                                                                                                                                                                                                                                                                                                        AF014775 246 bp DNA PRI 27-AUG-1997
Homo saptens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
AF014775 GI:2345115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cell_type="lymphoblastoid"
<1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH018"
/chromosome="6"
                                                                                to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 246
                                                                                                                                                                                                       198 CGAGAGCCTGCGGAACCTGCGGGCTAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /allele="HLA-B*1502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <1. .>246
                                                                            Align seg 1/1 to: AF014773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AF014775
US-08-653-294-34 x AF014773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-34 x AF014775
                                                                                                                                                                                                                                                                                                                         seq_name: gb_pr2:AF014775
                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AF014775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
```

source

FEATURES

gene

exon

CDS

BASE COUNT ORIGIN

SOURCE

FEATURES

```
2 (bases 1 to 246)
chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Direct Submission
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 bp DNA PRI 27-AUG-1997 class I antigen HLA-B gene (HLA-B*1502 allele),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Unpublished
[Dipublished 10.16]
                   Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung,E. and Bejchandra,S.
Bis alleles (B*1502)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                     /cell_type="lymphoblastoid"
<1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                     1. 246
/organism="Homo sapiens"
/oryanism="Homo sapiens"
/orsul_line="Thai DCH003"
/chromosome="6"
/map="6p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /allele="HLA-B*1502"
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACOUNTY OF THE COURT OF T
                                                                                                                                                                                                                                                                                                                                                                                                                                                            <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                          1. .246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                             /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                         /note="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AF014781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-34 x AF014781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_pr2:AF014783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AF014783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                    TITLE
JOURNAL
REFERENCE
AUTHORS
   REFERENCE
AUTHORS
                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Faculty of Medicine,
Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), exon 2 and partial cds. AF014781 GI:2345127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246 c. Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungyoung, E. and Bejchandra, S.

Bubsyoung, E. and Bejchandra, S.

Unpublished
                                                                                                                                                                                                2 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D. Rungroung, E. and Bejchandra, S.
Bungroung, E. and Bejchandra, S.
Direct Submission Medicine, Faculty of Med Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Med Siriraj Hospital, Mahidol University, Prannok Road, Bangkok Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10 Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                // 246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH002"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="lymphoblastoid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /allele="HLA-B*1502"
1. .246
                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AF014779 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=3
   AF014779
AF014779.1 GI:2345123
                                                                                                                                                                                                                                                                                                                                                                                                                                                       <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-34 x AF014779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_pr2:AF014781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
Locus AF014781
                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                        human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCUS
ACCESSION
VERSION
KEYWORDS
                                                                    ORGANISM
                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                    TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
```

ORIGIN

THE PERSON NAMED IN

TITLE JOURNAL

FEATURES

gene

exon

CDS

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

El (Abases I to 250)

Elsaleles (B*1525)

L (Apases I to 250)

C (Abases I to 250)

E (Abases I to 250)

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Direct Submission

L Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Sirira; Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
                                                                                                                                                                                                                                                                                                            /product="MHC class I antigen HLA-B"
/protein_id="AAB67823.1"
/protein_id="C1:2345135"
/d_xxef="C1:23451356"
/translation="PYTAMSRPGREPRFIAVGYUDDTQFVRFDSDAASPRMAPRAPW
IEQEGPEXWDRETQISKINTQTYRESIRNLRGYYNOSEA"
84 g 31 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele), aroun 2 and partial cds.
AF014787 GI:2345139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                            /cell_type="lymphoblastoid"
1. .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymphoblastoid"
1. .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1. .250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH3258"
/chromosome="6"
/map="5p21"
  /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH1109"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 CGAGAGAGCCTGCGGAACCTGCGGGGGTAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                           /allele="HLA-B*1525"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AF014785 from: 1
                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                 /gene="HLA-B"
                                                                                                                                                                                                                                                        <1. .>250
/gene="HLA-B"
                                                                                                                                       /gene="HLA-B"
                                                                              /map-"6p21
                                                                                                                                                                                                                                        /number=2
                                                                                                                                                                                                                 /note-"2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-34 x AF014785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr2:AF014787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
Locus AF014787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                               54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                         gene
                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                       Rungroung, E. and Bejchandra, S. Direct Submission States Submission Submitted (B-UDL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele), exon 2 and partial cds. AF014785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homosapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
BlS allales (8*1525)
Unpublished
2 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                /cell_type="lymphoblastoid"
<1. .>246
/gene="HLA-B"
                                                                                                                     1. .246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH016"
/chromosome="6"
/map="6p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                /allele="HLA-B*1502"
                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                           <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                     /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF014785.1 GI:2345135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          250 bp
                                                                                                                                                                                                                                                                                                                                                                             /number=2
                                                                                                                                                                                                                                                                                                                                                     /note="2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-34 x AF014783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AF014783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_pr2:AF014785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AF014785
                                                                              Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
```

BASE COUNT ORIGIN

LOCUS

ACCESSION

VERSION KEYWORDS

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

FEATURES

```
/genc- ......./
/codonctart-1
/product-"MHC class I antigen HLA-B"
/protein_id-"AAB67827.1"
/db_xref="G1:2345144"
/translation="FYTAMSRPGRGEPRFIAVGYVDDTOFVRFDSDAASPRMAPRAPW
IEQEGPEYNDRETQISKTNTOTYRESIRNLRGYYNQSEA"
IEQEGPEYNDRETQISKTNTOTYRESIRNLRGYYNQSEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 254)
Mitsuishi,Y.
Direct Submission
Submitted (04-Jun-1996) Tissue Typing Laboratory, UCLA School of Medicine, 950 Veteran Ave., Los Angeles, CA 90095, USA
Location/Qualifiers
1 . 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS HSB1501N1 254 bp DNA PRI 10-JUL-1996
DEFINITION Human MHC class I protein HLA-B heavy chain (B*1501new allele)
ACCESSION U59965.1 GI:1399896
VERYWORDS HLA B antigen; major histocompatibility complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="peripheral blood mononuclear cells"
/call_type="peripheral blood mononuclear cells"
/map="6p21.3"
<1. .254
/gene="HIA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: HSB1501N1 from: 1
                                                                                                                                                                                                                                                                                                                                                  from: 1
       /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number=2
81 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-34 x HSB1501N1
                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AF014789
                                                                                                                                                                                                                     Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-34 x AF014789
                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr2:HSB1501N1
                                                                                                                                  54 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                      /gene- ....................../codon_start=1
/codoct="MHC class I antigen HLA-B"
/product="MHC class I."
/protein_id="AAB67825.1"
/db_xref="G1:2345140"
/translation="FYTAMSREGEPEFIAVGYVDDTQFVRFDSDAASPRMAPRAPW
IEQEGPEYWDRETQISKTNTQTYRESLRNLRGYYNQSEA"
81 c 84 g 31 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theres 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
Direct Submission
Direct Submission
Submitted (18-JUJ-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AF014789 250 bp DNA PRI 27-AUG-1997
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Englandenes (B*1525)
Unpublished
                                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /ceil_type="lymphoblastoid"
1. .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. 250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cbll_line="Thai DCH025"
/chromosome="6"
/map="6921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /allele="HLA-B*1525"
1. 250
/gene="HLA-B"
/note="2"
/gene="HLA-B"
/allele="HLA-B*1525"
1. .250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF014789
AF014789.1 GI:2345143
                                                         /gene="HLA-B"
                                                                                                              <1. .>250
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="HLA-B"
                                                                           /note="2"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=2
<1. .>250
                                                                                                                                                                                                                                                                                                                                            Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-34 x AF014787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AF014787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pr2:AF014789
                                                                                                                                                                                                                                                          54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human .
                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
```

Company of the Company

THIS PAGE BLANK (USPTO)

```
Streptococcus pneumoniae po
Genomic DNA sequence of Str
ADP-91ucose-pyrophosphoryla
A. thermophilum thermostabl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-5407-1995 (first entry)
pHLA-B7 expression vector.
perpression vector: pHLA-B7; bicistronic mRNA;
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reading frame;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 J03112486-A.

10 J14-MAY-1991.

17 22-SEP-1989; 247697.

18 22-SEP-1989; JP-247697.

19 P-25-SEP-1989; JP-247697.

19 P-25-SEP-1989; JP-247697.

10 Colfu ) OLYMPUS OPTICAL KK.

10 P-25-SEP-1989; JP-247697.

11 P-25-SEP-1989; JP-247697.

12 P-25-SEP-1989; JP-247697.

13 P-25-SEP-1989; JP-247697.

14 P-25-SEP-1989; JP-247697.

15 P-25-SEP-1989; JP-247697.

16 P-25-SEP-1989; JP-247697.

17 P-25-SEP-1989; JP-247697.

18 P-25-SEP-1989; JP-247697.

19 P-25-SEP-1989; JP-247697.

20 Animals and prodn. of monoclonal antibodies specific for the companion of monoclonal antibodies specific for
                                                                                                                                                                                                                                                                                                                                                                                     HLA-B35 exon. Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers
1. .354
/*tag-
/*tag-
/ocate "pBR322 backbone contg. bacterial origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   replication 355. 1170 /*tag= b //note= "kanamycin resistance gene open reading fthe gene is taken from the transposable element rn903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag- c
/note- "SV40 polyA signal sequence"
   1305
1353
1763
2553
475.43
495.66
672.62
1.0e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: Q12115 from: 1 to: 1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (1410. .1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .1089
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295 CGAGAGGCCTGCGGAACCTGCGCGGCTAC
   101.43
101.11
98.73
95.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВЪ.
                                                                                                                                                                                                                                                                                   O12115 standard; DNA; 1089 BP. O12115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID Q75974 standard; cDNA; 4059
AC Q75974;
                                                                                                                                                                                                                                                                                                                                                    29-AUG-1991 (first entry)
   33.00
33.00
33.00
                                                                                                                                                                             seq_name: N_Geneseq_36:Q12115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 51.00
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:Q75974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-34 x Q12115
                                                                                                                                                                                                                                                  seq_documentation_block
   N_Geneseq_36:V43032
N_Geneseq_36:V32620
N_Geneseq_36:Q80003
N_Geneseq_36:V29686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                       4 Inductor Control Lord New Colling Services of the New Colling Services of Services of Human hSK3 coding Sequence. DNA Services of Human hSK3 coding Sequence. DNA Services of Human Secreted protein 5' SET Services of Human Secreted protein 5' SET Services of Services of Third Shimman Folistating Services of Serv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIA-B35 exon. HIA-B35 gene - u pliA-B7 expression vector. New pHIA-B7/Deta-2 microglobulin e HIA-C exon Cb-1. HIA-C gene, D HIAA-C exon Cb-2. HIA-C gene, D HUMAN CPRMZ DNA. New Chemoprot Human CPRMZ mutant DNA. New ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huntingtin gene antisense produ
Mouse TNRL3 DNA. New Tumor Necz
Isopentenyl transferase ipt gen
Musculus tumour necrosis A
                                                                                                                                                                                                                                                                            -MODEL-frame+_p2n.model -DEV-xlp
-Q-Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-Q-Cgn1_1/USPTO_spool/US08653294/runat_0402000_160701_15807/app_query.fasta.2
-Q-Cgn1_1/USPTO_spool/US08653294/runat_04D0000
-GAPGATT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-GAPGATT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-GAPGAD-4.500 -QGAPGAT-0.005 -XGAPOP-10.000 -XGAPGAT-0.500
-FGAPOP-4.500 -PGAPGAT-7.000 -YGAPOP-10.000 -YGAPGAT-0.500
-TRANS-human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-ALIGN-15 -MODE-LOCAL -OUTFWT-pfs -NORM-ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOS9 | HLA-B35 exon 4059 | HLA-B35 exon 4059 | PHLA-B7 expr 4051 | PHLA-B7 expr 4055 | PHLA-B7 expr 4051 | HLA-C exon C 1101 | HLA-C exon C 1101 | HLA-C exon C 1323 | Human CPRW2 1324 | Human CPRW2 1490 | Acyl-ACP-th 1659 | Rat truncated h 2224 | Rat rSK3 cor 2224 | Rat rSK3 cor 2224 | Human Small 1661 | Human Small 1661 | Human Small 1660 | Human Human Small 1660 | Human H
                                                                                                                                                software, version 4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110000
1110000
1110000
110000
110000
110000
110000
110000
110000
110000
110000
110000
110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 14

2 14

2 18 21

3 18 43

5 18 21

5 18 21

5 18 21

5 18 21

5 18 21

5 18 21

6 18 22

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

10 18 3

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ESCOre I
0.0767
0.3497
0.4411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.40
26.56
43.77
232.16
249.05
418.34
                                                                                                                                             About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
   OM of: US-08-653-294-34 to: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255.05
1159.05
1159.05
1159.05
1169.05
1173.05
1183.05
1183.05
1193.05
1193.05
1193.05
1193.05
1193.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
1195.05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139.96
123.93
120.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000
                                                                            Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
Query: US-08-653-294-34
Query length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:x08414 --
N_Geneseq_36:x41493 --
N_Geneseq_36:v30458_0 +-
N_Geneseq_36:v30459_0 +-
N_Geneseq_36:v30459_0 +-
                                                                                                                                                                                                                                               Command line parameters:
                                                                            Date: Feb 8, 2000 7:31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:V21210 + N_Geneseq_36:X20248_07 N_Geneseq_36:T94815 + N_Geneseq_36:T42475 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:V59528
N_Geneseq_36:N81608
N_Geneseq_36:Q52673
N_Geneseq_36:Q47076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_36:Q12117
N_Geneseq_36:X22446
N_Geneseq_36:X22450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:V35447
N_Geneseq_36:V35458
N_Geneseq_36:V35472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:090126
N_Geneseq_36:T38418
N_Geneseq_36:094624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Geneseq_36:Q12115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:012116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_36:Q56202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:T15158
N_Geneseq_36:Q94625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Geneseq_36:X33449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_36:V01731
N_Geneseq_36:Q43711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:X13139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:Q72980
N_Geneseq_36:X23425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Geneseq_36:V18599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq_36:T32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:V35473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36:N91381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:X13401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -THREADS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Genesed_
```

οţ

```
/note= "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence" 2979, 2984
/*tag= m
                                                                                                                                                                                                                                                                                                                                                               /*tag= g //note= "multiple cloning site, forms a junction between the HiA-B7 sequence and the EMCV-CITE sequence, and is used to facilitate subcloning" 1889. 2479
/*tag= h //note= "murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nucleotides 255-843 of cloned EMCV genomic DNA. It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HIA-B7 stop codon on this biscistronic mRNA to be recognised by the ribosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2480. .2839
/*tag 1
/note- "encodes beta-2 microglobulin; this cDNA is deriv. from chimpanzee (differs to the human 2840. .2846
/*tag 1
/note- "encodes beta-2 microglobulin; this cDNA is deriv. from chimpanzee (differs to the human 2840. .2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= o
/ntag= n
/note= "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
T1903*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag* p
/note* "pBR322 backbone contg. bacterial origin of
replication, it represents nucleotides 2244-3193"
                                                                                                                                                                                                                                                              "encodes putative HLA-B7 heavy chain mature
                            sequences. The oligonucleotide removes a polyadenylation signal sequence originally found in the RSV DNA sequence. "
                                                                                                                    535. .1620
/*tag= c
/note= "HLA-B7 heavy chain open reading frame"
                                                                                                                                                                                              /note- "encodes putative signal peptide of the HLA-B7 heavy chain" | 607. .1620 | /*tag- e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note = "synthetic linker to facilitate cloning"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "3' untranslated region of the beta-2
microglobulin mRNA"
2847. 2870
/*tag= k
   modifies this regulatory sequence to effect
higher level of expression of downstream
                                                                                          /*tag= b
/label= consensus_Kozak_signal_sequence
                                                                                                                                                                                                                                                                                                                           untranslated sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "synthetic linker"
'UTR 3111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (3151. .3967)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= n
                                                                                                                                                                                                                                                                                         1621. .1853
/*tag= f
                                                                                                                                                                                                                                                                                                                                       chain mRNA"
                                                                                                                                                                                                                                                                                                                                                      1854. .1888
                                                                                                                                                                   909.
                                                                                                                                                                                                                                                                            peptide"
                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                     signal_peptide
                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                             misc_signal
                                                                                                                                                                                                                                 mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9429469-A.
22-DEC-1994.
                                                                                                                                                                                                                                                                                            3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3'utr
                                                                                                                        cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cds
   Lew D., Marquet M.

10. Marquet M.

11. Lew D., Marquet M.

12. MPI; 95-036494/05.

13. MPI; 95-036494/05.

14. MPI; 95-036494/05.

15. Meaveries for gene therapy, partic for tumours - comprising one transcribed encoding one or more cistron(s) which express of a genetic material encoding one or more cistron(s) which express of the management or therapeutic peptide(s).

15. Marquet M. 27. Sopp; English.

15. This HLA-B7 antigen encoding plasmid was developed to incorporate many advantageous features, eg. the kanamycin resisitance gene. The cradication of two open reading frames encoding portions of SV40 viral encoding lowers the risk of tumourigenicity. The vector may also operate as a cassette into which cistrons may be inserted and removed at will for the transcription and subsequent translation of peptides of interest. The vector is used partic. for the treatment of neoplastic disease, eg. melanoma, and provides enhanced gene delivery and expression to the vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. .599
1. .599
1. .529

/*tag- a
/note= "Rous sarcoma virus LTR promoter domain, derived
for the Schmidt-Rupin strain nucleotides
8673-9146. This region also includes a 56 bp
region of a synthetic oligonucleotide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-AUG-1995 (first entry)
pHLA-B7/beta-2 microglobulin expression vector.
expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7;
light beta-2 microglobulin; class I major histocompatibility complex;
mHC; bicistronic mRNA; human leukocyte antigen; HLA;
covalently closed circular DNA; ds
                                                                                                                                                                     /*tag= g
/note= "Rous sarcoma virus 3' LTR promoter region"
                                                            /*tag- e
/note- "3' untranslated region of HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1033 G;
                                                                                                                                  /note= "HLA-B7 open reading frame"
complement (2886. .3415)
            /*tag- d
/note= "SV40 small t intron"
complement (1561. .1794)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: Q75974 from: 1
                                                                                       heavy chain mRNA"
complement (1795. .2880)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051 C;
complement (1412. .1560)
                                                                                                                                                                                                                  /*tag= h
/note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2589 CGAGAGCCTGCGGAACCTGCGCGGCTAC 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q75973 standard; cDNA; 4965 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     975 A;
                                                                                                                                                                                                  .4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-34 x Q75974/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q75973
                                                                                                                                                                                                                                                                        27-MAY-1994; U06069, 07-JUN-1993; US-074344. (UNMI ) UNIV MICHIGAN. (VICA-) VICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.00
                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4059 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                             22-DEC-1994.
27-MAY-1994;
                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
 intron
                                            3'utr
                                                                                                         cds
                                                                                                                                                       ltr
```

HLA-B7

```
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VULUAL DOLLY DILLALIZATION.

PI LEW D, MARQUEEL M. Nabel EG, Nabel GJ;

LEW D, MARQUEL INC.

DR WPI: 95-036494/05.

DR WPI: 95-036494/05.

TO GENETIC GOTE ENCORING ONE OF MORE CISTON(S) Which express mention material encoding one or more ciston(s) which express properties of timmunogenic or therapeutic peptide(s)

Claim B; Page 41-42; 50pp; English.

CT the PHLA-BY/Deta-2 microglobulin plasmid expression vector, in addition of the Annamycian resistance gene, contrains the plasmid DNA encoding the class I major hisotocompatibility complex (MHC) antigen. The plasmid is class I major hisotocompatibility complex (MHC) antigen. The plasmid is designed to express these two proteins via a bicistronic mRNA in class I major hisotocompatibility complex (MHC) antigen. The plasmid is celling a protein of transcription of the mRNA is dependent on a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long terminal respect. Termination of transcription is dependent upon the polyadenylation signal sequence deriv. from the bovine growth hormone comprolled by the CTER. Finally the replication of the plasmid in controlled by the CTER. Finally the presence of a bacterial origin of replication. The vector is used partic. for the treatment of neoplastic controlled by the presence of a characterial origin of in vivo.

CT in vivo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 1; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C antigen. See also Q12117 (same patent) and J03112486 and J03112487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      012116;
29-AUG-1991 (first entry)
HLA-C exon Cb-1.
Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1338 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouality: 51.00 Length: 10 Ratio: 5.100 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1293 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: Q75973 from: 1 to: 4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1171 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID Q12116 standard; DNA; 1101 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAY-1991.
22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLXU ) OLYMDUS OPTICAL KK.
WPI; 91-182989/25.
P-PSDB; R12465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:Q12116
27-MAY-1994; U06069.
07-JUN-1993; US-074344.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-34 x Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4965 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J03112485-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
```

```
CPRM1; human; chemoprotector regulated modifier; genotoxin; cytotoxin; CPRM2; CPRM3; mCPRM1; allele s; allele r; gene therapy; antibody; detoxification; detection; mutant; cancer; carcinogenic; aflatoxin; treatment; neurodegeneration; Alzheimer's disease; malondialdehyde; cyclo-oxygenase reaction; prostaglandin metabolism; ss. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 2: Page 1: 13pp: Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C antimals and prodn. of sequence and 103112486 and J03112487.

Sequence 1101 BP: 215 A; 335 C; 379 G; 172 T;
                                                                                                                                                                                                                                                                                                                             49-AUG-1991 (first entry)
HLA-C exon Cb-2.
Human leukocyte antigen; probe; major histocompatibility complex;
MHC; class I; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 90.000
Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                               Align seg 1/1 to: Q12116 from: 1 to: 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: Q12117 from: 1 to: 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 CGAGTGAGCCTGCGGAACCTGCGCGCGTAC 324
                                                                                                                                                                                      1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 74. .994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID x22446 standard; DNA; 1323 BP.
                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID Q12117 standard; DNA; 1101 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-MAX-1991.
22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
P-PSDB; R12466.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X22446;
20-MAY-1999 (first entry)
Human CPRM2 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 44.00
Ratio: 4.889
Percent Similarity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:X22446
  4.889
90.000
                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:Q12117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-34_x Q12117
                                                                                   alignment_block:
US-08-653-294-34 x Q12116
      Quality:
Ratio:
                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J03112485-A.
```

N

```
Align seg 1/1
     8888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The actual control of metabolites, particularly aflatoxins userum.

The actoxification of metabolites, particularly aflatoxins

Claim 2; Fig 8; 31pp; German.

This sequence encodes a novel protein designated CPRM2 (chemoprotector regulated modifier) that inhibits the effects of genotoxic and/or regulated modifier) that inhibits the effects of genotoxic and/or cytotoxic substances. The invention describes the isolation of CPRM1, CPRM3, mcPRM1, allele s, and mcPRM1, allele r. Transformants containing such proteins are used to produce recombinant proteins and nucleic acids for use in gene therapy and to raise antibodies which are used to (i) detoxify geno- and/or cyto-toxic metabolites and (ii) detect or seed to (i) detoxify geno- and/or cyto-toxic metabolites and (ii) detect or containing containing indicative of increased risk of cancer, e.g. prenatally). The proteins can be used to eliminate carcinogenic allatoxins and to treat neurodegeneration, e.g. Alzhehmer's disease, associated with production of malondialdehyde, a toxic product or the cyclo-oxygenase reaction and prostaglandin metabolism.

Squence 1323 BP; 331 A; 368 C; 286 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes a novel protein designated CPRM2 which is a mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CPRM1; mouse: chemoprotector regulated modifier; genotoxin; cytotoxin; CPRM2; CPRM3; mCPRM1; allele s; allele r; gene therapy; antibody; detoxification; detection; mutant; cancer; carcinogenic; aflatoxin; treatment; neurodegeneration; Alzheimer's disease; malondialdehyde; cyclo-oxygenase reaction; prostaglandin metabolism; ss.
                                                                                                                                                                                    New chemoprotector regulated modifier proteins - useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New chemoprotector regulated modifier proteins - useful in the detoxification of metabolites, particularly aflatoxins Disclosure; Fig 12; 31pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: X22446 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a /product= "CPRM2 mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1058 AAAGAAAGTGTGAAAACAAAAGAGGTTAC 1029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                     30-DEC-1998.
24-JUN-1998. D01796.
24-JUN-1997; DE-026823.
(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-JUN-1997; DE-026823.
(DEKR.) DEUT KREBSFORSCHUNGSZENTRUM.
Praml C, Schwab M;
WPI; 99-081282/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
 /*tag= a
/product= "CPRM2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID X22450 standard; DNA; 1324 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-MAY-1999 (first entry)
Human CPRM2 mutant DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-653-294-34 x X22446/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:X22450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-DEC-1998.
24-JUN-1998; D01796.
                                                                                                                         Praml C, Schwab M;
WPI; 99-081282/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                             P-PSDB; W93087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; W93091
                                  WO9859055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9859055-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
```

```
Claim 2; Page 6; 7pp; Japanese.

This sequence represents the coding sequence for the Cuphea leptopoda acyl-ACP-thiosesterase (AAT). This sequence was isolated by synthesising a AAT cDNA, and using that sequence to probe for a fragment of the AAT gene, which was then amplified. AAT is a key enzyme in the synthesis of middle chain aliphatic acids, and as such is useful in pharmaceutical preparations, and foods.

Sequence 1490 BP; 351 A; 332 C; 402 G; 405 T;
chemoprotector regulated modifier that inhibits the effects of genotoxic and/or cytotoxic substances. The invention describes the isolation of CPRMI, CPRMI, allele s, and mCPRMI, allele r. Transformants containing such proteins are used to produce recombinant proteins and nucleic acids for use in gene therapy and to raise antibodies which are used to (1) detoxify geno- and/or cyto-toxic metabolites and (11) detect presence of CPRM proteins (or nucleic acid encoding them, including detection of mutations indicative of increased risk of cancer, e.g. prenatally). The proteins can be used to eliminate acrinopenic aflatoxins and to treat neurodegeneration, e.g. Alzheimer's disease, associated with production of malondialdehyde, a toxic product or the cyclo-oxygenase reaction and prostaglandin metabolism. Sequence 1324 BP; 332 A; 368 C; 338 G; 286 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cuphea leptopoda; aliphatic acid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding Cuphea leptopoda Hemsl. acyl-ACP-thio:esterase - for synthesis of middle chain aliphatic acids, useful in pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 1324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.00 Length: 10
4.333 Gaps: 0
90.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1994; JP-320547.
(NOR) NORINBUISANSHO CHUGOKU NOGYO SHIKENBACH
WPI; 96-365584/37.
P-PSDB; W02020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= Acyl-ACP-thioesterase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to reverse of: T32217 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T32217 standard; cDNA to mRNA; 1490 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acyl-ACP-thioesterase coding sequence. Acyl-ACP-thioesterase; AAT; cuphea lepmiddle chain aliphatic acid; ss. Cuphea leptopoda hemsi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 30. .1289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: X22450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-34 x X22450/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-FEB-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-34 x T32217/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:T32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio: 4.222
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-1994; 320547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J08173165-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prepns. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
```

```
DNA encoding calcium-activated potassium channel - useful in assays

T to identify compounds which increase or decrease potassium ion flux

Claim 3: Page 112: 151pp; English.

This sequence encodes the human small conductance calcium-activated

C potassium channel protein 3 (InSX3) of the invention. The proteins of the

invention are monomers of a calcium-activated potassium channel, where

C humaning in a calculated molecular weight of between 40 and

CC shows and (il) has a unit conductance of between 2 and 60 ps when the

CC monomer is in the functional polymeric form of a potassium chain and is

CC expressed in a Xenopus cocyte. Antibodies specific for the protein, and

CC probes specific for the DNA can be used to detect the presence of the

CC protein or DNA sequences in a sample. Host cells expression of the

CC protein can be used in assays to identify compounds which increase or

CC ell can also be used for the recombinant production of the protein. The

CC ell can also be used for the recombinant production of the protein. The

CC ell can also be used for determine mutations in the SK and IK

CC genes in a computer system. The proteins encoded by the SK and IK

CC an be used in a computer system for determining their three dimensional

Structure, which is useful for determining that bind to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding calcium-activated potassium channel - useful in assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1998 (first entry)
Rat rSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 3;
rSK3; rat; potassium ion flux; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                352 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 1674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 3.800 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: V35458 from: 1
                                                                                                                                                                                                  (ICAG-) ICAGEN INC.
(UYOR-) UNIV OREGON HEALTH SCI.
Adelnan DP, Bond CT, Maylie J, Silvia CP;
WPI; 98-207332/18.
P-PSDB; W63708.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ICAG-) ICAGEN INC.
(UYOR-) UNIV OREGON HEALTH SCI.
Adelman DP, Bond CT, Maylle J, Silvia CP;
WPI; 98-207332/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 CGGGAGGCGCTGAGGCGCTTC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
2. .2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID V35472 standard; cDNA; 2224 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-34 x V35458/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
                          19-MAR-1998.
10-SEP-1997; U16033.
17-APR-1997; US-044233.
11-SEP-1996; US-026451.
07-MAR-1997; US-040052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:V35472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-SEP-1997; U16033.
17-APR-1997; US-045233.
11-SEP-1996; US-026451.
07-MAR-1997; US-040052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1674 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09811139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
PERSE SERVICE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding calcium-activated potassium channel - useful in assays

To identify compounds which increase or decrease potassium ion flux

Claim 3: Page 105; 151pp; English.

This sequence encodes the rat small conductance calcium-activated

Claim 3: Page 105; 151pp; English.

This sequence encodes the rat small conductance calcium-activated

Contains the potassium channel, where can monomers of a calcium-activated potassium channel, where

Conformation are monomers of a calcium-activated potassium channel, where

Conformation are monomers of a calcium-activated potassium channel, where

Conformation are monomers of a calcium-activated of Detween 2 and 60 ps when the

Monomer is in the functional polymeric form of a potassium chain and is

conformation and sequences in a sample. Host cells expression of the

protein can be used in a sample. Host cells expression of the

Content or DNA sequences in a sample. Host cells expression of the

Content or DNA sequences in a sample. Host cells expression of the

Content or DNA sequences in a sample. Host cells expression of the

Content or DNA sequences in a sample. Host cells expression of the

Content or DNA sequences of deterting the protein. The transfected host

Coll can also be used for the recombinant production of the protein. The

Coll can also be used for determine mutations in the SK and IK

Genes in a computer system. The proteins encoded by the SK and IK

Contents of the computer system for determining their three dimensional

Contents of the contents of the contents of the protein of the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1998 (first entry)
Truncated human hSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 3;
hSK3; human; potassium ion flux; ss.
                                                                                                                                                                                                                                                                                                                                                01-OCT-1998 (first entry)
Rat trundated rSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 1;
rSK3: rat; potassium ion flux; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           398 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1997; U16033.
17-APR-1997; US-04533.
07-MAR-1997; US-04651.
(ICAG-) ICAGEN INC.
(UCAG-) ICAGEN INC.
(UGAC-) US-0400CT, Maylie J, Silvia CP; WPI: 98-207332/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: V35447 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       499 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                               2 GluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID V35458 standard; cDNA; 1674 BP.
AC V35458;
                                                                                                                                                                                                                                       seq_documentation_block:
ID V35447 standard; cDNA; 1659 BP.
AC V35447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           404 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-34 x V35447/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:V35458
                                                                                                                                                                        seq_name: N_Geneseq_36:V35447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1659 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; W63703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9811139-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
```

ID DE COS

```
to identify compounds which increase or decrease potassium ion flux claim 3; Page 123-124; 151pp; English.

This sequence encodes the rat small conductance calcium-activated potassium channel protein 3 (rsk3) of the invention. The proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer; (i) has a calculated molecular weight of between 40 and 80 kDa; and (ii) has a unit conductance of between 2 and 60 pS when the monomer is in the functional polymeric form of a potassium chain and is captessed in a Kenopus occyte. Antibodies specific for the protein, and probes specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expression of the protein or DNA sequences in a sample. Host cells expression of the protein can be used in assays to identify compounds which increase or decrease the potassium ion flux through the protein. The transfected host cell can also be used for the recombinant production of the protein. The SK and IK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding calcium-activated potassium channel - useful in assays to identify compounds which increase or decrease potassium ion flux claim 3; page 128-129; 151pp; English.

This sequence encodes the human small conductance calcium-activated potassium channel protein 3 (hSK3) of the invention. The proteins of the invention are monomers of a calcium-activated potassium channel, where the monomer: (i) has a calcium-activated potassium channel, where the monomer is in the functional polymeric form of a potassium chain and is expressed in a Xenopus cocyte. Antibodies specific for the protein, and probes specific for the DNA can be used to detect the presence of the protein or DNA sequences in a sample. Host cells expression of the protein can be used in assays to identify compounds which increase or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human hSK3 coding sequence.
Small conductance calcium-activated potassium channel protein 3;
hSK3; human; potassium ion flux; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 38.00 Length: 10
Ratio: 3.800 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        537 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adelman JP, Bond CT, Maylle J, Silvia CP;
WPI; 98-207332/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            588 CGAGAGGCGCTGAGGCGCTGAGGGCTTC 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualiflers
252. .2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: V35472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UYOR-) UNIV OREGON HEALTH SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V35473 standard; cDNA; 2462 BP.
V35473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              531 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-34 x V35472/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag- a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:V35473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1996; US-026451.
07-MAR-1997; US-040052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-APR-1997; US-045233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-SEP-1997; U16033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ICAG-) ICAGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W63717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9811139-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                             \frac{1}{2} \frac{1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A PAR E PAR
```

```
decrease the potassium ion flux through the protein. The transfected host cell can also be used for the recombinant production of the protein. The DNA sequences can also be used for determine mutations in the SK and IK genes in a computer system. The proteins encoded by the SK and IK genes can be used in a computer system for determining their three dimensional structure, which is useful for determining ligands that bind to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human small conductance calcium activated potassium channel gene. Human small conductance calcium activated potassium channel; hKCa3/KCNN3, bipolar disease; schizophrenia; treatment; diagnosis; netcion; transgenic animal; gene therapy; neuropsychiatric disorder; neurological disorder; neuromuscular disorder; immunological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  such disorders. Use of the wild type gene in gene therapy to treat these disorders is also contemplated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human small conductance calcium activated potassium channel-3 useful for diagnosis, treatment and prevention of particularly schizophrenia and bipolar disorders claim 3; Figure 5; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disorders associated with a dysfunctional or altered small conductance calcium-activated potassium channel-3 (hKCa3/KCNN3) comprise neuropsychiatric, neurological, neuromuscular and immunological disorders, specifically bipolar disease and schizophrenia. Transgenic animals comprising the hKCa3/KCNN3 gene as a transgene in their somatic and germ cell lines can be used as models for studying these conditions and their treatments. Antibodies (Ab) directed against the hKCa3/KCNN3 polypeptide or conservative variants of the polypeptide can be used to conservative variants of the polypeptide can be used to detect those at risk from these disorders and also in therapy against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
287. 2482
/*tag= a
/*product= "Small conductance calcium activated
2482. 2487
                                                                                                                                       Ë
                                                                                                                                         479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ChECC ) UNIV CALIFORNIA.
Chandy KG, Fantino E, Gargus JJ, Gutman G, Kalman K;
WPI: 99-132165/11.
                                                                                                                                                                                                                                                                                                                                                       to: 2462
                                                                                                                                                                                                             Percent Similarity: 100.000 Percent Identity: 70.000
                                                                                                                                       ö
                                                                                                                                       617
                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                       814 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- Poly-A signal
2509. .2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poly-A region
                                                                                                                                                                                                                                                                                                                                                                                                                               850 CGGGAGGCGCTGAGGCGGCTGAGGGGCTTC 821
                                                                                                                                                                                                                                                                                                                                                                                         1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                     to reverse of: V35473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X08414 standard; cDNA; 2521 BP.
                                                                                                                                       552 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-34 x V35473/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:x08414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-1998; US-070741
15-JUL-1997; US-052556
                                                                                                                                     BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-1998; U14902
                                                                                                                                     2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; W96312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9903889-A1
                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_site
                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                       proteins.
                                                                                                                                       Seguence
    888888888
```

g

```
1 ArgGluSerLeuArgAsnLeuArgGly 9
                                                                                  seq_name: N_Geneseq_36:V30458_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                                           seq_documentation_block
                                                                                                                                                                                        V30458_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                    Pression into acids encoding human secreted proteins - obtained from the nucleic acids encoding human secreted proteins - obtained from umbilical cord, lymph ganglia, I ymphocytes and placental itssue

lymphocytes and placental itssue

Claim 1; Page 268-269; 411pp; English.

X41379 to X41526 represent 5' expressed sequence tags (ESTS) for human secreted proteins, and encode the proteins given in Y12521 to Y12668, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differantiation activity, hemmatopoiesis regulating activity, chemotactic/
chemokinetic activity, haemostatic and thrombolytic activity, receptor/
ligand activity, antiinflammatory activity, tumour inhibition activity and chromosome mapping products can be used in forensic, gene therapy and chromosome mapping products. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide or the insertion of a polypeptide into a cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human: secreted protein, EST: expressed sequence teg; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopolesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; antiinflammatory; tumour inhibition; antitumour; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUN-1999 (first entry)
Human secreted protein 5' EST SEQ ID NO: 152 from WO 9906553
    490 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                      to: 2521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                          Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: X41493 from: 1 to: 416
      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 G;
    624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-FEB-1999.
31-JUL-1998: IB1237.
01-AGC-1997; US-90S051.
(GEXT ) GENSET.
Duclert A, Dumas Milne Edwards J, Lacroix B;
WPI; 99-153783/13.
                                                                                      Length:
                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: X08414 from: 1
      833 C;
                                                                                                                                                                                                                                                                                                                    870 CGGGAGGCGCTGAGGCGGCTGAGGGGCTTC 841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 C;
                                                                                                                                                                                                                                                                          1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                _documentation_block:
_X41493 standard; cDNA; 416 BP
      574 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-34 x X41493/rev
                                                                                                                                                                    alignment_block:
US-08-653-294-34 x X08414/rev
                                                                                                          Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.00
4.625
88.889
                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:X41493
                                                                                    38.00
      2521 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                      Quality:
                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; Y12635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO9906553-A2.
                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
        Sednence
                                                                                                                                                                                                                                                                                                                                                                                                                                             X41493;
```

```
/product="(semi)aldehyde dehydrogenase-like protein"
complement (426949. .428028)
                                                                                                                                                                        14-oCT-1998 (first entry)
Rhizobium species plasmid pNGR234a.
Symbiosis; open reading frame; ORF; plasmid; vector; transportation;
degradation; metabolism; host range; nitrogen fixation; nodulation;
legume; plant; ds.
Rhizobium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'product= "glutamate dehydrogenase-like protein"
      COCUS V30458 Accession V30458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "aminotransferase-like protein"
/note= "homologous to the BioA gene"
124056. .425594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    product= "encapsulation-like protein"
note= "homologous to the CapA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "homologous to the GLUD1 gene"
complement (430538. .431284)
                                                                                                                                                                                                                                                                                                                                                                                                  Journal "oligopeptide permease" /note= "homologous to the OppC gene" 418673. 419680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name= "ORF K2"
/product= "oligopeptide permease"
/note= "homologous to the OppD gene"
419677. .420738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product "oligopeptide permease" note "homologous to the OppF gene" 20774, .422159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product=""transposase homologue"
/note= "homologous to the Tnp gene"
complement (433880. .434110)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'product=""transposase homologue"
'note= "homologous to the Tnp gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "transposase homologue"
complement (431296. .432840)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "ORF K10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'standard_name- "ORF K3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "ORF K4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'standard_name= "ORF K5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= g
/standard_name= "ORF K7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'standard_name= "ORF K6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /standard_name= "ORF K9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /standard_name= "ORF K8"
                                                                     210000
310000
410000
510000
                                                 10000
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                          417796. .418671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22628. .424031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28292. .429623
                                                            V30458_1 100001
V30458_2 200001
V30458_3 300001
V30458_4 400001
V30458_5 standard; DNA; 534720 BF
V30458
Sequence split_into 6 fragments
Fragment Name Begin
```

```
/product- "alpha-subunit of FeMo protein of nitrogenase"
454590. .456131
                                                                                                                                                                                                                                                                                                                 /gene= "nifk"
/product= "beta-subunit of FeMo protein of nitrogenase"
456187, ,457677
                                                         /standard_name= "ORF L3"
/product= "putative protein with degradative function"
450341, .451396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "ORF L12"
/product= "protein similar to part of the Fe protein
                                                                                                                              /standard_name= "ORF L4"
/product= "luciferase alpha-subunit-like protein"
//note= "homologous to the LuxA gene"
452980. .454494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "ORF L9"
/product= "protein involved in FeMo co-factor
blosynthesis"
                                                                                                                                                                                                                                                                                                                                                                            /standard_name= "ORF L8"
/product= "protein involved in FeMo co-factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /standard_name= "ORF L15"
/product= "processing protease-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "ORF L10"
/product= "protein of unknown function"
/note= "homologous to the Nifx gene"
459579, .460067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "ORF L13"
/product= "protein of unknown function"
463201. .464739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name= "ORF I14"
/product= "peptidase-like protein"
/note= "homologous to the bi-MPP gene"
/*tag= ak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of nitrogenase"
/note= "homologous to the NifH gene"
461228. .461545
             /note= "homologous to the LinA gene"
448497. .450203
                                                                                                                                                                                                                                                                                                                                                                                                       blosynthesis" homologous to the NifB gene" 457687, 459096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "homologous to the FixF gene"
459093. .459575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 110000
                                                                                                                                                                                                                                                                                                 'standard_name= "ORF L7"
                                                                                                                                                                                                                 /standard_name= "ORF L6"
protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgGluSerLeuArgAsnLeuArgGly 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.00
4.625
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: V30458_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-34 x V30458_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                               CDS
                                                                                                 CDS
                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= y
/standard_name= "ORF L2"
/product= "gamma-hexachlorocyclohexane-dechlorinase-11ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "protein required for nitrogenase activity" complement (438605. .439912)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "protein required for nitrogenase activity" complement (439923. .441032)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product- "protein required for nitrogenase activity"
complement (441042, .441899)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "protein required for nitrogenase activity" complement (442316. .442636)
                                                                                                                                                                                                                                                                                                                                                                            /product- "positive regulator of nif, fix and other genes"
                                                                                                                                                                             /product="ferrodoxin/ferrodoxin-like protein"
/note= "homologous to the FdxN gene"
complement (434753. 436234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="dctA"
/product= "c4-dicarboxylate transport protein"
/note= "homologous to the DctAI gene"
                                                                                                                                                                                                                             /*tag= n
/standard_name= "ORF K14"
/standard_name= "ORF K14"
/product= "nifB"
/product= "protein involved in FeMo co-factor
blosynthesis"
complement (436460. .438130)
                                                                            /*tag= 1
/standard_name= "ORF K12"
/product= "protein of unknown function"
complement (434517. .434711)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_name= "ORF L1"
/product= "cytochrome P450-11ke protein"
/note= "homologous to the CamC gene"
447844. .448500
                        /product="protein of unknown function"
/note= "homologous to the FixU gene"
complement (434107. .434433)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ^resp.
/standard_name- "ORF K20
/product- "protein of unknown function"
complement (443313. .443879)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /standard_name= "ORF K21"
/product= "protein of unknown function"
144337. .445029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "ORF K22"
/product= "ferrodoxin.like protein"
/note= "homologous to the N1fQ gene"
445088. .446602
                                                                                                                                                                                                                                                                                                                                                                                                            complement (438297. .438590)
                                                                                                                                                             /standard_name= "ORF K13"
                                                                                                                                                                                                                                                                                                                              /*tag= o
/standard_name= "ORF K15"
/gene= "nifA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name= "ORF K17"
/gene= "fixC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= s
/standard_name= "ORF K19"
/gene= "fixA"
                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= p
/standard_name= "ORF K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'standard_name- "ORF K18"
            /standard_name= "ORF K11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= w
'standard_name= "ORF K23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene= "fixx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'gene= "fixB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /standard_r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag= x
                                                            CDS
                                                                                                                              CDS
                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
```

15658 CGCGAAAGTCTTAGGAATCTCTTGGGG 15684

THIS PAGE BLANK (USPTO)

```
1 AQ468916 HS_5140_B2_H09_T7A
1 AA203261 zx55d11.r1 Soares_f
1 F14616 SSO4H02 Porcine small
                                                                                                                                                                                                                                                                                                                                                                                                                      Human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherial; Primates; Catarrhini; Hominidae; Homo.

Eutherial; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 103)

Badams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C. Man-Wai,C. Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fitzhugh,W.M., Fritchman,J.L., Geoglagen,N.S., Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Ulterback,T.R., Weldman,J.F., Li,Y., Dimke,D., Feng,D.F., Ferrie,A., Tescher C., Mastings,G.A., Dimke,D., Feng,D.F., Ferrie,A., Tescher C., Hastings,G.A., Kozak,D.L., Kubch,S.G.A., Heswillion,D.Y., Hudson,P., Kima,K., Kozak,D.L., Rubon,A.K., Tescher C., Yu,G.L., Rubon,S.M., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence

Nature 377 (6547 Suppl.), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
712 Medical Center Drive, Rockville, MD 20850 USA
723 Medical Center Drive, Rockville, MD 20850 USA
7213 3018699423
Fax: 3018699423
Fax: 3018699423
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverses
Location/Qualifiers
                                                                                                                                                                                                                                    ដ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="ARCC (inhost):120083"
/db_xref=taxon:9606"
/db_xrefi=taxon:9606"
/dcv_stage="adult"
/dev_stage="adult"
/note="Organ: adrenal gland; Vector: pBluescript SK-;
Site_1: EcoRI: Site_2: XhoI"
35 c 29 g 13 t
                                                                                                                                                            seq_documentation_block:
LOCUS AA319533 103 bp mRNA EST 19-APR-1997
LOCUS AA319572 Adrenal gland tumor Homo sapiens cDNA 5' end similar similar to major histocompatibility complex, class I, B (GB:M16102), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               on Sep 12, 1996 this sequence version replaced gi:1393672.
Other_ESTS: THC169519
Contact: Kerlavage, AR
Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 100.000
72.47
135.60
29.97
137.02
132.13
143.90
                                                                                                                                                                                                                                                                                                                      AA319533
AA319533.1 GI:1971860
40.00
40.00
39.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-34 x AA319533
                                                                                                                  seq_name: gb_est12:AA319533
gb_gss13:AQ468916
gb_est11:AA203261
gb_est4:F14616
                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA083156 zn08d04.rl Stratagenė
AA121088 zm22d05.rl Stratagene
AQ333000 HS_5003_A2_A08_r7 RPCI
AA158109 zo57h10 sl Stratagene
AA160714 zo77e11.rl Stratagene
                                                                                                                                                                                             Command line parameters:
-MODEL-framet-p2n.model -DEV-Xlp
-Q-/cgnl_1/USFTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-Q-/cgnl_1/USFTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-DB-EST -OFMT-fastap -SUFFIX-rst -GAPOP=12.000 -GAPDT-4.000
-MINMATCH-0.100 -LOOPCL-0.000 -LOOPEXT-0.000 -GAPOP=4.500
-GGAPEXT-7.000 -XGAPOP=10.000 -XGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-LIST-45 -DOCALIGN-200 -THR.ZCORE-pct -ALIGN-15 -MODE-LOCAL
-GIST-45 -DOCALIGN-200 -THR.ZCORE-pct -ALIGN-15 -MODE-LOCAL
-OUTFMT-Pfs -NORM-SXt -MINLEN-0 -MXLEN-1000000 -USER-US08653294
                                                                                                                  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EScore
   out_format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.33
66.33
7.46
7.46
7.46
7.98
8.98
8.98
8.98
8.98
8.98
9.12
9.68
110.59
110.59
110.59
110.59
110.59
110.59
110.59
110.59
110.59
110.59
110.59
110.59
110.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               194 48 1185 64 1185 64 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68 1185 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141.70
139.63
138.21
137.85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152.30
152.01
150.41
   EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
query: 105.08-653-294-34
query length: 10
batabase: EST:*
Database sequences: 4538634
batabase length: 1887811982
Search time (sec): 7600.090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     551.00

551.00

551.00

551.00

551.00

551.00

551.00

551.00

551.00

551.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00

561.00
   OM of: US-08-653-294-34 to:
                                                         Date: Feb 8, 2000 6:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est12:AA319533
gb_est13:AA35240
gb_est13:AA352960
gb_est13:AA352960
gb_est13:AA352960
gb_est13:AA352960
gb_est13:AA310808
gb_est17:W40489
gb_est77:W40489
gb_est77:W40489
gb_est77:AA310808
gb_est77:AA310808
gb_est77:AA310808
gb_est77:AA36389601
gb_est77:AA36389601
gb_est73:AA3689801
gb_est73:AA3689801
gb_est73:AA36862
gb_est73:AA3689801
gb_est13:AA36306
gb_est13:AA36306
gb_est13:AA36306
gb_est26:AA33284
gb_est27:AA10530
gb_est27:AA10530
gb_est27:AA10530
gb_est28:AA945159
gb_est27:AA100800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_gss11:AQ333000
gb_est10:AA158109
gb_est10:AA160714
```

```
52 a
                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

E 1 (Dases 1 to 189)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult.C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man Wai.C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fitchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblow, E., Hinkle, P.S., Strigey, T.F., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Bednarik, D.P., Greene, J.M., Fischer, C., Hastings, G.A., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H., Fraer, C., Man, A., Man, M., Mu, J.S., Greene, J.M., Culle, Melson, P.S., Olsen, H., Fraer, C., Man, A., Man, M., Mu, J.S., Greene, J.M., Kozak, D.L., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Fraer, C. M., Jasser, P.S., Panen, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
                                                                                                                                                                     Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced gi:1404737.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
    to: 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .189
/organism="Homo sapiens"
                                                                   1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                      AA361477.1 GI:2013795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_ESTs: THC169519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
0
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
to: AA319533
                                                                                                                                  seq_name: gb_est13:AA361477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12140200
                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
  Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                          ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
```

```
E (bases I to 218)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Leen, N.H., Kirkness, E.F., Walnstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Earndon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Fliggerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Heddlow, E., Hinkle, P.S., Jr.,

Kelley, J.M., Relley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weldman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Bednarik, D.P., Grene, J.M., Gruber, C., Hastings, G.A.,

Raymond, L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wel, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.

Fraser, C.M. and venter, J.C.

Fraser, C.M. and venter, J.C.

Fraser, C.M. and venter was a series of the series of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS
LOCUS
AA352603
DEFINITION EST60621 Activated T-cells XX Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, B*62.3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: Mi3 Reverse to the first continuation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Vector: pBluescript SR-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On May 8, 1995 this sequence version replaced gi:800964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="ATCC (inhost):152802"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells xx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA352603
AA352603.1 GI:2004923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Other_ESTs: THC172938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70 c
                                                                                                                                                                                                                                  to: AA361477
alignment_block:
US-08-653-294-34 x AA361477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est13:AA352603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 270)

Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock, K.G., Gocayne,J.D., White,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fitzhugh,W.M., Fitzhugh,G., Hond,M.C., Hedblom,E., Hinkie,P.S.,Jr., Kelley,J.M., Kelley,J.C., Lul,L.I., Marmaros,S.M., Merrick,J.W., Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M., Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shifey,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hadson,P., Kim,A.K., Kozak,D.L., Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L., Welly,T.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Traser,C.M. and Venter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: arkerlavetigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.hfml)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOGUS AAA352960 270 bp mRNA EST 21-APR-1997
DEFINITION EST61101 ACTIVATED T-cells XX Homo sapiens CDNA 5' end similar to major histocompatibility complex, class I, B61, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12140200 O No. 1 No. 1 No. 2 N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bioinformatics
The Institute for Genomic Research
Tyl2 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="ATCC (inhost):153240"
/db_xref="taxon:9606"
/clone_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 CGAGAGGCCTGCGGAACCTGCGCGGNTAC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA352960.
AA352960.1 GI:2005353
                                                                                                                                                             Ouality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AA294911
                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-34 x AA294911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est13:AA352960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sednence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Frimates; Catarrhini; Hominidae; Homo.

10 (Dases 1 to 259)

11 (Dases 1 to 259)

12 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bulke, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wal, C., Man-Wal, C., Hand, C., Hand, C.L., Hand, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhquan, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hand, M.C., I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.L., Saudek, D.M., Shiley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednailt, D.D., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., Rozak, D.L., Kunsch, C., Hungjun, J., Li, H., Malssner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Fischer, C.M., and Venter, J.C., The Stander, R. Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Fischer, C.M., and Venter, J.C., The Stander, J. S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hg1/hg1.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"

87 c 75 g 30 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12140200
On Nov 29, 1993 this sequence version replaced gi:430148.
Other_ESTs: THC172938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="ATCC (inhost):190413"
/db_xref="taxon:9606"
/clone_lib="Panoreas tumor I"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                     :
:
                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .259
                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AA294911
AA294911.1 GI:1947266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kerlavage, AR
                                                                                Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AA352603
                                                                                                                                                                                                              alignment_block:
US-08-653-294-34 x AA352603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est12:AA294911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
```

SHOT SHEET SHEET

```
alignment_scores
                                                                                                                                                                                                                              Align seg 1/1
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 373)
(Dases 1 to 373)
(Disses, S. Dietrich, W. DuBuque, T., Favello, M., Cliapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Clish, M., Hautman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Trevaskis, E., Underwood, K., Soares, M.B., Tan, F., Thierry-Meg, J., Pravskis, E., Underwood, K., Wolldmann, P., Waterston, R., Wilson, R., and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Fax: 314 286 1810
Final Estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the INRAGE Consortium (info@image.llnl.gov) for further information. Insert Lengh: 1592
Seq primer: -28M13 rev2 from Anersham
High quality sequence stop: 268.
                     Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block: 01-DEC-1996
LOCUS AA058454 373 bp mRNA EST 01-DEC-1996
DEFINITION z167407.r1 Stratagene colon (#937204) Homo sapiens CDNA clone INAGE:509677 5' similar to gb:MZ4039_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Sep 12, 1996 this sequence version replaced g1:1393357
                                                          5 others
                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 100.000
 /dev_stage="adult"
/note="Vector: pBluescript SK-;
                                                          u
                                                                                                                                                                                                                                                                                       ;
t
                                                                                                                                                                                                                                                                                                                                            1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                            ρ
                                                          88
                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA058454.1 GI:1551280
                                                          80
C
                                                                                                                                                   Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AA352960
                                                                                                                                                                                                                            alignment_block:
US-08-653-294-34 x AA352960
                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est8:AA058454
                                         "Iodx
                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seguence.
                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human,
                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                            ORIGIN
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases) 1 to 397)

1111/er,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Mardas,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le, Moore,B., Moorte,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Weg,J., Pravaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28ml3 revi ET from Amersham
High quality sequence stop: 295.
Localion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Nov 29, 1993 this sequence version replaced g1:430429.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63108
others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 others
                                                                                                                                         Percent Identity: 100.000
ų
                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. 397
/organism="Homo sapiens"
/db_xref="GDB:5588245"
/db_xref="taxon:9606"
/clone="iMAGE:648507"
57
                                                                                                                                                                                                                                                                                                                           229 CGAGAGACCTGCGGAACCTGCGCGGCTAC 258
                                                                                                                                                                                                                                                                                     1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
  b
                                                                                                                                                                                                                                             from: 1
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA224068
AA224068.1 GI:1844610
  O
                                                                                               Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                           to: AA058454
119
                                                                                                                                                                                 alignment_block:
US-08-653-294-34 x AA058454
                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est11:AA224068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Marra, M.
  ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97044478
73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human
```

**X** 

```
seg_documentation_block:
LOCUS AA166317 405 bp mRNA EST 09-MAR-1998
DEFINITION ZO56c07.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:590892 5' similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ACCESSION AA160317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Feb. 314 286 1810
Fax: 314 286 1810
Fax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 405)

11 (bases 1 to 405)

11 (larrin, 1005)

11 (larrin, Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptce, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-NCI human EST Project

Unpublished (1997)

On Sep 12, 1996 this sequence version replaced gi:1406818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 others
                                Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 t
                                                                                                                                                                                                                                                                                                        to: 397
                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA160317.1 GI:1734956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                    Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                        alignment_block:
US-08-653-294-34 x AA224068
                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: AA224068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-34 x AA160317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est10:AA160317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

```
/organism="Homo sapiens"
/db_xref="GD8:1263173"
/db_xref="tack.gb8:1263173"
/db_xref="tack.gb8:1263173"
/dlone="Inhadze:32869"
/clone="Inhadze:32869"
/clone="the pancreatic islet"
/tissue_type="pancreatic islet"
/ida_host="SolR cells (kanamycin resistant)"
/note="forgan: pancreas; Vector: pBluescript SK-; Site_1:
/note="forgan: pancreas; Vector: pBluescript SK-; Vector: pBluescript SK-; Vector: pBluescript SK-; Vector:
                                                                                                                                                                                                                                                                                                                                               seq_documentation_block: 427 bp mRNA EST 20-MAY-1996
LOCUS W40489
DEFINITION 2c84401.r1 Pancreatic Islet Homo sapiens cDNA clone IMAGE:328969'5'
similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35
RCESSION W40489
W40489.1 GI:1324496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 427)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dierrich,N., DuBuque,T., Favello,A., Gish,W.,
Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,
Mardis,E., Moorris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Frevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Generation and analysis of 280,000 human expressed sequence tags Genome_Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
This clone is available royalty-free through LLNL ; contact the
TMAGE Consortium (info@image.linl.gov) for further information.
Seq primer: mob.REGA+ET
High quality sequence stop: 397.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On Jan 25, 1995 this sequence version replaced gi:637865.
Contact: Wilson RK
Washington University School of Medicine
4444 Froest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                  ::
ئ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluSerLeuArgAsnLeuArgGlyTyr
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
    to: AA160317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: W40489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-34 x W40489
                                                                                                                                                                                                                                                                 seq_name: gb_est7:W40489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
```

大 一 大大大大大

Wed Feb

us-08-653-294-34.rst

```
seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AA663896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo saptens
                                                                                                                                               seq_name: gb_est9:C18310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                                                                                          numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . namuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryotta; Matazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (basea 1 to 43)

Bult, C. J. Lee, N. H. Kirkness, E. F., Weinstock, K. G., Gocayne, J. D., White, O., Sutton, G., Blake, J. A., Brandon, R. C., Man-Wal, C., Sutton, R. A., Cline, T. R., Cotton, M. D., Earle-Hughes, J., Fine, L. D., Clayton, R. A., Cline, T. R., Cotton, M. D., Farle-Hughes, J. Fine, L. D., Clayton, R. A., Glane, C. L., Hanna, M. C., Hedblom, E. L., Geoghagen, N. S., Glodek, A., Gnehm, C. L., Hanna, M. C., Hedblom, E. L., Hanna, M. C., Holblom, D. T., Palligrino, S. M., Noreno-Palanques, R. F., McDonald, L. A., Nguyen, D. T., Pelligrino, S. M., Phillips, C. A., Kyder, S. E., Scott, J. L., Saudek, D. M., Shirley, R., Small, K. V., Spriggs, T. A., Utterback, T. R., Weldman, J. F., Li, Y., Dimke, D. Fengi, D. F., Ferrie, A., Flscher, C., Hastings, G. A., Hastings, G. A., Hungjun, J., Li, H., Meissner, P. S., Olsen, H., Raymond, L., Weil, Y. F., Roche, T. Wing, J., Kim, A. K., Ensche, J., Fannon, M., Wing, J., Kim, A., Kim, A., Kamon, P. J., Fannon, M., Raymond, L., Weil, Y. F., Roche, J., Raymond, L., Weil, Y. F., Roche, J., Haseltine, W. A., Fields, C., Fraser, C. M., Francho, M., Husson, P. J., Fenley, C. M., Fraser, C., Haseltine, W. A., Fields, C., Fraser, C. M., Raymond, C., Weil, Y. F., Roche, J. Haseltine, W. A., Fields, C., Fraser, C. M., Raymond, C., Weil, Y. Francon, C. M., Husson, F. Fields, C., Fraser, C. M., Raymond, C., Weil, Y. Francon, C. M., Husson, F. Fields, C., Fraser, C. M., Raymond, C., Weil, W. W., Fields, C., Fraser, C., M., Raymond, C., Weil, W., Fields, C., Fraser, C., M., Raymond, C., Weil, M., Fields, C., Fraser, C., M., Raymond, C., Weil, M., Fields, C., Fraser, C., M., Raymond, C., Weil, M., Fields, C., Fraser, C., M., Raymond, C., Weil, M., Fields, C., Fraser, C., M., Raymond, C., Weil, M., Fields, C., Fraser, C., M., Raymond, C., Weil, M., Fields, C., Fraser, C., M., M., Raymond, C., Weil, M., Fields, C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                  For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Sep 12, 1996 this sequence version replaced g1:1397854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"ATCC (inhost):156811"
/db_xref-"taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
279 CGAGAGACCTGCGAAACCTGCGCGGCTAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                    AA310808
AA310808.1 GI:1963136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Other_ESTs: THC180721
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      144 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5.100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-34 x AA310808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: AA310808
                                                       seq_name: gb_est12:AA310808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
```

```
Eutheria: Mammalia; Eutheria: Mammalia; Eutheria: Primates; Catarrhini: Hominidae: Mammalia; Eutheria: Primates; Catarrhini: Hominidae: Homo.

Eutheria: Primates; Catarrhini: Hominidae: Homo.

E 1 (Dases 1 to 475)

Kyushkir, H., Nagata, M., Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H., Suzuki, M., Takaichi, A., Takada, F., Shimada, Y., Shinomiya, H., Nakamura, Y. and Takahashi, E.

Otsuka CDNA project

Unpublished (1996)

On Sep 12, 1996 this sequence version replaced gi:1393837.

Contact: Tsutomu Fujiwara

Otsuka GEN Research Institute

Otsuka GEN Research Institute

Otsuka Pharmaceutical Co., Ltd

463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION ae74d01.51 Stratagene schizo brain 511 Homo sapiens cDNA clone IMAGE:969889 3' similar to 9b:M38203 HLA CLASS I HISTOCOMPATIBILITY ANTICEN, B-62 B*1504 ALPHA (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 479)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
                                                                                                                                             C18310 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone GEN-560D07 5', mRNA sequence.
C18310
E18310.1 GI:1579912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="GEN-560D07"
/clone_11b="Human placenta cDNA (TFujiwara)"
/tissue_type="Placenta"
in 161 c 154 g 68 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .475
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 475
299 CGAGAGAGCCTGCGGAACCTGCGGGGCTAC 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: C18310 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA663896.1 GI:2617887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     479 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cuality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est17:AA663896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-34 x C18310
```

Allen acut de po

-

Wed Feb

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/dev_stage="34 years old"
/dev_stage="34 years old"
/dev_stage="36 kanamycin resistant,"
/note="vector: Bluescript SR:; Site_1: EcoRI; Library
/note="vector: Bluescript SR:; Site_1: EcoRI; Library
/note="vector: Bluescript SR:; Site_1: EcoRI; Library
/note="vector: Bluescript SR: Schizophrenic suicide.
/Sold secucasian, SOR aleutian. Schizophrenic suicide.
/Sandom primed into EcoRI site of ZAP II vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N.; Torrey, Er., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Umpublished) Stanley Neuropathology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."

10 thers
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, T., Wylie, T., Waterston, R. and Wilson, R. WashU-NCI human EST Project
L. Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394858.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLML; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 430.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:

LOCUS AL039796 503 bp mRNA EST 29-SEP-1999
DEFINITION DKFZp434B1912_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKFZp434B1912 5', mRNA sequence.

ACCESSION AL039796 1 GI:5408804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                              1. 479
//organism="Homo sapiens"
//db_xref="taxon:9606"
//clone="IMAGE:969889"
//clone=lib="$tratagene schizo brain $11"
//sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 CGAGAGAGCCTGCGGAACCTGCGCGGCTAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EST (Duesterhoeft, et al.)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AA663896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-34 x AA663896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est35:AL039796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiemann,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
```

```
AA263135 710 bp mRNA EST 02-JUL-1998
PMY0598 KGI-a Lambda Zap Express CDNA library Homo sapiens CDNA 5',
mRNA sequence.
AA263135
AA263135.1 GI:1898941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.

Human.
                                                                                                                                                                   Am Klopferspitz 18a D-82152 Martinsried, Germany This is the 5' sequence of the clone insert clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qlagen within the cDNA sequencing consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :: pSport1; Site_1: Not1; Site_2: Sall"
165 g 68 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oncology Research Laboratories
The Toronto Hospital
CRCS-424, 67 College St., Toronto, Ontario M5G 2M1, Canada
Tel: 416 3403433
Email: r.hawley@utoronto.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vo s1 sequence available.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6,
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Localition/Qualifiers
1. 503
/organism="Homo sapiens"
/dp.xref="taxon:9606"
/clone="DKFZp434B1912"
/clone="DKFZp434B1912"
/tissue_type="testis"
/dev_stage="aduit"
/lab_host="DH10B"
On Jun 2, 1999 this sequence version replaced g1:4967270.
Contact: Duesterhoeft A
MIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                On May 5, 1995 this sequence version replaced gi:797738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone was randomly picked from KGla primary library.
Seq primer: 5. GAAATAACCCTCACTAAAGGG 3'
High quality sequence stop: 710.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 51.00 Length: 10 Ratio: 5.100 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 300 CGAGAGACCTGCGGAACCTGCGCGGCTAC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector:
172 c 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Hawley RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AL039796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-34 x AL039796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est11:AA263135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
```

```
BASE COUNT
                                                                                                                                                                                                                                                                                                   ORIGIN
                                                                          /clone_lib="KG1-a Lambda Zap Express cDNA library"
/cell_type="promyeloblast"
/cell_type="promyeloblast"
/cell_type="promyeloblast"
/cell_type="promyeloblast"
/note="vector: Lambda Zap Express (Stratagene); Site_l:
ECORI.Site_2: XhoI; Unidirectional cloning sites:
ECORI.Site_2: XhoI; Unidirectional cloning sites:
ECORI.XhoI mRNA was purified from KG1-a cell line, cDNA was synthesized using an XhoI-OllgodT linker primer. ECORI adaptors were ligated, followed by digestion with XhoI for directional cloning into predigested Lambda Zap Express"
224 c 227 g 109 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo, Ph.D. cnb. arrayed by: Greg Lennon, Ph.D. cnb. Library Arrayed by: Greg Lennon, Ph.D. cnb. Asquencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A1424623 209 bp mRNA EST 30-MAR-1999
1134901... NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:2098128 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1to 209)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on Apr 21, 1998 this sequence version replaced g1:3072294. Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550 Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .209
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2098128"
/clone="IMAGE:2098128"
/clone="type="glioblastoma (pooled)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 710
1. .710
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert Length: 1183 Std Error:
Seq primer: -400P from Gibco
High quality sequence stop: 208
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 CGAGAGAGCCTGCGGAACCTGCGCGCGTAC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgGluSerLeuArgAsnLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AA263135 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRNA sequence.
A1424623
A1424623.1 GI:4270554
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-34 x AA263135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est27:AI424623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS A1424623
                                                                                                                                                                                                                                                                                                                               ಡ
                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human.
                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
        source
                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
```

4.

```
to: 209
                                                                                                                                            Percent Identity: 100.000
                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                to reverse of: AI424623
                                                                                                                                                                                                       1 ArgGluSerLeuArgAsnLeuArgGly 9
                                                                                                                                                                        :
                                                                                                                                                             alignment_block:
US-08-653-294-34 * AI424623/rev
                                                                                                                         Quality: 44.00
Ratio: 4.889
Percent Similarity: 100.000
                                                                                63
                                                                                                                   alignment_scores:
                                                                                                                                                                                       Align seg 1/1
```

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

' Search time 133.56 Seconds
(without alignments)
3.547 Million cell updates/sec February 8, 2000, 04:05:44 Run on:

US-08-653-294-35 Title:

102 1 YGRLNRLSERRESLRNLRGY 20 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Length DB ID Description  20 1 R952913 HLA-B7 CTL II 20 1 W33790 Peptide B7. 20 1 W33791 Peptide B7. 20 1 W33791 Peptide B7. 20 1 W33791 Peptide B7. 20 1 W33792 Peptide B7. 20 1 W33796 Peptide B7. 25 1 R83073 Peptide B7. 25 1 R95431 PLA-B7.60-8 25 1 R95431 PLA-B7.60-8 25 1 R95419 Peptide B7. 25 1 R95792 Peptide B7. 25 1 R95792 Peptide B7. 25 1 R95792 Peptide B7. 25 1 R95419 Peptide B7. 25 1 R41206 Peptide B2. 26 1 W33793 Peptide B2. 27 1 R41206 Peptide B2. 28 1 R41206 Peptide B2. 29 1 W33793 Peptide B2. 20 1 W33791 Peptide B2. 20 1 R92009 Peptide B2. 20 1 R92009 Peptide B2. 22 1 R92009 Peptide B2. 23 1 W48711 PEPTA SENI	Result		* Ouery			SUMMARIES	
102 100.0 20 1 R92913 HIA-B7 CTL N 102 100.0 20 1 R95415 HIA-B7 CTL N 102 100.0 20 1 H33790 Peptide B7.8 102 100.0 20 1 H33790 Peptide B7.8 100.0 20 1 H33790 Peptide B7.8 10.0 10 10 1 R93061 HIA-B7 CTL N 10.0 20 1 H33790 Peptide B7.8 10.0 10 1 H33796 Peptide B7.8 10.0 10 1 H33796 Peptide B7.8 10.0 10 1 H33796 Peptide B7.8 10.0 25 1 R93073 HIA-BW62.60-8 10.0 25 1 R93073 HIA-BW62.60-8 10.0 25 1 R95419 HIA-BW62.60-8 10.0 25 1 R95419 HIA-BW62.60-8 10.0 25 1 R95419 HIA-BW62.60-8 10.0 25 1 R92910 HIA-BW46.60-8 10.0 25 1 R93073 HIA-C exon Glyphosate Glyphos		COL	ĭĭi		DB	qı	Description
102 100.0 20 1 R95415 HIA-B7.84-78 102 100.0 20 1 W33790 Peptide B7.8 100.0 10 1 R83061 HIA-B7.6 CTL R5.0 10 1 W37515 Peptide B7.5 1 50.0 10 1 W3796 Peptide B7.5 1 50.0 25 1 R83073 Peptide B7.6 R8307 Peptide B7.7 R8307 Peptide B7.6 R8307 Peptide B7.7 R8307 Peptide B7.6 R8307 Peptide B7.7 R8307 Peptide B7	П	0	8	20	Н	37	-B7 CTL mod
102 100.0 20 1 W33790 Peptide B7.8 102 100.0 20 1 W33790 Peptide B7.1	~	0	8	20	Н	7	84-75-8
102 100.0 20 1 W33797 Peptide B7.8 51 50.0 10 1 R44209 Peptide Fra 51 50.0 10 1 R84209 Peptide Fra 51 50.0 10 1 W3786 Peptide Fra 61 51 50.0 10 1 W3786 Peptide B7.7 51 50.0 25 1 R41207 Peptide B7.7 51 50.0 25 1 R41207 Peptide B7.7 51 50.0 25 1 R41207 Peptide Fra 61 51 50.0 25 1 R41207 Peptide Fra 61 51 50.0 25 1 R41207 Peptide Fra 61 50.0 25 1 R4204 Peptide Fra 61 50.0 25 1 R4204 Peptide Fra 61 50.0 25 1 R4204 Peptide Fra 62 51 50.0 25 1 R4204 Peptide Fra 62 51 50.0 25 1 R4204 Peptide Fra 62 51 50.0 25 1 R4204 Peptide B7.7 5 46 6 50 1 W26792 Peptide B7.7 5 46 4 43.1 20 1 W3793 Peptide Fra 62 51 R41206 Peptide B7.7 6 6 6 1 R12466 Peptide B7.7 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	m	0	8	20	Н	5	B7.84-
51 50.0 10 1 R41209 Peptide frag 15 50.0 10 1 R432061 Peptide frag 15 50.0 10 1 NV7515 Peptide B7.1 S1 50.0 10 1 NV7515 Peptide B7.1 S1 50.0 25 1 R41207 Peptide B7.1 S1 50.0 25 1 R4244 HIA-B7.6 C0-8 4 4 43.1 20 1 W42792 Wouse TIE-2 HIA-B7.0 C0-8 1 W52910 Peptide B27 6 4 4 43.1 20 1 W3793 Peptide B27 6 4 4 43.1 20 1 W3793 Peptide B27 6 6 6 5 1 R82910 Peptide B27 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	4	0	8	20	Н	2	B7.
51 50.0 10 1 R83061 HIÀ-B7 CTL in the color of the color	ហ	51	0	10	Н	2	de fragme
51 50.0 10 1 W07515 Peptide B7.7 F.c.ll modul   51 50.0 10 1 W33786 Peptide B7.7 F.c.ll   51 50.0 25 1 R41207 Peptide B7.7 F.c.ll   51 50.0 25 1 R41207 Peptide B7.7 F.c.ll   52 50.0 25 1 R41207 Peptide Frag   53 50.0 25 1 R41207 Peptide Frag   54 50.0 25 1 R95419 Peptide Frag   55 50.0 25 1 R95419 Peptide Frag   56 50 1 W26792 Peptide Frag   57 50 1 W26792 Peptide B7.7 Fo.8 F.c.ll   58 50 1 W26792 Peptide Frag   58 50 1 W26792 Peptide B7.7 Fo.8 F.c.ll   59 1 W26792 Peptide B7.7 Fo.8 F.c.ll   50 1 W33793 Peptide B7.7 Fo.8 F.c.ll   50 1 W33793 Peptide B7.7 Fo.8 F.c.ll   50 1 W33793 Peptide B7.7 F.c.ll   50 1 R266 Peptide B7.7 F.c.ll   50 1 W33793 Peptide B7.7 F.c.ll   50 1 W33793 Peptide B7.7 F.c.ll   50 1 R92908 Peptide B7.7 F.c.ll   50 1 W33791 Peptide B7.7 F.c.ll   50 1 W37791	ဖ	51	0	10	Н	9	HLA-B7 CTL modulat
51 50.0 10 1 W33786 Peptide B7.7 51 50.0 10 1 W33796 Peptide B7.7 51 50.0 25 1 R83073 Peptide F3.1 50.0 25 1 R83073 Peptide F3.2 50.0 362 1 R12464 Pir.A-B%62.60-87 50.0 362 1 R12464 Pir.A-B%62.60-87 50.0 362 1 R12464 Pir.A-B%62.60-97 50.0 362 1 R12464 Pir.A-B%62.60-97 50.0 1 R3793 Peptide B27 Peptide B27 Peptide P3.1 20 1 R3793 Peptide B27 Peptide P3.1 25 1 R41206 Peptide F74 4 3.1 25 1 R83072 Peptide F74 4 3.1 25 1 R95418 Peptide Para Para Para Para Para Para Para Par	7	51	0	10	П	12	odulatin
51 50.0 10 1 W33796 Peptide B7.7 5 50.0 25 1 R41207 Peptide B7.7 5 50.0 25 1 R83073 HLA-B462 CTR 1 R85419 HLA-B462 CTR 2 S 1 R85210 HLA-B462 CTR 2 S 1 R85210 HLA-B462 CTR 2 S 1 R82210 HLA-B462 CTR 2 S 1 R82210 HLA-B466 CTR 2 S 1 R82210 HLA-B466 CTR 2 S 1 R82419 HLA-B2702 CTR 2 S 1 R82419 HLA-B2702 CTR 2 S 1 R82419 HLA-B2702 CTR 2 S 1 R82411 HAA-B2702 CTR 2 S 1 R82411 HPIV-3 JS 15 HPIV-3 JS 17	æ	51	0	10	Н	78	B7.75-84
51 50.0 25 1 R41207 Peptide frag 183   51 50.0 25 1 R83073   51 50.0 25 1 R83073   51 50.0 25 1 R83073   52 5 1 R83073   53 50.0 25 1 R85419   54 50.0 25 1 R85419   55 50.0 25 1 R85419   56 605 1 R62838   56 605 1 W62838   57 5 60 605 1 W62838   58 60 7 W62838   58 60 7 W62838   58 60 8 1 W62838    58 60 8 1 W62838   58 60 8 1 W62838    58 60 8 1 W62838    58 60 8 1 W62838    58 60 8 1 W62838    58 60 8 1 W62838    58 60 8 1 W62838    58 60 8 1 W	S	21	0	10	7	5	B7.75-8
51 50.0 25 1 R83073 HLÄ-Bw62 CTI   51 50.0 25 1 R895431 HLÄ-Bw62.COI   51 50.0 25 1 R95449 HLA-Bw62.CO-S   52 5 1 R95449 HLA-Bw62.CO-S   53 50.0 362 1 R12464 HLA-Bw62.COI   44 43.1 20 1 W62838 MOUSE TIE-2   44 43.1 20 1 R92910 HLA-Bw702 CT   44 43.1 25 1 R84206 HLA-Bw702 CT   44 43.1 25 1 R84206 HLA-Bw46 CTI   44 43.1 25 1 R84705 HLA-Bw46 CTI   44 43.1 366 1 R12465 HLA-Bw46 CTI   44 43.1 366 1 R12465 HLA-Bw46 CTI   42 41.2 22 1 R92909 HLA-Bw702 CT   43 42.2 43.0 1 R20642 GLyphosate   42 41.2 20 1 W33791 Peptide BZ702 CT   42 41.2 20 1 W33791 Peptide BZ702 CT   43 42 2 41.2 223 1 W48711 HPIV-3 35 16 HZA-BY   44 41.2 2233 1 W48712 HPIV-3 3V STR1   45 41.2 2233 1 W48713 HPIV-3 3V STR1   46 41.2 2233 1 W48713 HPIV-3 3V STR1   47 41.2 2233 1 W48713 HPIV-3 3V STR1   48 41.2 2233 1 W48713 HUMMAN MACCOI	0	51	0	25	٦	2	fragmen
51         50.0         25         1         R995431         HILA-B7, 60-84           51         50.0         362         1         R45419         HLA-B462.60         HLA-B462.60           51         50.0         362         1         W62838         Mouse TIE-2         HLA-B462.60           4         45.1         50         1         W7592         Mouse TIE-2         HLA-B702.01           44         43.1         20         1         W3793         Peptide B270         HLA-B702.01           44         43.1         25         1         R4206         HLA-B702.01         HLA-B46.01         B2702.01         HLA-B46.01         B2702.01         HLA-B46.01         B2702.01         HLA-B46.01         B2702.01         HLA-B46.01         B2702.01         HLA-B46.01         B2702.01         B2702.01         HLA-B46.01         B2702.01         HLA-B46.01         B2702.01         B	-	51	0	25	Н	7	HLA-Bw62 CTL modul
51 50.0 25 1 R95419 HLA-Bw62.60- 51 50.0 25 1 R12464 HLA-Bw62.60- 46 45.1 509 1 W26792 McOuse TIE-2 44 43.1 20 1 W3793 McOuse TIE-2 44 43.1 25 1 R41206 Peptide B270 C7 44 43.1 25 1 R41206 Peptide Frag 44 43.1 25 1 R83072 HLA-Bw46.C07 44 43.1 366 1 R12465 HLA-Bw46.C07 44 43.1 366 1 R12466 HLA-Bw46.C07 44 43.1 366 1 R12466 HLA-Bw46.C07 43 42.2 430 1 R2042 G1yphosate C19 42 41.2 20 1 R92909 HLA-B2702 C1 42 41.2 20 1 W33791 Peptide B270 42 41.2 2233 1 W48711 HPIV-3 JS 14 41 41.2 2233 1 W48712 HPIV-3 JS 16 41 40.2 2133 1 W48713 HPIV-3 FRh1 41 40.2 2131 1 W48713 HPIV-3 FRh1 42 41.2 2233 1 W48713 HPIV-3 PRh1 44 41.2 2233 1 W48713 HPIV-3 SPRh 45 41.2 2233 1 W48713 HPIV-3 SPRh	7	51	0	25	٦	2	0-84. C
51         50.0         362         1         R12464         HLA-B35 anti           47.5         46.6         605         1         W65792         Mouse TIE-2           44         43.1         20         1         R92910         Peptide B2702 CJ           44         43.1         20         1         W3793         Peptide B2702 CJ           44         43.1         25         1         R4206         Peptide B2702 CJ           44         43.1         25         1         R84206         HLA-Bw46 CFI           44         43.1         36         1         R12465         HLA-Bw46 CGI           44         43.1         366         1         R12465         HLA-Bw46 CGI           44         43.1         366         1         R07033         Breast cance           43         42.2         43.0         1         R246.5         HLA-C exon           43         42.2         43.1         1         R22262         HLA-C exon         Glyphosate cance           43         42.2         43.1         1         R2262         HLA-B3702 CJ           42         41.2         20         1         R92909         HLA-B3702 CJ	ж	51	0	a	Н	ᅼ	.60-84.
47.5         46.6         605         1         W62838         Glycine max           46         45.1         509         1         W2792         Mouse TIE-2           44         43.1         20         1         W3793         Peptide B270           44         43.1         25         1         R41206         Peptide B270           44         43.1         25         1         R446         FILA-BW46         CII           44         43.1         36         1         R12465         HLA-BW46         COI           44         43.1         366         1         R12465         HLA-C         COO           44         43.1         366         1         R12465         HLA-C         COO           43         42.2         43.0         1         R20426         G1yphosate         G1yphosate           42         41.2	4	S	0	ø	Н	9	antigen
46 45.1 509 1 W26792 Mouse TIE-2 44 43.1 20 1 R392910 Peptide B2702 CJ 44 43.1 25 1 R41206 Peptide B2702 CJ 44 43.1 25 1 R83072 HIAA-BAV6 CJ 44 43.1 366 1 R12465 HIAA-BAV6 CJ 44 43.1 366 1 R12466 HIAA-BAV6 CJ 44 43.1 366 1 R12466 HIAA-C exon CJ 43 42.2 43.0 1 R20642 GJ 43 42.2 43.0 1 R20642 GJ 42 41.2 20 1 R92909 HIAA-B2702 CJ 42 41.2 20 1 W33791 Peptide B2702 CJ 42 41.2 2233 1 W48711 HPIV-3 JS 14 42 41.2 2233 1 W48712 HPIV-3 SEN1 41 40.2 2131 W48713 HPIV-3 SEN1 41 40.2 217 1 W46424 HUMMAN MACTOR	'n	۲.	9	0	-	3	×
44 43.1 20 1 R92910 PHZ-B702 CT 44 43.1 20 1 W33793 Peptide fized 44 43.1 25 1 R83072 Peptide fized 44 43.1 25 1 R83072 Peptide fized 44 43.1 25 1 R83072 Peptide fized 44 43.1 25 1 R95418 PLZ-BW46 CTI 44 43.1 366 1 R12465 PLZ-C CTI 44 43.1 366 1 R12465 PLZ-C CTI 64 43.1 366 1 R12465 PLZ-C CTI 64 43.1 366 1 R20642 PLZ-C CTI 64 43.1 1 R20642 PLZ-C CTI 64 43.1 1 R20642 PLZ-C CTI 64 64.2 41.2 20 1 R92909 PEPTIGE B2702 CTI 64 64.2 41.2 20 1 W33791 PEPTIGE B2702 CTI 64 64.2 41.2 2233 1 W48711 PHIV-3 JS 18 42 41.2 2233 1 W48712 PHIV-3 JS 18 42 41.2 2233 1 W48713 PHIV-3 JS 18 42 41.2 2233 1 W48713 PHIV-3 JS 18 PRIV-3 PRIN HIV-3 JS 18 PRIN HIV-3 JC 19 PRIV-3 PRIN HIV-3 JC 19 PRIN MARTIN HIPLY-3 JC 19 PRIN MARTIN HIPLY-3 JC 19 PRIN MARTIN HIPLY-3 JC 19 PRIN MARTIN MARTIN HIPLY-3 JC 19 PRIN MARTIN MARTIN MARTIN HIPLY-3 JC 19 PRIN MARTIN MARTIN MARTIN MARTIN MARTIN MARTIN HIPLY-3 JC 10 PRIN MARTIN MARTIN MARTIN MARTIN HIPLY-3 JC 10 PRIN MARTIN	o	46	ß	0	Н	5	N
44 43.1 20 1 W33793 Peptide B27( 44 43.1 25 1 R41206 Peptide Frad 44 43.1 25 1 R83072 HLA-Bw46 Cf0- 44 43.1 366 1 R12465 HLA-C CXON C4 44 43.1 366 1 R12465 HLA-C CXON C4 44 43.1 366 1 Y07033 Breast CANC C4 43 42.2 43.0 1 R20642 Glyphosate CANC C4 42 41.2 20 1 R92909 HLA-BX702 C7 42 41.2 20 1 W33791 Peptide B270 42 41.2 2233 1 W48711 HPIV-3 JS 18 42 41.2 2233 1 W48712 HPIV-3 JS 18 42 41.2 2233 1 W48713 HPIV-3 JS 18 41 40.2 217 1 W46424 HUMMAN MACTOR	~	44	m	20	-1	금	2 CTL
44 43.1 25 1 RA1206 Peptide fra 44 43.1 25 1 R83072 HLA-Bw46 CG 44 43.1 25 1 R83072 HLA-Bw46 CG 44 43.1 366 1 R12465 HLA-C exon 43.1 366 1 R12466 HLA-C exon 43.1 366 1 R12466 HLA-C exon 43.1 366 1 R22462 HLA-C exon 43.2 43.0 1 R20642 Glyphosate 43 42.2 43.0 1 R20642 Glyphosate 42 41.2 20 1 R92909 HLA-B2702 CG 42 41.2 20 1 W33791 Peptide B27 42 41.2 223 1 W48711 HPIV-3 JS 1 HPIV-3 JS 1 42 41.2 2233 1 W48712 HPIV-3 JS 1 HPIV-3 JC 1 40.2 217 1 W46713 HPIV-3 JC 1 HUMan macro	œ		m	20	Н	2	B27(
44 43.1 25 1 R88072 HLA-Bw46 CT 44 43.1 25 1 R891072 HLA-Bw46 CT 44 43.1 366 1 R12465 HLA-C exon 44 43.1 366 1 R12465 HLA-C exon 44 43.1 366 1 R00642 Glyphosate 43 42.2 430 1 R22662 Glyphosate 42 41.2 20 1 R92908 HLA-B2702 C 42 41.2 20 1 W33791 Peptide B2702 C 42 41.2 2231 W48711 HPIV-3 JS 1 HPIV-3 JC 1 40.2 233 1 W48712 HPIV-3 JC 1 HUMBAD MACKO	σ.		m	25	-	2	fragmen
44 43.1 25 1 R95418 HLA-Bw46.6G 44 43.1 366 1 R12465 HLA-C exon 44 43.1 366 1 Y07033 HLA-C exon 44 43.1 366 1 Y07033 Glyphosate 43 42.2 43.0 1 R22664 Glyphosate 42 41.2 20 1 R92908 HLA-B2702 C 42 41.2 20 1 W33791 Peptide B77 42 41.2 223 1 W48711 HPIV-3 JS 1 42 41.2 2233 1 W48712 HPIV-3 JS 1 42 41.2 2233 1 W48712 HPIV-3 JS 1 42 41.2 2233 1 W48713 HPIV-3 JS 1 41 40.2 217 1 W46424 Human macro	0		m	25	Н	7	CTL mod
44 43.1 366 1 R12465 HLA-C exon 44 43.1 366 1 R12466 Evon 44 43.1 366 1 R12466 Breast cancel 43.1 366 1 R2466 Breast cancel 43.1 366 1 R20642 Glyphosate 43.2 43.2 43.1 R20642 Glyphosate 43.4 2.2 41.2 20 1 R92909 Breast Cancel 42.4 2.2 20 1 W33791 Breast Cancel 63.7 Breast Cancel	_		m	25	~	듸	.60-84. C
44         43.1         366         1 R.2466         HLA-C exon           44         43.1         366         1 Y07033         Breast can           43         42.2         43.0         1 R.20642         Glyphosate           42         41.2         43.1         1 R.22562         Glyphosate           42         41.2         20         1 R.92909         HLA-B2702           42         41.2         20         1 W33791         Peptide B27           42         41.2         20         1 W33792         Peptide B27           42         41.2         2233         1 W48711         HPIV-3 JS JS J           42         41.2         2233         1 W48712         HPIV-3 JS FRhl           42         41.2         2233         1 W48713         HPIV-3 JS FRhl           41         40.2         217         1 W46424         Human macro	~		m	9	-	9	9
44 43.1 366 1 Y07033 Breast cancellate to the concentration of the conce	_		m	9	Н	9	exou Cp-
43     42.2     430     1     R20642     Glyphosate       43     42.2     431     1     R22562     Glyphosate       42     41.2     20     1     R92909     HLA-B2702     C       42     41.2     20     1     W33791     Peptide B27       42     41.2     20     1     W33792     Peptide B27       42     41.2     2233     1     W48711     HPIV-3     JS 1       42     41.2     2233     1     W48712     HPIV-3     JS 1       42     41.2     2233     1     W48713     HPIV-3     JC 1       41     40.2     217     1     W46424     Human macro	₹,		m	9	Н	33	ä
43     42.2     431     1 R22262     Glyphosate       42     41.2     20     1 R92909     HLA-B2702       42     41.2     20     1 W33791     Peptide B27       42     41.2     20     1 W33792     Peptide B27       42     41.2     2233     1 W48711     HPIV-3 JS J       42     41.2     2233     1 W48712     HPIV-3 FRhI       42     41.2     2233     1 W48713     HPIV-3 FRhI       41     40.2     217     1 W46424     Human macro	'n		~	3	-	54	e oxi
42 41.2 20 1 R92909 HIA-B2702 CT 42 41.2 20 1 R92908 HIA-B2702 CT 42 41.2 20 1 W33791 Peptide B270 CT 42 41.2 20 1 W33792 Peptide B270 42 41.2 2233 1 W48711 HPIV-3 JS is 42 41.2 2233 1 W48712 HPIV-3 JS is 42 41.2 2233 1 W48713 HPIV-3 WEND 41 40.2 217 1 W46424 Human macrop	o		2	m	-	226	
42 41.2 20 1 R92908 HLA-B2702 CT 42 41.2 20 1 W33792 Peptide B270 42 41.2 20 1 W33792 Peptide B270 42 41.2 2233 1 W48711 HPIV-3 JS is 42 41.2 2233 1 W48712 HPIV-3 JS is 42 41.2 2233 1 W48713 HPIV-3 PRhl 40.2 217 1 W46424 Human macrop	7		н	20	Н	290	2 CIL
42 41.2 20 1 W33791 Peptide B270 42 41.2 223 1 W48711 HPIV-3 DS 1S 42 41.2 2233 1 W48712 HPIV-3 DS 1S 42 41.2 2233 1 W48712 HPIV-3 FRb1 42 41.2 2233 1 W48713 HPIV-3 FRb1 41 40.2 217 1 W46424 Human macrop	മ		щ	20	Н	290	-B2702 CT
42 41.2 20 1 W33792 Peptide B270 42 41.2 2233 1 W48711 HPIV-3 JS 1S 42 41.2 2233 1 W48712 HPIV-3 FRh1 42 41.2 2233 1 W48713 HPIV-3 FRh1 41 40.2 217 1 W46424 Human macrop	0		~	20	Н	379	e B2702.
42 41.2 2233 1 W48711 HPIV-3 JS is 42 41.2 2233 1 W48712 HPIV-3 FRh1 HPIV-3 FRh1 HPIV-3 FRh1 42 41.2 2233 1 W48713 HPIV-9 Vero 41 40.2 217 1 W46424 Human macrop	0		М	20	Н	379	B2702.84-
42 41.2 2233 1 W48712 HPIV-3 FRh1 42 41.2 2233 1 W48713 HPIV-3 Vero 41 40.2 217 1 W46424 Human macrop	_	42	ч	23	Н	371	JS 1S
42 41.2 2233 1 W48713 HPIV-3 Vero 41 40.2 217 1 W46424 Human macrop	~		н	23	Н	871	
41 40.2 217 1 W46424 Human macrop	m		н	23	Н	871	-3 Vero
			0	Н	Н	642	macrop

H. pylori GHPO 144 Consensus sequence	Human L5/3 tumour Human L5/3 tumour Human L5/3 partial Human L5/3 partial	Macrophage stimula Human L5/3 tumour Macrophage stimula	Human growth facto Human MSP protein.
W98326 P80911 P66507	R66598 W14266 W14267	W07691 R66602 W07692	W14270 W82789
219	705 705 705	710 711 711	711
2.0.0	444	4 4 6 6 7 7 7 7	40.2
444	4 <b>4 4</b> 4	4 4 4 1 1 1 1	<b>4 4 1 4 1</b>
3 3 3 4	. w w 4 . w o O	4 4 4 1 2 6	44 5 5

## ALIGNMENTS

Gaps ö Length 20; Indels Ouery Match 100.0%; Score 102; DB 1; Best Local Similarity 100.0%; Pred. No. 1.3e-09; Matches 20; Conservative 0; Mismatches 0;

ö

1 YGRLNRLSERRESLRNLRGY 20 1 YGRLNRLSERRESLRNLRGY 20 ò

7 쉱

195415 standard; peptide; 20 AA.
R95415.
R95415.
R95415.
R95415.
R95415.
R95415.
R95415.
R954175.84 Palindrome.
R1A-B7.84-75-84 Palindrome.
R1A-B7.84-75-84 Palindrome.
R1A-B7.84-75-84 Palindrome.
R1A-B7.84-75-84 Palindrome.
R0511; calclum influx: cytotein; mammal; heat shock protein; Hsc70; APC; B cell; calclum influx: cytoteixic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
R05513288-A1.
R99513288-A1.

为 法 社会

```
Synthetic.
                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
   88888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
                                                                                                                              Composes. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 18: 29pp: English.

Example: Page 20pp: Engli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treating autolimmune diseases

Example 1; Page 19; 41pp; English.

Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R a376-77L) (a379-84) or (aa80 = 1 or N; aa81, aa84 = a hydrophobic or Small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-1998 (first entry)
Peptide B7.84-75-75-84 tested for immunomodulating activity.
Immunomodulating dimer: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beulow R, Clayberger C, Krensky AM; wPI; 98-086530/V08. New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 102; DB 1; Length 20; 100.0%; Pred. No. 1.3e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-1997.
22-NAX-1997, U08689.
24-NAX-1996, US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                   STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W33790 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                       Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YGRLNRLSERRESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YGRLNRLSERRESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
                                                                                                         WPI; 95-194027/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo saptens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
```

ò

쉽

```
PP 27-NOV-1997.

PR 12-NAV-1997.

PR 22-NAV-1997.

PR 22-NAV-1997.

PR 22-NAV-1997.

PR 22-NAV-1997.

PR 22-NAV-1996.

PR 22-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rhemmatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1998 (first entry)
Peptide B7.84-75-75-84 tested for immunomodulating activity.
Immunomodulating dime: immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 102; DB 1;
100.0%; Pred. No. 1.3e-09;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 102; DB 1;
100.0%; Pred. No. 1.3e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W33797 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     used for detection and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YGRLNRLSERRESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YGRLNRLSERRESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YGRLNRLSERRESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YGRLNRLSERRESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 100.
                                                                                                                                                                                                                                                                                                                               20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rejection.
```

ᠬ

The state of the s

```
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                   12-APR-1996; U04710.
12-MAY-1995; US-440504.
                Query Match
Best Local Similarity
Matches 10; Conserv
                                                                     RESLRNLRGY 20
                                                                                        1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                             WO9635443-A1.
                                                                                                                                                                                                                                                                                                                                            14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rejection
                                                                                                                                                                                                                                                                                                                                                                                                    Buelow R;
                                                                                                                                          ^
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          œ
                                                                                                                                         RESULT
                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a fragment of a class I major histocompatibility complex (MHC) antigen. This sequence corresponds to residues 75-84 of the alpha-1 domain of the class I MHC HLA-B. This sequence, and the peptide fragments represented by R83062-R83085, R83090-R83096 and recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited treatments). The peptides particularly modulate (or inhibit) the activity of the peptides particularly modulate (or inhibit) the sequence 10 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MXY-1996 (first entry)
HLA-B7 CTL modulating peptide (B7.75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B7.
                                                                                                                                                                                                                       Mew peptide(s) based on class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets claim 11; Page 54; 61pp; English.
The peptide is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition. This peptide sequence is more commonly found within larger peptide compounds of not more than 30 amino acids in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                      15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukccyte antigen: HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 51; DB 1; Length 10;
Pred. No. 0.043;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prea. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1995.
05-ARR-1995; U04349.
05-ARR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                       16-SEP-1993.
25-FEB-1993: U01758.
02-MRR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 13; Page 66; 80pp; English.
                            R41209 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R83061 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                     10 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
W09526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
RESULT
R41209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
R83061
                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ದ್ದ
```

```
Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of clinical symptoms of insulin dependent diabetes by modulating Tell madiated attack on target cells

of clinical symptoms of insulin dependent diabetes by modulating Tell mediated attack on target cells

cell mediated attack on target cells

cell mediated attack on target cells

the method of the invention. These sequences are based on a portion of the method of the invention. These sequences are based on a portion of the major histocompatability complex (MHC) class I antigen (see W07510. The method is for affecting the course of an autoimmune disease involving Trcell mediated destruction of tissue in mammals. These peptides are used especially to treat insulin-dependent diabetes

chopy in the classes. Other diseases that can be treated are multiple sclerosis, rheumatoid arthritis, psoriasis, pemphigus vulgaris, slogren's disease, thyroid disease, Hashimoto's thyroiditis, myssthemia gravis, etc. The peptides modulate T-cell mediated attack on autologous target cells and may also reduce inflammation, swelling, and release of cytokines, perforins, granzymes etc. associated with T cell activation.
                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       04-AUG-1997 (first entry)

T-cell modulating peptide #4.

T-cell modulating peptide #4.

T-cell modulator: autoimmune disease; tissue destruction; alphal-domain; mammal; major histocompatability complex; MHC class I; antigen; perforin; insulin-dependent diabetes mellitus; multiple sclerosis; inflammation; theumatoid arthritis; psoriasis; pemphigus vulgaris; Sjoyren's disease; thyroiditis; myaschenia gravis; granzyme; autologous target cell; cytokine release; T cell activation; therapy.
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-JUN-1998 (first entry)
Peptide B7.75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                           Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.0%; Score 51; DB 1; Length 10; 100.0%; Pred. No. 0.043; Live 0; Mismatches 0; Indels
                                                                                    0; Indels
                       Score 51; DB 1;
Pred. No. 0.043;
0; Mismatches C
50.0%; Scc.
100.0%; Pred
0; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.00.
100.08; Pre-
                                                                                                                                                                                                                                                                                                                                                                                 W07515 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W33786 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SANG-) SANGSTAT MEDICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
WO9744351-Al
```

Wed Feb

```
Delicable Relations of the periods o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-NOV-1997.

22-MAY-1997; 108689.

PR 24-MAY-1995; US-63294.

PR 52-MAY-1995; US-63294.

R STRD ) UNIV LELAND STANFORD JUNIOR.

Beallow R, Claryberger C, Krensky AM;

PR 1: 99-086530/08.

New immunomodulating dimer peptide(s) - based on a Class I HLA-B

PR 1 alpha-1 domaln, used for preventing rejection of transplants or

reating autoimmune diseases

Example 1; Page 19; 41pp; English.

PR 24-MAY-1996

PR 24-MAY-1996

PR 25-MAY-1996

PR 25-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide B7.75 84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51; DB 1; Length 10;
Pred. No. 0.043;
0; Mismatches 0; Indels
                                                                                       (STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W33796 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; (
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                               US-653294
                               22-MAY-1997; U08689
24-MAY-1996; US-653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W33796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HIA-Bw62 CTL modulating peptide (Bw62.60-84).
Yotocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-Bw62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New peptide(s) based on Class I HLA antigen domains - used for modulating cytotoxic T-lymphocyte activity towards targets modulating cytotoxic T-lymphocyte activity towards targets and lass for terminus English.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytotoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and neoplasia and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAR-1994 (first entry)
Peptide fragment of Class I HLA peptide.
Human leukocyte antigen: HLA; peptide; transplantation; neoplasia;
parasitic disease; cytotoxic I lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 51; DB 1; Length 10; 100.0%; Pred. No. 0.043; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 51; DB 1; Length 25; 100.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; Preu. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-SEP-1993.
25-FEB-1993; U01758.
02-MRR-1992; US-844716.
(STR.) UNIY LELAND STANFORD JUNIOR.
Clayberger CA. Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R41207 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R83073 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R83073;
16-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1995.
05-APR-1995; U04349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RESLRNLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
W09526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
R83073
ID 883073
AC R83073
DT 16-MAX
DE HLA-BW
KW CYLOED
KW CIRSS
OS SYNTHE
PN WO9526
PD NO9526
PD 05-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT RESULT RAISON RA
           888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
```

```
Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                    16 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-B35 antigen.
                                                                                                                                                                                                                                                      HLA-Bw62.60-84
                                                                                                                                                                                                                                     12-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                         18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R12464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
R12464
                                                                                  5
                                                                                                                셤
                                                                                                                                                                                                       셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               While of the properties of the properties of the proteins and properties of the properties of the properties of the protein of CTLS.

PS Example 12, 29pp; English.

Example 12, 20pp; English.

Example 26.84

Example 26.84

Insert passociated antigens. This sequence represents the protein processor of the 25 containing a coverage of the 25 containing a covalently that the heat shock protein HSc70. p74 is annohoteric detergent, and then passed through an affinity column covalently bound HLA-B7702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcum influx, and inhibits compounds can be screened for their effect on the cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate Compounds can be screened for their effect on the cytolysis. Candidate compound and p74.

Compounds can be screened for their effect on the cytolysis of containing the amount of binding between the candidate compound and p74.

Containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete containing T-cells and antigen presenting cells (APCS), by adding to the conners.

Containing T-cells and antigen presenting cells (APCS), by adding to the conners.
                                                                                                        Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC ULA-BWG2. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the settivity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; recal lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                               Clayberger C, Krensky AM, Parham P;
WPI: 95-538882446.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                         Length 25;
                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 1;
Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                           50.0%; Scc.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R95431 standard; peptide; 25 AA.
R95431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-NOV-1994; U12985
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                           11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 RESLRNLRGY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clayberger C, Kre
WPI; 95-194027/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-NOV-1996
HLA-B7.60-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
 g
                                                                                                                                                                                                                                                                                                                                                                                                                              ð
```

```
Clayberger C, Krensky AM;

RHI; 95-194027/25.

Clayberger C, Krensky AM;

WPI; 95-194027/25.

Compans. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Frample, Page 9; 29pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of known leucocyte-associated antigens. This sequence represents the R95413, and R95415-R95431 represent palindromes and fragments of known leucocyte-associated antigens. This sequence represents the HA-BW62.60-84. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein p74 from a sective with the heat shock protein Hsc70. P74 from Del isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with the extracellular fragment of p74 combined with the extracellular fragment of p74 combined with the extracellular portion of p74 and of p74 and of p74 and of p74 and p84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolysis. Candidate compounds the amount of binding between the candidate compound and determining the amount of binding between the candidate composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA; p74; alphal-hellx; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human leukocyte antigen; probe; major histocompatibility complex;
                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Score 51; DB 1; Length 25; 100.0%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                       0.11;
50.0%; Scor.
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Pred. ....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R12464 standard; Protein; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                     R95419 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RESLRNLRGY 20
                                                                                                                                               11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC; class I.
Homo sapiens.
J03112486-A.
```

ö

us-08-653-294-35.rag

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ij
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                              N-PSDB, 012115.

HIA-B35 gene - used in DNA probe and transformant cells for immunising animals, for developing monoclonal antibody.

Claim 1; Page 1; 11pp; Japanese.

Probes comprising part of the sequence encoding this sequence can be used to identify Class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-B35 antigen. See also J03112485 and J03112487.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel anti-microbial protein from e.g. Macadamia integrifolia useful for controlling microbial infestations of plants or mammals Claim 1: Page 63-65; 96pp; English.

The sequence is that of an antimicrobial protein which can be used to control microbial infestations in plants and mammalian animals.
                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .,
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 605;
                                                                                                                                                                                                                                                              Query Match 50.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-DEC-1997; AU0874.
20-DEC-1996; AU-004275.
(RETH-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
BOWER II. GOULLER KC, Green JL, Manners JM, Marcus JP;
WPI; 98-377279/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                              W62838;
27-OCT-1998 (first entry)
Glycine max antimicrobial protein.
antimicrobial protein; infestation; control.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 46.6%; Score 47.5; D
Best Local Similarity 47.8%; Pred. No. 11;
Matches 11; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              W62838 standard; Protein; 605 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YGR---LNRLSERRESLRNLRGY 20
                                  22-SEP-1989; JP-247697.
(OLYU ) OLYMPUS OPTICAL KK.
                                                                                                                                                                                                                                                                                                                                                   99 RESLRNLRGY 108
                 22-SEP-1989; 247697
22-SEP-1989; JP-247
                                                                                                                                                                                                                                                                                                                               11 RESLRNLRGY 20
                                                                  WPI; 91-182991/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycine max. WO9827805-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
W62838
ò
                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
```

Search completed: February 8, 2000, 04:05:44 Job time: 9361 sec

211 YGRIRVLORFNORSPOLONLRDY 233

g

Н

us-08-653-294-35.rpr

```
Compugen Ltd.
GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
```

February 7, 2000, 18:04:41; Search time 111.22 Seconds (without alignments) 8.482 Million cell updates/sec OM protein - protein search, using sw model US-08-653-294-35 102 1 YGRLNRLSERRESLRNLRGY 20 BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table: Run on:

142080 Total number of hits satisfying chosen parameters:

142080 seqs, 47169319 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_62:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Result

Description	MHC class I antige	MHC class I antige	MHC class I antige	н	Ħ	class I	ILA-B39	یډ	sur		MHC class I lympho		class I histocompa	н	Н	н	Η	class I histocompa	class I	class I	class I	MHC class I histoc	ss I hist	ass I	H	H	MHC class I histoc	MHC HLA-B8 chain -	HLA-B*5602 - human	lymphocyte antigen
£ £	138875	138876	ന	138874	159188	HLHU40	168774	S24439	168701	136956	168747	I54308	S24436	S24437	S24438	S24440	S24433	S03538	I54418	HLHUB7	277966	G01230	S16789	A45880	137519	137520	137522	8443	172755	8
DB	5	~	~	7	~	Н	7	~	~	~	~	~	~	~	~	7	~	ď	~	Н	~	~	7	~	~	~	~	7	~	~
Length	1 M	3	m	3	æ	7	7	~	0	0	S	2	354	S	354	S	S	S	9	9	9	9	9	ø	ø	O	ø	ø	362	S.
Watch		50.0					50.0			٠.	50.0	50.0	50.0	50.0	50.0			50.0		50.0							50.0			20.0
Score	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51	51
No.	-	7	m	4	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30

HLA-B*5501 - human HLA-B*5502 - human HLA-B*5501 - human MHC class I histoc HLA-B alpha-chain Iymphocyte antigen HLA-B*58*401 - human MHC class I protei HLA-B\$5 variant - Iymphocyte antigen MHC HLA-BW42, HLA- MHC HLA-BW42, HLA- MHC HLA-BB18 chain
172752 172753 172754 138437 138437 155505 155505 156649 156649 156655 156865 161869
00000000000000000000000000000000000000
51 51 51 51 51 51 51

## ALIGNMENTS

MHC class I antigen - human (fragment)
C;Species: Homo saplens (man)
C;Species: Homo saplens (man)
C;Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 23-Jul-1999
C;Accession: 138875
E;Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stef
Immunogenetics 42, 19-27, 1995
A;Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A;Reference number: 138860; MUID:95317819
A;Accession: 138875
A;Accession: 138875
A;Accession: 138875
A;Accession: 138875
A;Accession: 1-137 <RES
A;Accession: 1-137 <RES
A;Accession: 1-137 <RES
A;Accession: 1-137 <RES
A;Cross-references: EMBL:U15639; NID:9930332; PIDN:AAA74046.1; PID:9930333
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology

Gaps ö Length 137; Ouery Match 50.0%; Score 51; DB 2; Best Local Similarity 100.0%; Pred. No. 0.91; Matches 10; Conservative 0; Mismatches (

ö

11 RESLRNLRGY 20 40 RESLRNLRGY 49 ŏ g RESULT 2
138876

MHC class I antigen - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 23-Jul-1999
C; Accession: 138876
A; Tachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stef Immunogenetics 42, 19-27, 1995
A; Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A; Recence number: 138876
A; Accession: 138876
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule t

Gaps ö Length 137; 0; Indels 50.0%; Score 51; DB 2; 100.0%; Pred. No. 0.91; iive 0; Mismatches Query Match 50.0 Best Local Similarity 100. Matches 10; Conservative

ö

40 RESLRNLRGY 49 11 RESLRNLRGY 20 g à

ö

```
A; Gene: GDB:HLA-B
A; Cross-references: GDB:120048; OMIM:142830
A; Map position: 6p21.3-6p21.3
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterodimer; membrane protein; transplantation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: 168774
R;Mueller, C.A.; Engler Blum, G.; Gekeler, V.; Stelert, I.; Weiss, E.; Schmidt, H.
Immunogenetics 30, 200-207, 1989
A;Title: Genetic and serological heterogeneity of the supertypic HIA-B locus specific
A;Reference number: 154463; MUID:89379286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A02186
R;Lopez de Castro, J.A.; Bragado, R.; Strong, D.M.; Strominger, J.L.
Blochemistry 22, 3961-3969, 1983
A;Title: Primary structure of papain-solubilized human histocompatibility antigen HLA A;Reference number: A02186; MUID:84000412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Comment: Comparison of a number of class I allelic sequences (-B40 vs. -B7 and -A2 y restricted to the alpha-1 and alpha-2 domains. The most conspicuous clustering of v ossible alloantigenic determinants of these antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC class I histocompatibility antigen HLA-B40 alpha chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 02-Sep-1997
A;Map position: 6p21.3-6p21.3
A;Introns: 90/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Cross-references: GB:M29865; NID:g187676; PIDN:AAA36223.1; PID:g187677
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-90/Domain: alpha-1 <F21>
F:91-181/Domain: alpha-2 <F22>
F:91-260/Domain: immunoglobulin homology <IMM>
F:195-260/Domain: immunoglobulin homology <IMM>
F:86/Binding site: carboydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 270;
1.8;
                                                                                                                                                                                                                                                                                         Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 274;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                              DB 2;
1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                         50.0%; Score 51;
llarity 100.0%; Pred. No.
Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 51; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 51; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC HLA-B39 chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 1-270 <LOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-274 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A. Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-274 <RI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: 168774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                Cispectes: Homo sapiens (man) (insument) (insument) (insument) (inspectes) authors sapiens (man) (insument) (i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disc., and antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Species: Homo sapiens (man)
C:Accession: 138974
R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefanc R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefanc R:Garber, T.L.; Butler, L.M.; Trachtenberg, E.A.; Erlich, H.A.; Rickards, O.; De Stefanc A:Title: HLA-B alleles of the Cayapa of Ecuador: new B39 and B15 alleles.
A:Accession: 138874
A:Accession: 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Accession: I59188
R; Bronson, S; K; Pei, J; Taillon-Miller, P.; Chorney, M.J.; Geraghty, D.E.; Chaplin, D. Proc. Natl. Acad. Sci. U.S.A. 88, 1676-1680, 1991
A; Title: Isolation and characterization of yeast artificial chromosome clones linking th A; Reference number: I59188; MUID:91156671
A; Accession: I59188
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB:M59841; NID:9187697; PIDN:AAA59623.1; PID:9187698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 51; DB 2; Length 137; 100.0%; Pred. No. 0.91; 1ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51; DB 2; Length 137;
Pred. No. 0.91;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHC cell surface glycoprotein - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: GDB:HLA-B
A;Cross-references: GDB:120048; OMIM:142830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%; Scor.
100.0%; Pre
                                                                                                                                                             class I antigen - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-181 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 RESLRNLRGY 20
```

g ç

40

ö g

```
C; Species: Homo saplens (man)
C; Species: Homo saplens (man)
C; Species (2-101-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C; Accession: Is4308
R; Rodriguez, S:G.; Johnson, A.H.; Hurley, C.K.
Hum. Immunol, 37, 192-194, 1993
A; Title: Molecular Characterization of HLA-B71 from an African American individual.
A; Reference number: I54308; MoID:94064392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
C;Accession: 16847
Immunogenetics 29, 297-307, 1989
A;Title: Allelic variation in HLA-B and HLA-C sequences and the evolution of the B A;Accession: 168747
A;Accession: 168747
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
       02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999 C;Accession: 136956
B;Parham, P: Lawlor. Do.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: 136956; MUID: 89235215
A;Accession: 136956 MUID: 89235215
A;Accession: 136956 MUID: 89235215
A;Accession: 136956 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 130856
A;Residues: 1-308 FAES>
A;Residues: 1-308 FAES>
A;Cross-references: GB:M24044; NID:g176812; PIDN:AAA35423.1; PID:g176813
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1.350 <RES>
A;Cross-references: GB:M28204; NID:9576472; PIDN:AAA53257.1; PID:9576473
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A: Map position: 6p21.3-6p21.3
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Accession: I54308
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-350 <RES>
A;Cross-references: GB:L07950; NID:g307236; PIDN:AAA59683.1; PID:g307237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.0%; Score 51; DB 2;
llarity 100.0%; Pred. No. 2.3;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 51; DB 2; ilarity 100.0%; Pred. No. 2.1; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GDB:120048; OMIM:142830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
154308
MHC HLA B71 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           금
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                     C. Accession: S24439

R. Watkins, D. I.; McAdam, S. N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Matrics, D. I.; McAdam, S. N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Matrics, D. I.; McAdam, S. N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Matrics, D. I.; McAdam, S. N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbella: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate A; Reference number: S24439

A; Reference number: S24027; MUID: 92269956

A; Reference number: S24027; MUID: 92269956

A; Molecule type: MRNA
A; Residues: 1-274 <WAT>
C; Genetics:
A; Gene: HLA-B-3901
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords: glycoprotein
F; 1-274/Product: class I histocompatibility antigen HLA-B-3901 *status predicted <WAT>
F; 1-194/Droduct: class I histocompatibility antigen HLA-B-3901 *status predicted <EXI>F; 1-194/Droduct: class I histocompatibility antigen HLA-B-3901 *status predicted <EXI>F; 1-274/Product: class I histocompatibility antigen HLA-B-3901 *status predicted <EXI>F; 1-274/Product: class I histocompatibility antigen HLA-B-3901 *status predicted <EXI>F; 1-274/Product: class I histocompatibility subjectived <EXI
F; 1-274/Product: class I histocompat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: 168701

B; Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.

B; Arnot, D.; Lillie, J.W.; Auffray, C.; Kappes, D.; Strominger, J.L.

Immunogenetics 20, 237-252, 1987

A; Reference number: 154412; MUID:84287690

A; Reference number: 1548701

A; Accession: 168701

A; Residue; preliminary; translated from GB/EMBL/DDBJ

A; Residue; preliminary; translated from GB/EMBL/DDBJ

A; Residues: 1-300 cRES>

A; Residues: 1-300 cRES>

A; Residues: 1-300 cRES>

A; Cross-references: GB:MA7540; NID:9187733; PIDN:AAA59638.1; PID:9386890

C; Superfamily: class I histocompatibility antigen; immunoglobulin homology

C; Keywords: Surface antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Homo sapiens (man)
Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                      class I histocompatibility antigen HLA-B-3901 - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 01-Nov-1996 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 51; DB 2; Length 274; Best Local Similarity 100.0%; Pred. No. 1.8; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.0%; Score 51; DB 100.0%; Pred. No. 2; ive 0; Mismatches
              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell surface antigen - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHC ChlA chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RESLRNLRGY 20
                                                                                                                                                 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111111111
75 RESLRNLRGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 RESLRNLRGY 20
                                                                                                                    111111111
75 RESLRNLRGY
          10;
                                                                                                                                                                                                                                                        œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
```

HLA-

ó

```
Search completed: February 7, 2000, 18:04:41 Job time: 22207 sec
                                                       Best_Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100. Matches 10; Conservative
                                                                                                                                                                                                                                                                  11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Molecule type: mRNA
;Residues: 1-354 <WAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: HLA-B-4801
               Query Match
                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
$22436
class I histocompatibility antigen HLA-B-3504 precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
C;Accession: $24436
R;Warkins, D. I.; McAdam, S. N.; Liu, X.; Strang, C. R.; Milford, E. L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indicate A; Reference number: $24027; MuID: 92269956
A;Reference number: $24027; MuID: 92269956
A;Reference number: $24027; MuID: 92269956
A;Reference number: $24027; MuID: 92269956
A;Residues: 1354 <WAT>
C;Genetics:
A;Residues: 1354 <WAT>
C;Genetics:
A;Gene: HLA-B-3504
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Reynodas: glycoprotedin; transmembrane predicted <SIG>F:17-299/Domain: alpha-2 #status predicted <EXT>F:17-299/Domain: alpha-2 #status predicted <EXT>F:107-188/Domain: alpha-2 #status predicted <ITMN>F:324-334/Domain: intracellular #status predicted <ITMN>F:324-335/Domain: intracellular #status predicted <ITMN>F:324-335/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S24437
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Garbe Nature 357, 329-333, 1992
A;Title: Watercombinant HLA-B alleles in a tribe of South American Amerindians indicate A;Reference number: S244027; MUID:92269956
A;Accession: S24437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: HLA-B-4802
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
C; Keywords; glycoprotein; transmembrane protein
E; Hypoponain: signal sequence #status predicted <SIG>
E; Hypoponain: signal sequence #status predicted <SIG>
E; Hypoponain: signal sequence #status predicted <EXT>
E; Hypoponain: alpha-2 #status predicted <EXT>
E; Hypoponain: alpha-2 #status predicted <EXT>
E; Hypoponain: immunoglobulin homology <IMM>
E; Hypoponain: transmembrane #status predicted <IMM>
E; Hypoponain: intracellular #status predicted <INM>
E; Hypoponain: intracellular #status predicted <INT>
E; Hypoponain: 
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                            Gaps
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;102/Binding site: carbohydrate (Asn) (covalent) #status predicted F;117-180,219-275/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; Score 51; DB 2; Length 354; 100.0%; Pred. No. 2.4;
                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
          Pred. No. 2.3;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Pred. No. 2...
ilarity 100.0%; P
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                          Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91 RESLRNLRGY 100
                                                                                                                                                   11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-354 <WAT>
                                                                                                                                                                                                                                              66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                              g
                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
```

```
C;Accession: S24438
R;Watkins, D.I.; McAdam, S.N.; Liu, X.; Strang, C.R.; Milford, E.L.; Levine, C.G.; Ga Nature 357, 329-333, 1992
A;Title: New recombinant HLA-B alleles in a tribe of South American Amerindians indic A;Reference number: S24027; WUID:92269956
A;Accession: S24438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: glycoprotein; transmembrane protein
F:1-17/Domain: signal sequence #status predicted <SIG>
F:17-354/Product: class I histocompatibility antigen HiA-B-4801 #status predicted <WA
F:17-299/Domain: extracellular #status predicted <EXT>
F:107-198/Domain: alpha-2 #status predicted <EXZ>
F:212-277/Domain: immunoglobulin homology <IMM>
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 18-Jul-1997 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                     class I histocompatibility antigen HLA-B-4801 precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;300-323/Domain: transmembrane #status predicted <TMM>
7343-334/Domain: intracellular #status predicted <INT>
F;102/Binding site: carbohlular(covalent) #status predicted
F;107-180,219-275/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 2; Length 354;
Pred. No. 2.4;
Length 354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
DB 2;
2.4;
                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
Score 51;
Pred. No.
50.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50.0%;
```

glycine max pseudomonas homo sapien glycine max homo sapien homo sapien homo sapien homo sapien

Н

Perfect score:

Run on:

δ

Sednence:

Scoring table:

Searched:

```
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-60(B-40) B*4001 ALPHA CHAIN (FRAGMENT).
                                                                                                                                                                                                                      MEDIINE: 84000412.
LOPEZ DE CASTRO J.A., BRAGADO R., STRONG D.M., STROMINGER J.L.;
"Primary structure of papain-solubilized human histocompatibility
antigen HLA-B40 (-Bw60). An outline of alloantigenic determinants.";
Blochemistry 22:3961.3969(1983).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                             P30498 P
P13916 9
Q05395 P
P30499 P
P10321 P
P30484 P
P30484 P
P30686 P
P30500 P
P30500 P
P30500 P
                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                             Length 270;
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 51; DB 1; Best Local Similarity 100.0%; Pred. No. 0.59; Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 AA
                                                                                                                              270 AA
                                                                                           ALIGNMENTS
1263_HUMAN
GLCA_SOYBN
HRPJ_PSESY
1C01_HUMAN
GLCX_SOYBN
1CXX_HUMAN
1C01_PANTR
1C02_HUMAN
1C02_HUMAN
1C05_HUMAN
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 25, (Rel. 25, 1) (Rel. 25, 1) (Rel. 38, 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                     84
11 RESLRNLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1824_HUMAN
P30470;
01-APR-1993 (
01-APR-1993 (
15-JUL-1999 (
                                                                                                                            1B33_HUMAN
P01890;
[1]
SEQUENCE.
                                                                                                               RESULT 1
1B33_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
1B24_HUMAN
 000000444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                            pan troglod
homo sapien
pan troglod
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                        saplen
                                                                                                                                                                                                                                                                                                                                                                                                                                       sapien
sapien
sapien
sapien
                                                                                                                                                                                                                                                                               homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapien
                                                Search time 68.63 Seconds (without alignments) 8.703 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapien
                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                       homo
homo
homo
homo
homo
homo
homo
                                                                                                                                                                                                                                                                  Description
                                                                                                                                                                                                                                                                              P01890
P30470
                                                                                                                                                                                                                                                                                            82229
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                 8, 2000, 01:26:01;
                                                                                                                            82229 seqs, 29864866 residues
                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                1B04_HUMAN
1B07_HUMAN
1B08_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                     1B27_HUMAN
1B28_HUMAN
1B31_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                         1832_HUMAN
1834_HUMAN
1835_HUMAN
1836_HUMAN
                                                                                                                                                                                                                                                                                            1A02_PANTR
1B02_HUMAN
1B02_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B38_HUMAN
1B39_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1B43_HUMAN
1B46_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1B55_HUMAN
1B56_HUMAN
                                                                                                                                                                                     summaries
                                                                                                                                                                                                                                                                                                                                     LB10_HUMAN
                                                                                                                                                                                                                                                                                                                                             LB11_HUMAN
                                                                                                                                                                                                                                                                                                                                                   B12_HUMAN
                                                                                                                                                                                                                                                                                                                                                            LB13_HUMAN
                                                                                                                                                                                                                                                                                                                                                                  1B21_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                LB23_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                        LB25_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                              LB26_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B48_HUMAN
                                                                                                                                                                                                                                                                                                                                                                          IB22 HUMAN
                                   sw model
                                                                                  102
1 YGRLNRLSERRESLRNLRGY 20
                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                  protein - protein search, using
                                                                                                                                                                              Post-processing: Minimum Match 0%
Listing first 45
                                                                           US-08-653-294-35
                                                                                                                                                                                                                                                                 DB
                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                   SwissProt_38:*
                                                                                                                                                                                                                                                         Query
Match Length
                                                                                                                                                                                                                                                                                                  February
```

Score

Result No.

Database :

ö

Gaps

Wed Feb

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ð
                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN
B-35 B*3504 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR'1990 (Rel. 14, Created)
01-APR'1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 14, Last sequence update)
CHAR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPAISHLITY ANTIGEN, A-5 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanzee).
Elekaryota: Metazoa; Chimcata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                 ဥ
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3504 ALPHA CHAIN PRECURSOR (FRAGMENT).
HLA-B OR HLAB.
                                                                                   MEDLINE; 92269956.
WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L.,
LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H.,
TROUP G.M., HUGHES A.L., LETVIN N.L.,
"New recombinant HLA B alleles in a tribe of South American
Americaldians indicate rapid evolution of MHC class I loci.";
Nature 357:329-333(1992).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                         THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 51; DB 1; Length 354; 100.0%; Pred. No. 0.8; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 6564795A CRC32;
                                                                                                                                                                                                                                                                                                                                       PFAM; PF00047; ig; 1.
PFAM; PF00129; MG_I; 1.
MC_I; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 AA
                                                                                                                                                                                                                                                                                                             EMBL; M86403; -; NOT_ANNOTATED_CDS. HSSP; P30685; 1A1N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W.
                                                                                                                                                                                                                                                                                                                       HSSP; P30685; 1A1N.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
354 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                   [1]
SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1A02_PANTR
P16210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 90207291...
ENNIS P.D., ZEMMOUR J., SALTER R.D., FARHAM P.;
Rapid cloning of HLA-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                    LAWLON D.A., WARREN E., WARD F.E., PARHAM P.;
LAWLON D.A., WARREN E., WARD F.E., PARHAM P.;
Immunol. Rev. 113:147-185(1990).
-I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 90315860.
PARHAM P., BENJAMIN R.J., CHEN B.P., CLAYBERGER C., ENNIS P.D.,
KRENSKY A.M., LAWLOR D.A., LITTMAN D.R., NORMENT A.M., ORR H.T.,
SALTER R.D., ZEMMOUR J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-7 B*0702 ALPHA CHAIN
PRECURSOR (B7.2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 362; 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-5 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97E6CE8A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; P30685; 1AIN.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 1g; 1.
PFAM; PF00129; MRC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%; Score 51; DB
100.0%; Pred. No. 0.8
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40487 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M30679; AAA87971.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 RESLRNLRGY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 RESLRNLRGY 20
90201944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1B02_HUP
P01889;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1B02_HUMAN
```

m

F. .

STANDARD;

89030641

```
*Mucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
                                                                         01-7AN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-2 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                        Submitted (FEB-1989) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                           Pan troglodytes (Chimpanzee).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                     MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G., KLEIN J.;
                                                                                                                                                                                                                                                                                                                                               -!- SUBUNIT: DIMER C
MICROGLOBULIN).
                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                   1B02_PANTR
P13751;
                                                                                                                                                                                                                                                                       [2]
REVISIONS.
                                                                                                                                                                                                                                                                                               MAYER W.;
                           RESULT 5
1B02_PANTR
                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                              MEDLINE; 85287366.
SOOD A.K., PAN J., BIRO P.A., PEREIRA D., SRIVASTAVA R., REDDY V.B.,
DUCEMAN B.W., WEISSMAN S.M.;
"Structure and polymorphism of class I MHC antigen mRNA.";
Immunogenetics 22:101-121(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                       SEQUENCE OF 25-295.
MEDLINE: 80088278
ORR H.T., LOPEZ DE CASTRO J.A., LANCET D., STROMINGER J.L.;
"Complete amino acid sequence of a papain-solubilized human
histocompatibility antigen, HLA-B7. 2. Sequence determination and
search for homologies.";
Biochemistry 18:5711-5720(1979).
"Diversity of class I HLA molecules: functional and evolutionary interactions with T cells.";
                                                                                                                                                                                                                                                                                           THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                       SEQUENCE FROM N.A.
ELLEXSON M.E., ZHANG L., HILDEBRAND W.H.;
Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AALA -> GPW (IN REF. 3).
Q -> E (IN REF. 5).
W -> S (IN REF. 3).
R -> G (IN REF. 3).
GL -> RP (IN REF. 3).
                         Cold Spring Harb. Symp. Quant. Biol. 54:529-543(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B-7 B*0702 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . -> RP (IN REF. 3)
87B2ED84 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M32317; AAA36230.1; -.
EMBL; M16102; AAA56522.1; ALT_SEQ.
EMBL; U29057; AAA91229.1; -.
PIR; A02185; HLHUB7.
PIR; B35997; B35997.
HSSP, P04660; 1AGB.
MIN; 142830; -.
PROSITE: PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40460 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; G1
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362
110
188
283
18
18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 AA;
                                                                                                                                                                                                                                                                                                                       MICROGLOBULIN)
                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
```

DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ilensib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                              CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                              CHLA CLASS I HISTOCOMPA:
B-2 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
;, 4BF65A6C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 51; DB 1;
100.0%; Pred. No. 0.82;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                                                                                                        HSSP; P30685; IAIN.
PROSTTE; P800290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW.
                                                                                                                                        EMBL; X13116; CAA31508.1; -. PIR; S03538; S03538.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1B04_HUMAN
P30460:
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                             MHC I;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a
a
a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
```

ö

Gaps

ö

Query Match 50.0%; Score 51; DB 1; Length 362; Best Local Similarity 100.0%; Pred. No. 0.82; Matches 10; Conservative 0; Mismatches 0; Indels

66

11 RESLRNLRGY 20

ò g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed 'Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Diversity and diversification of HLA-A,B,C alieles.";
J. Immunol. 142.3397-3950(1989).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-14 B*1401 ALPHA CHAIN
                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
     362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M24040; AAA59661.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40358
     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 RESLRNLRGY
                                                                                                                                                                                                         HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1B08_HUMAN
P30463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1808_HUMAN
        NO STATE THE TENT OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antagonist HIV-1 Gag peptides induce structural changes in HLA B8.";
J. Exp. Med. 184:2279-2286(1996).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 97130420.
REID S.W., MCADAM S., SMITH K.J., KLENERMAN P., O'CALLAGHAN C.A.,
HARLOS K., JAKOBSEN B.K., MCMICHAEL A.J., BELL J.I., STUART D.I.,
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLASS I HISTOCOMPATIBILLITY ANTIGEN, B-8 B*0801 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51; DB 1; Length 362;
Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIN, TETE, PS00290; IG_MHC; 1.
PROSITE: PS00247; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE: 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
"Injversity and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B-8 B+0801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 25-300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
1467B8EB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Sco...
100.0%; Pred. No. v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M24036; AAA52662.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1114
2206
3309
3333
1110
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1AGB; 16-JUN-97.
1AGC; 16-JUN-97.
1AGD; 16-JUN-97.
1AGE; 16-JUN-97.
1AGE; 16-JUN-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MICROGLOBULIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HLA-B OR HLAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142830;
                                                                                                                   PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
```

SIGNAL

CHAIN

DOMAIN DOMAIN

RESULT 7 1807\_HUMAN

66

용

ô

Best Loca Matches

```
ö
                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN
PRECURSOR.
                                                                            ö
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
                                             Length 362;
                                                                            Indels
                                                                            ö
                                                Score 51; DB 1;
Pred. No. 0.82;
9BED8199 CRC32
                                                                                                                                                                                                                   362 AA
                                                            Best Local Similarity 100.0%; pred. No. 0.6
Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                             (Human).
                                                                                                                                                                                                                                                                                                                                HLA-B OR HLAB.
                                                                                                                                                                                                                   OC OE DIT
```

us-08-653-294-35.rsp

```
99 RESLRNLRGY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1B11_HUMAN
P30465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
1811_HUMAN
AC P30465;
DT 01-APR-
DT 01-APR-
DT 15-UUL-
DE HLA CLI
DE CHAIN |
COS HOMO SI
OC EUKATY
COC EUKATY
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
 å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1B10_HUMAN STANDARD; PRT; 362 AA.
P30464.
01-ARR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HLA CLLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-65(B-14) B*1402 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                 MEDLINE; 89235215.

PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;

PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;

"Diversity and diversification of HLA-A,B,C alleles.";

J. Immunol. 142:3937-3950(1989).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.

-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 92196792.
LITTLE A.-M., PARHAM P.;
"The HLA-BAP5 subtype of B15: molecular characterization and comparison with rossreacting antigens.";
Tissue Antigens 38:186-190(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
 Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Y SIMILARITY.
Y SIMILARITY.
Y SIMILARITY.
BE68AC9E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB 1;
Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                  EMBL; M24032; AAA59664.1; --
HSSP; P30460; 1AGB.
MIM; 142830; --
PROSITE; P500290; IG_MHC; 1.
PFAM; PF00129; MHC_1; 1.
PFAM; PF00129; MHC_1; 1.
MC_1; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Scor.
100.0%; Pred. No. v...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40342 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLA-B OR HLAB.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 RESLRNLRGY 20
                                   SEQUENCE FROM N.A MEDLINE; 89235215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1B10_HUMAN
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-75(B-15) B*1502 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
CXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
MADLINE, 3905650B
MADRIGAL J.A., BELICH M.P., HILDEBRAND W.H., BENJAMIN R.J.,
LITTLE A.-M., ZEMMOUR J., ENNIS P.D., WARD F.E., PETZL-ERLER M.L.,
MARTELL R.W., DU TOIT E.D., PARRAM P.,
"Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72(BW-70) B*1503 ALPHA
CHAIN PRECURSOR.
HIA-B OR HLAB.
                                                                                                                                                                                                         5
F
TISSUE-BLOOD:
MEDLINE; 96369309.
LIN L., TOKUNAGA K., TANAKA H., NAKAJIMA F., IMANISHI T.,
KASHTAKSE K., BANNAI M., MIZUNO S., AKAZA T., TADOKORO K.,
SHIBATA Y., JUJI T.;
FURTHER MOLECULAR diversity in the HLA-B15 group.";
Tissue Antigens 47:265-274 (1996).
--- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS
THE IMMONE SYSTEM.
--- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8CF9BCD0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M75138; AAA59630.1; -.
EMBL; D50293; BAA08824.1; -.
HSSP; P306885; 1AlN.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00147; Ig; 1.
PFAM; PF00129; MHC_L; 1.
MHC_L; Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40338 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100 Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110
188
283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
```

```
HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1B13_HUMAN
P30466;
                                                                                                                                                                                                                                                                                                                                                                DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       윱
                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                    HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, BW-72/BW-70) Bv1503 ALPHA CHAIN. EXTRACELLULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3. CONNECTING PEPTIDE.
J. Immunol. 149:3411-3415(1992).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-APR-1993 (Rel. 25, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 92269956.
WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L., LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H., TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HLA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci.";
                 THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                            Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAMOS M., BARBER D.F., LAYRISSE Z., DE CASTRO J.A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; 99D70546 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 51; DB 1;
Pred. No. 0.82;
); Mismatches
                                                                                                                                                   EMBL; X61709; CAA43878.1; -.
PIR; S16789; S16789.
HSSP; P91688; JAIN.
MIM; 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00147; 19; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Scor.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                           40387 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 357:329-333(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-B OR HLAB
                             -!- SUBUNIT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1B12_HUMAN
P30513;
                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
1B12_HUMAN
                                                                                                                                                                                                                                                       CHAIN
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-62 B*1504 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1] SEQUENCE FROM N.A. MEDLINE; 89235215.
PARHAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.;
DIDVESTIFY and diversification of HLA-A,B,C alleles.";
J. Immunol. 142:3937-3950(1989).
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                   THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; E80FC24C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB Pred. No. 0.8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
PFAM; PF00129; MHC_I; 1.
SIGNAL I Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.0%; Sco
ilarity 100.0%; Pr
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M84382; AAA59632.1; --
EMBL; U70528; AAB16918.1; --
PIR; S24433; S24433.
HSSP; P30685; IAIN.
MIM; 142830; --
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                   -!- SUBUNIT: DIMER (MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
1115
207
299
310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
1813_HUMAN
10 13466
DT 01-APR
DT 15-UAR
DT 15-UAR
DE HLA-B
CS HOMO S
CC ELKALY
CC ELKALY
CC ELKALY
CC THE
CC TH
```

```
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "An altered position of the alpha 2 helix of MHC class I is revealed by the crystal structure of HLA-B*3501."; Immunity 4:203-214(1996).
                                                                                                                                                                                                                                                                      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE; 89339610.
OOBA T., HAYASHI H., KARAKI S., TANABE M., KANO K., TAKIGUCHI M.;
"Inhe structure of HLA-B35 suggests that it is derived from HLA-Bw58
by two genetic mechanisms.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
MENSSEN R., ORTH P., ZIEGLER A., SARNGER W.;
SUDMILLED (APR-1998) to the PDB data bank.
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 96209671.
SMITH K.J., REID S.W., STUART D.I., MCMICHAEL A.J., JONES E.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               !- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 25-300.
                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 51; DB 1;
100.0%; Pred. No. 0.82;
ive 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY.
038EC3FC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     362 AA.
                                                                                                     EMBL; M24039; AAA59662.1; --
HSSP; P30460; IAGB.
MIM: 142830; --
PROSITE; PS00290; IG_MHC; 1.
PFAM: PF00147; 19; 1.
PFAM: PF00129; MHC_I: 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 30:76-80(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                       24
362
                                                                                                                                                                                                                                                                                                                                                        298
309
333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                         299
310
334
110
125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RESLRNLRGY 20
                                                                                                                                                                                                                                                             7
7
7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1B21_HUMAN
P30685;
                                                                                                                                                                                                                                                                                                                                     DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                             MHC I;
SIGNAL
                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1921_HUMAN
1D 1821_HI

                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66
    õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outsation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-B35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE: 91365651.
CHERTROPE I.P., HERRERA M., FAINBOIM L., SATZ M.L.;
CHERTROPE L.P., HERRERA M., FAINBOIM L., SATZ M.L.;
COMPLETE OUTCOCCIONE encoding HIA-B:
"Complete nucleotide sequence of a genomic clone encoding HIA-B:
identification of a new variant of HIA-B35.";
Hum. Immunol. 31:153-158(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMONE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 362;
                                                                                                                                                                                                                                                                                                                             MIM; 142830; ...
PROSITE: PS00290; IG_MHC; 1.
PRAM; PF00047; MHC_L; 1.
PFAM; PF00129; MHC_L; 1.
MHC I; Transmembrane; Glycoprotein; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51; DB 1;
Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC TAIL.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEC1C675 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                362 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                        M28110; AAA59617.1; JOINED.
M28111; AAA59617.1; JOINED.
M28111; AAA59617.1; JOINED.
M28112; AAA59617.1; JOINED.
M28113; AAA59617.1; JOINED.
M28114; AAA59617.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MM.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.0%; 8
100.0%;
                                                                                                                                        EMBL; M28115; AAA59617.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
Best Local Similarity 100.
Watches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                            PIR; A45880; A45880.
PDB; IAIN; 08-APR-98.
PDB; IA9B; 18-NOV-98.
PDB; IA9E; 18-NOV-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255
115
207
209
339
110
125
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
1B22_HUMAN
ID 1B22_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P30468;
                                                                                                                                                                                                            EMBL; 1
EMBL; 1
EMBL; 1
                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         66
```

**原門 銀行**原

DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-

MICROGLOBULIN).

us-08-653-294-35.rsp

```
between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3502 ALPHA CHAIN. EXTRACELULAR ALPHA-1. EXTRACELLULAR ALPHA-2. EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BECK Y., SATZ L., TAKAMIYA Y., NAKAYAMA S., LING L., ISHIKAWA Y., NAGANO T., UCHIDA H., TOKUNAGA K., MULLER C., JUJI T., TAKIGUCHI M.: POlymorphism of human minor histocompatibility antigens: T cell recognition of human minor histocompatibility peptides presented by HLA-BIS subtype molecules.";
J. Exp. Med. 181:2037-2048(1995)
J. E. FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE: 92176661.
ZEMMOUR J., LITTLE A.M., SCHENDEL D.J., PARHAM P.;
"The HLA-A.B 'negative' mutant cell line CIR expresses a novel
HLA-B35 allele, which also has a point mutation in the translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3503 ALPHA CHAIN
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 51; DB 1; Length 362; 100.0%; Pred. No. 0.82; 1.ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                    CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                           D7B5C2C9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 AA.
                                                                                                                                                                              PFAM: PF00047; 19: 1.
PFAM: PF00129; MHC_I: 1.
PFAM: PF00129; MHC_I: 1.
SIGNAL I Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  initiation codon.";
J. Immunol. 148:1941-1948(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                            MW.
                                                                                                                                  EMBL; M63454; AAA59682.1; -. HSSP; P30685; 1AlN.
                                                                                                                                                                                                                                                                                                                                                                                                                            40564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                      1114
206
298
308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 RESLRNLRGY 108
                                                                                                                                                                                                                                                                                                                                                                                                                           362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95279930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HLA-B OR HLAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1B23_HUMAN
P30469;
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                              DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
1B23_HUMAN
                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

Search completed: February 8, 2000, 01:26:02 Job time: 1562 sec

FESTRNINGY 108

66

11 RESLRNLRGY 20

ò ద

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                           B-35 B*3503 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
7; 4222D30A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  50.0%; Score 51; DB 1;
llarity 100.0%; Pred. No. 0.82;
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC TAIL
                                                                                                                                                                                                                                       Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                ÄΣ
                                                                                                                                         EMBL; M81798; AAAS9684.1; -.
EMBL; D50299; BAA08828.1; -.
HSSP; P30685; 1AlN.
                                                                                                                                                                                 MIM: 142830; -.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              40515
                                                                                                                                                                                                                                       I; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                     110
125
227
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                               FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                      MHC I;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                  DOMAIN
```

homo homo homo

1

sapien sapien

homo homo homo homo homo homo homo

sapien sapien sapien

homo homo homo

homo homo homo homo homo

OM protein

Run on:

Sequence:

Minimum DB Maximum DB

Database

Searched:

```
029662
029676
029678
077960
029716
                                                    019576
019581
019581
019583
092671
029677
                                                                                                                                                  029663
029665
029664
029707
P79665
                                                                                                                                                                                                                      P79666
019777
019778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                               019776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK STUNGROUNG E., BECCHANDRA S.; Submitted duful-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF014769; AAB67807.1; -. FPRAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.0%; Score 51; DB 7; Length 81; 100.0%; Pred. No. 1.2; 1.4e 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 81.
. AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 AA
                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         019525 PRELIMINARY; PRT;
019525;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last seque
01-NOV-1998 (TrEMBLrel. 08, Last annot
MAC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TremBirel. 05, Last sed
01-NOV-1998 (TremBirel. 08, Last ann
MHC CLASS I ANTIGEN HLA-B (FRAGMENT)
HLA-B.
                                                                                                                                                  029663
029665
029664
029707
P79665
019777
                                                                                                                                                                                                                                                019778
019776
029662
029676
                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 05, TrEMBLrel. 05, (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                             019523
019523;
01-JAN-1998 (
 NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
019525
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 homo sapien
homo sapien
homo sapien
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homo sapien
homo sapien
                                                                                            Search time 176.54 Seconds (without alignments)
7.855 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       homo s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OHOU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           019523 M
019525 M
019529 M
019529 M
019531 M
019531 M
019531 M
019541 M
019542 M
019542 M
019542 M
019543 M
019550 M
019
                                                                                                                                                                                                                                                                               225878
                          Compugen Ltd.
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
             GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                   225878 seqs, 69334122 residues
                                                                                                 ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                              8, 2000, 19:16:17
                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Listing first 45 summaries
                                                                    protein search, using sw model
                                                                                                                                                                  102
1 YGRLNRLSERRESLRNLRGY 20
                                                                                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             019523
019525
019527
019523
019533
019533
019534
019543
019543
019548
019548
019548
019548
019548
019559
019559
019559
019559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_fungi:*
sp_human:*
sp_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_organelle:*
sp_phage:*
                                                                                                                                                     US-08-653-294-35
                                                                                                                                                                                                                                                                                                                                                                                                      sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sp_virus:*
                                                                                                                                                                                                                                                                                                        seq length: 0 seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                          SPTREMBL_12
                                                                                              February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521
521
521
521
521
521
521
521
```

ö

Gaps

ö

Result

ä

ö

```
81
                                                                                                                                                                                               MHC.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                019531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
019531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
019533
ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID DATE OF THE PRINCE OF THE P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
CHANDRAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.,
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014773; AAB67811.1; -.
PFAM; PF00129; MHC_I; 1.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                     SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
SUDBHITTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
BMBL; AF014771; ABB67809.1; -
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 50.0%; Score 51; DB 7; Length 81; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 50.0%; Score 51; DB 7; Length 81; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JNOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HIA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 1
81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                1 1
81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    019527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 019529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       019529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ო
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
019529
1D 529
1D DT 019529
DT 019 DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 019
DT 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
1019527
10 AC 0119527
10 DT 011
DT 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
ò
```

```
Gaps
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
       <u>`</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
RUNGROUNG E., BEJCHANDRA S.:
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014775; AAB6'B13.1; --
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK
SUNGROUNG E., BEJCHANDRA S.;
SUDMITTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO14777; AAB67815.1; -
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
CHANDANAXINGYONG D., SIRIKONG M., LUANGIRAKOOL K., SRINAK ISTUGROUNG E., BEJCHANDRA S.;
SUDMILTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFOJ4779; AAB67817.1; -
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                       Length 81;
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ul-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-07-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HIA-B (FRAGMENI).
                                                                                                                                                                                                                                                                  50.0%; Score 51; DB 7;
100.0%; Pred. No. 1.2;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%; Score 51; DB 7;
100.0%; Pred. No. 1.2;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                81 AA; 9405 MW;
                                                                                                                                                                                                                                                                     Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                          66 RESLRNLRGY 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 RESLRNLRGY 75
```

ö

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
BENBL; AF014785; AAB67823.1; -.
PENBL; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGROUNG E., BEJCHANDRA S.;
SUBMILTED (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014787; AAB67825.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 50.0%; Score 51; DB 7; Length 83; Best Local Similarity 100.0%; Pred. No: 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7; Length 83;
1.2;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                 01-JAN-1998 (Trembirel. 05, Created)
01-JAN-1998 (Trembirel. 05, Last sequence update)
01-NOV-1998 (Trembirel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-INOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
HLA-B.
                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                     DB 7;
                   50.0%; Score 51; DB 7; 100.0%; Pred. No. 1.2; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 1
83 83
83 AA; 9731 MW; 24B8D666 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 1
83 83
83 AA; 9731 MW; 24B8D666 CRC32;
                                                                                                                                                                                                                                                   83 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0%; Score 51; DB Best Local Similarity 100.0%; Pred. No. 1.7 Matches 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                   PRT;
                     Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                             11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            019541
                                                                                                                                                                                                                                               019539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
019541
                                                                                                                                                                                                          თ
                                                                                                                                                                                                        RESULT
019539
                                                                                                                                            a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STARRANGO STARRA
                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D.,
RUNGKOUNG E., BEJCHANDRA S.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO14783; AAB67821.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHANDANAYINGYONG D., SIRIKONG M., LUANGTRAKOOL K., SRINAK D., RUNGROUNG E., BEJCHANDRA S.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF014781; ARB67819.1; -PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhin1; Hominidae; Homo.
                                                                                                                      Query Match 50.0%; Score 51; DB 7; Length 81; Best Local Similarity 100.0%; Pred. No. 1.2; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                 PRELIMINARY; PRT; 81 AA. 019535; C19535; C1-JAN-1998 (TrEMBLrel. 05, Created) (1-JAN-1998 (TrEMBLrel. 05, Last sequence update) MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               019537 PRELIMINARY, PRT; 81 AA. 019537. 01-JAN-1998 (TrEMBLrel. 05, Created) 01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JAN-1998 (TrEMBLrel. 08, Last annotation update) MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 50.0%; Score 51; DB 7; 11 Similarity 100.0%; Pred. No. 1.2; 10; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 1
81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 1
81 81
81 AA; 9405 MW; 073087CE CRC32;
                                                              073087CE CRC32;
                       1
81
9405 MW;
                       1
81
81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 RESLRNLRGY 20
                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
NON_TER
SEQUENCE
MHC.
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                         RESULT
019535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
019537
                                                                                                                                                                                                                                                                                                                                                                          FT SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
```

ö

à g

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.0%; Score 51; DB 7; Length 89; 100.0%; Pred. No. 1.3; 0; Indels 1.4e 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. CHANG G.H.;
CHOPEK M., CAO K., ZHANG G.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, 1088249; AB4848493.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. CHANG G.H.;
CHOPER M., CAO K., ZHANG G.H.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases:
EMBL, 1088264; AAB48498.1; -
PFAM; PF00129; MHC_I; 1.
                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NAY-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I HLA-B (FFRGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 1
89 89
89 AA; 10501 MW; FA3EFCDC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 AA; 10489 MW; A7D3DF93 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 51; DB 7; Pred. No. 1.3; 0; Mismatches
89 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111111111
74 RESLRNLRGY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P79620
P79620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        019548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
P79620
ID P79620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15 019548 AC 019548 AC 019548 DT 01-7AN DT 01-NAN DT 01-NAN
   DDT AND DE LEAD DE LEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1)
SEQUENCE FROM N.A.
SHIKONG M., LUANGTRAKOOL K., SRINAK I
RUNGROUNG E., BEJCHANDRA S.;
SUBMITTEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF014789; AAB6787.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 83; 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 50.0%; Score 51; DB 4; Length 89; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

CARTER V., DUNN P.P.;

Identification of a novel HLA-B*07 allele.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ237594; CAB40714.1; -.
                                                                                                                                                                                                                                                                               01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC CLASS I ANTIGEN HLA-B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09Y452 PRELIMINARY; PRT; 89 AA. 09Y452. 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) HUMAN LEUCOCYTE ANTIGEN B (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 89
89 AA; 10609 MW; 659B735B CRC32;
                                                                                                                                                                                                                                          83 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 1
83 83
83 AA; 9731 MW; 24B8D666 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50.0%; Score 51; DB 100.0%; Pred. No. 1.2
                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 50.0
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                    11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 RESLRNLRGY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
```

ó

ö

RESULT 13 P79615

ò

```
OC Eutheria: Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA CAO K., BURDETT L., ZHANG H., FERNANDEZ-VINA M.;
RL Submitted (JUL.1997) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF016299; AAB69444.1; -..
DR PFAM; PF00129; MHC_I; 1.
KW MHC.
FT NON_TER 89 89 A3: 10550 MW; 11452E40 CRC32;
```

Query Match 50.0%; Score 51; DB 7; Length 89;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy 11 RESLENIRGY 20
11 | | | | | | | | | | | | | | |
Db 74 RESLENIRGY 83

ó

Search completed: February 8, 2000, 19:16:17 Job time: 21504 sec

THIS PAGE BLANK (USPTO)

```
i U55022 Human MHC class I ant
i U91330 Homo sapiens MHC clas
i AF181842 Homo sapiens MHC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur.epm.orni.gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, Http://gnomic.stanford.edu/chris/GENSCANW.html), and NetPlantGene (http://www.cbs.dtu.GK/netpgene/cbsnetpgene.html), and NetPlantGene (http://www.cbs.dtu.GK/netpgene/cbsnetpgene.html), saraches of the complete sequence against a peptide database and the Arabidopsis EST database at TiGR (http://www.tigr.org/tdb/at/at.html).
Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as 'unknown' proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are predicted by tRNAscan-SE (Sean Eddy,
                                                                                                                                                                                                                              Eukaryota; thallana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
euchyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
Arabidopsis.

Lin,X., Kaul,S., Shea,T.P., Fujii,C.Y., Shen,M., Vanhken,S.E.,
Barnstead,M.E., Mason,T.M., Bowman,C.L., Ronning,C.M., Benito,M.,
Carrera,A.J., Creasy,T.H., Buell,C.R., Town,C.D., Nierman,W.C.,
Fraser,C.M. and Venter,J.C.
Arabidopsis thallana chromosome II BAC F7HI genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xiaoying Lin

The institute for Genomic Research
9712 Medical Center Dr.

Rockville, MD 20850, USA
e-mail: Xiin@tigr.org
BAC clone F7H1 is from Arabidopsis chromosome II and is near the molecular marker mi398

The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-APR-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
4 (bases 1 to 84544)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (18-JUN-1999) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
5 (bases 1 to 84544)
                                                                                                                ATACOO7134 84544 bp DNA PLN 01-JUL-1999
Arabidopsis thaliana chromosome II BAC F7H1 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (Ol-JUE-1999) The Institute for Genomic Research,
Medical Center Dr., Rockville, MD 20850, USA
On Apr 24, 1999 this sequence version replaced g1:4580447.
Address all correspondence to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (21-MAR-1999) The Institute for Genomic Research, Medical Center Dr, Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 84544)
   270
270
270
 14.03
14.03
14.03
136.49
136.49
136.49
                                                                                                                                                                                   AC007134.8 GI:4678196
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 84544)
Lin,X. and Kaul,S.
Direct Submission
                                                                                                                                                    complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                   seq_name: gb_pl2:ATAC007134
                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                    thale cress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in, x.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in, X
gb_pr2:HSHLABV01
gb_pr2:HSHLADTT1
gb_pr4:HUM31HLA1
                                                                                                                               DEFINITION
                                                                                                                                                                ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 U59965 Human MHC class I proteil D89333 Homo sapiens DNA for MHC AJ131852 Homo sapiens HLA-B gen AJ007605 Homo sapiens HLA-B*151 M28110 Human MHC class I call
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF014769 Homo sapiens MHC class AF014771 Homo sapiens MHC class AF014773 Homo sapiens MHC class AF014773 Homo sapiens MHC class AF014777 Homo sapiens MHC class AF01478 Homo sapiens MHC class AF014781 Homo sapiens MHC class AF014785 Homo sapiens MHC class AF014789 Homo sapiens MHC class AF014789 Homo sapiens MHC class AF014789 Homo sapiens MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AJ23713 Homo sapiens Hick B gen
AJ237213 Homo sapiens Hick B gen
AJ243131 Homo sapiens Hick B gen
AJ24373 Homo sapiens Hick B gen
AJ24317 Homo sapiens Hick B gen
AJ24317 Homo sapiens Hick B gen
UG7330 Human Hick Class I antige
AF017080 Homo sapiens MHC class
U76392 Human Hick B gene, allele
U76394 Human Hick B gene, allele
U76396 Human Hick B gene, allele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocumentation.
1 AC007134 Arabidopsis thallana
1 AC010932 Homo sapiens chromo (191332 Human cell line THAI DCH (191334 Human cell line THAI DCH (191334 Human cell line THAI DCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human MHC class I antige
Human class I MHC antige
Human MHC class I antige
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF002275 Homo sapiens MHC class
AF016299 Homo sapiens MHC class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human MHC class I antige
Homo sapiens MHC class 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF002268 Homo sapiens MHC class
AF008926 Homo sapiens MHC class
                                                                                                           Command line parameters:
-MODEL-frame+_p2n.model_DEV=xlp
-Q=/cgnl_l/GSPTO_spool_VS08653294/runat_04022000_160701_15779/app_query.fasta.2
-Q=/cgnl_l/GSPTO_spool_VS08653294/runat_04022000_160701_15779/app_query.fasta.2
-DB-Genembl -QFWT=fastap -SUFFTX=rge -GAPOP=12.000 -GAPEXT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=4.500
-FGAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -TRR_SCORE=pct -ALIGN=15 -MODE-LOCAL
-OUTFWHT=ff -NORM=ext -MINLEN=0 -MAXLEN=1000000 -USER=US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 Documentation
                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U67746 H
U80670 H
U90244 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       U67748 1
U93913 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84544 203273
   out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   285.036
955.036
1337.28
1337.28
1337.28
1337.28
1337.29
1337.20
1337.20
1337.20
1336.49
1336.49
1336.49
1336.49
1336.49
1336.49
1336.49
1336.49
1336.49
1336.49
 GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query: US-08-653-294-35
Query length: 20
Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176,920000
 OM of: US-08-653-294-35 to:
                                Date: Feb 8, 2000 10:25 PM
                                                                                                                                                                                                                                                                                                                   Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9b_pr2:HSB0801S1
9b_pr2:HSB1505V1
9b_pr2:HSB3501V1
9b_pr2:HSB3511H1
9b_pr2:HSB3901V1
9b_pr2:HSB39061S1
9b_pr2:HSB39061S1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9b_pr2: HSHLABKI

9b_pr2: HSHLABKI

9b_pr2: AF014770

9b_pr2: AF014771

9b_pr2: AF014777

9b_pr2: AF014777

9b_pr2: AF014777

9b_pr2: AF01478

9b_pr2: AF014789

9b_pr2: AF014789

9b_pr2: AF014789

9b_pr2: AF014789

9b_pr2: HSN13852

9b_pr1: HSN13852

9b_pr1: HSN13852

9b_pr1: HSN13852

9b_pr1: HSN13852

9b_pr1: HSN13713

9b_pr2: HSN13713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
gb_pl2:ATAC007134
gb_htg6:AC010932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pr2:HSB5001V1
gb_pr2:HSB5602S1
gb_pr2:HSHLAB60N1
gb_pr2:HSHLABMR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UMMHB350S2
```

us-08-653-294-35.rge

```
4 LeuAsnArgLeuSerGluArgArgGluSerLeuArgAsnLeuArgGlyTy 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
        repeat_region
                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                         mRNA
                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="overlap with BAC clone F19G14 (AC006438:1. .4157)."
928. .1330
http://genome.wustl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Regions of genomic sequence that are not annotated as genes but have predicted exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                        /note="8353 nt before this point were not included in the submitted sequence, due to overlap with another BAC" complement(1. .4157)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAAFQVSEITQSPSMDPTVCYVQNGPNKGRPICSFYNRVGHIAERCYKKHGFPDGFTP
KGKAGEKLOKPKPLAANVAESSEVNTSLESMYGNLSKEQLOOFIAMFSSQLQNTPPST
YATASTSQSDNLGICFSPSTYSFIGILTVARHTLSSATWVIDSGATHHYSHDRSLFSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LDTSVLSÄVNLPTGPTVKISGVGTLKLNDDILLKNVLFIPEFRLNLISISSLTDDIGS
RVIFDKNSCEIQDLIKGRMLGQGRRVANLYLLDVGDQSISVNAVVDISMWHRRLGHAS
LQRLDAISDSLGTTRHKNKGSDFCHVCHLAKQRKLSFPTSNKVCKEIFDLLHIDVWGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FSVETVEGY KYFLIIVDDHSRATWMYLLKTKSEVLTVFPAFIQQVENQY KVKVKAVRS
DNAPELKFTSFYAEKG IVSFHSCPETPEQNSVVERKHQHILNVARALMEQSQVPLSLW
GDCVLTAVFILINRTPSQLLMNKTPY BILTGTAPAY BOLGTGCLCY SSTSPKORHKFO
PRSRACLFLGY PSGYTKMDLESTWYFISRNVQFHEEVFPLAKNPGSESSLKLFTP
MYPVSSGIISDTHAFSSLPSQIISDLPQISSQRVRKPPAHLMDYHCNTMQSDHKYPI
SSTISYSKISPSHMCYINNITKIPIPTNYABAQOTKEWCEAVDAEIGAMEKTNTWEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRTTHLTAAYRVLQYIKGTVGQGLFYSASSDLTLKGFADSDWASCQDSRRSTTSFTMF
VGDSLISWRSKKQHTVSRSSAEAEYRALALATCEMVWLFTLLVSLQASPPVPILYSDS
TAAIYIATNPVFHERTKHIKLDCHTVRERLDNGELKLLHVRTEDQVADILTKPLFPYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="G1:4678198"
/translation="MVPGEWKATENFGLTYAKFKATNHRYKMGFWAKTRVVRMEPLSD
SYYLSLTSFIDVLTGGLNQNYLIDVVGQIVNVGEMETINVHNKPTKKINFELRDHK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FNYTNLPRTYNLTQEIQDFRQGTLSLSEYYTRLKTLWDQLDSTEALDEPCTCGRAMRL
QQRAEQAKIVKFLAGLNESYAIVRRQIIAKKALPSLGEVYHILDQDNSQQSFSNVVAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KLLLKVSASKKWFLKQLDVSNAFLNGELEEEIFMKIPEGYAERKGIVLPSNVVLRLKR
SIYGLKQASRQWFKKFSSSLLSLGFKKTHGDHTLFLKMYDGEFVIVLVYVDDIVIAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEAAAAQLTEELDQRFKLRDLGDLKYFLGLEVARTTAGISICQRKYALELLQSTGMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CKPVSVPMIPNLKMRKDDGDLIEDIEQYRRIVGKLMYLTITRPDITFAVNKLCQFSSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation-"MVTVARVTRKSTRSKAGTSSVTRKSRSTGAVTTPPNSPPVNRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ASRALTSSESGDPTQSPFFLHSADHPGLNIISHRLDETNYGDWSVAMLISLDAKNKTG
FIDGTLSRPLESDLNFRLWSRCNSMYKSWLLNSVSPQIIRSILRMNDASDIWRDLNSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLPKGKKAVGCKWVFTLKFLADGNLERYKARLVAKGYTQKEGLDYTDTFSPVAKMTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="similar to retroviral aspartyl proteases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="similar to replication protein Al" /protein_id="AAD26944.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"similar to reverse transcriptase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10299. .10369
/rpt_famlly="(GAAAA)n"
join<<13346. .13547,13635. .>13735)
/gene="F7H1.3"
                                                                                                                                              Location/Qualifiers
1. 8454
/ 8454
/ Organism="Arabidopsis thaliana"
/ Cultivar="Columbia"
/ Ch_xref="taxon:3702"
/ Chromosome="II"
/ map-"mi398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(13346. .13547,13635. .13735)
/gene="F7H1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein_id="AAD26943.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEHLKSKMSILNIFSCSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="F19G14.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <13346. .>13735
/gene="F7H1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <2020. .>6384
/gene="F7H1.2"
<2020. .>6384
/gene="F7H1.2"
                                                                                                                                                                                                                                                                                                                                                     /clone="F7H1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   928. .1330
/gene="F7H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            opnesd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                       FEATURES
```

```
/translation="MEALVVVHKVASEGGRRPKTTVSDESGSHSREKGKSFQVKDSPE
NNYATGKVDSLERGHFSSSYNQERQSEEQRR"
complement(21381. 21407)
/rpt_family="POLY_A"
complement(<21932. >22627)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DESKIAEESFRIDYFINIMDQAIMCIEIRFEQFQYYEQIFGFLFGYKRLKYAEDDELR
TSCMKLEASLKHDVHSDYDGEDLFMELKLLKDVLPKEITKPYEVLKFIKIMDSCYPNT
WIAYRILLTIPYSVALAERTFSKLKLIKKYLRSTMSQERLNGLALISV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTHPPRSTCDSSPROHLPLPKKNARIWSSGAWKSRLYSFSTYFLRFRDLGFIQNHTKA
LCLSAGAGHALMALSQIGLSDVTAVELVDSIPLVKRADPHNLPFFDGVFDFAFTAHLA
EALFPWQFVEEMERTVRRGGFCVVSVDECGGDDVRDIARLFHNSKVVDVANVTLEGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MIGGFNSDMKEHIRRANKGEIHCHFPSHKSONELTELLANDTRM
MILKKIKDAKYFSVILDSIPDVSRKEOMTFLIRCVDVSTCSPKIEEFFLIFLHIKDRR
EYTDNPGHRSDVESLTESETHGIGGFFFLFGMIIWYDLLAAVNIVSKSLOFEDMDLEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'translation="MERNVEKMLKRVSIVFLSIGTVLMVIMILQTPKTCISPEAPSKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AISQLGGLVTYLKNYKETGFEKAKVESTQIAIEMKIAPVFPKKSVKKKKQFVEDVEKI
                                                                                                                                                       /note="predicted by genscan and genefinder"
21092. .21322
/gene="F7H1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="predicted by genscan and genefinder" complement(21932. .22627)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  join(<23753. .24059,24489. .>25330)
/gene="F7H1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 17
Gaps: 0
Percent Identity: 52.941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted by genscan and g
join(23753. .24059,24489. .25330)
/gene="F7H1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 84544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted by genscan" 28186. .28689 /gene="F7H1.7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note-"hypothetical protein"
                                                                                                                                                                                                                                        /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(<21932. .>22627)
                                                                                                                                                                                                                                                                              /protein_id="AAD26945.1"
/db_xref="G1:4678199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAD26947.1"
/db_xref="GI:4678201"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAD26946.1"
/db_xref="G1:4678200"
                                                 /rpt_family="(GAA)n"
<21092. .>1322
/gene="F7H1.4"
<21092. .>21322
/gene="F7H1.4"
/rpt_family="(CAT)n"
18429. .18462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <23753. .>25330
/gene="F7H1.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .>28689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <28186. .>28689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KTSILFKVQDSPT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="F7H1.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="F7Hl.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="F7H1.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="F7H1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: ATAC007134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-35 x ATAC007134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.00
3.467
88.235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <28186.
```

bp in length length bp in length length

of 2109 unknown

length

length

in length in length bp in length bp in length op in length in length op in length bp in length

of 2874

length

of 2310 unknown

length

ength

of 2971 unknown

of 2459

length

unknown

```
1. .203273

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="15"

/map="15"

/clone="RP11-296E22"

/clone="RPC1-11 Human Male BAC"

/clone="RPC1-11 Human Male BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 7521 bp in length gap of unknown length contig of 10549 bp in length gap of unknown length gap of unknown length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of unknown length
contig of 11935 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig of 12152 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 18579 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length contig of 12666 bp in gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown length
contig of 8907 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of a 203273: contig coation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of contig gap of contig gap of
                                    contig
gap of
                                                                       contig
gap of
                                                                                                          contig
gap of
                                                                                                                                               contig
gap of
                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                    contig
gap of
                                                                                                                                                                                                                                                                                    contig
gap of
                                                                                                                                                                                                                                                                                                                        contig
gap of
                                                                                                                                                                                                                                                                                                                                                         contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
   9116:
                                      11451;
                                                                       14012:
                                                                                                        15805:
                                                                                                                                           17914:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183255:
                                                                                                                                                                              20644:
                                                                                                                                                                                                                                                  26283:
                                                                                                                                                                                                                                                                                     28593:
                                                                                                                                                                                                                                                                                                                        31564:
                                                                                                                                                                                                                                                                                                                                                         34023:
                                                                                                                                                                                                                                                                                                                                                                                            36890:
                                                                                                                                                                                                                                                                                                                                                                                                                               41485:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49438:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53273:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61902:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67950:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74487:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82190:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91448:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98969:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109518:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119016:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127923:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139858:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152524:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164676:
                                                                                                                                                                                                                 23409:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45667:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56613:
                                                                                                                                                                                                                                                  23410
                                    9177
                                                                       11452
                                                                                                        14013
                                                                                                                                           15806
                                                                                                                                                                              17915
                                                                                                                                                                                                                 20645
                                                                                                                                                                                                                                                                                                                        28594
                                                                                                                                                                                                                                                                                                                                                         31565
                                                                                                                                                                                                                                                                                                                                                                                            34024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61903
   7637
                                                                                                                                                                                                                                                                                                                                                                                                                               36891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183256
                                                                                                                                                                                                                                                                                     26284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 139859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                 Upublished

S (bases 1 to 203273)

Baldwin, J., Barna M., Beckelly, R., Boguslavkiy, L., Boukhgaiter, B.,

Baldwin, J., Barna M., Beckelly, R., Boguslavkiy, L., Boukhgaiter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gaçe, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

McEwan, P., McGurk, A., McKernan, K., Madonald, P., Marquis, N.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Myman, D., Ye, W., J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (28-SEP-1999) Whitehead Institute/MIT Center for Genome

Rosearch, 320 Charles Street, Cambridge, MA 02141, USA

On Nov 30, 1999 this sequence version replaced gl:5931431.

All repeats were identified using RepeatMasker:

Sant, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                     seq_documentation_block:
LOCUS AC010932 203273 bp DNA HTG 30-NOV-1999
DEFINITION Homo sapiens chromosome 15 clone RP11-296E22 map 15, *** SEQUENCING
IN PROGRESS ***, 36 unordered pieces.
                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 203273)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RPI1-296E22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 36 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
Center project Information
Center project name: 11684
Center clone name: 296_E_22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 1957 bp in length
gap of unknown length
contig of 1082 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 1375 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig of 1671
gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
                                                                                                                                                                                                                                AC010932
AC010932.2 GI:6479157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1375:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3332:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4414:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6085:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7636:
                                                                                                                                                                                                                                                                 HTG; HTGS_PHASE1.
                                                                                                                       seq_name: gb_htg6:AC010932
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9809
                                                                                                                                                                                                                                                                                     human.
                                                                                    78810 T 78810
                                                     20 r 20
                                                                                                                                                                                                                                                             KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
```

COMMENT

unknown length of 10549 bp in length

unknown length of 9258 bp in length

ength

unknown

of 6537 bp in length

ength

unknown of 7703

ength

ength

of 5289 of 6048 unknown

op in length bp in length in length

of 3340

ength

length

ength

unknown

ength

ength

unknown unknown

4182 of 3771 of 3835 unknown unknown unknown

ength

unknown

4595

ength

of 2867

unknown length of 12666 bp in length

of 20018 bp in length

```
Direct Submission
Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMBAN Cell line THAI DCH012 MHC class I HLA-B gene (allele HLA-B 55), exon 2. U91336 U91336.1 GI:1906679
                                     HSHLABM1 243 bp DNA PRI 26-MAR-1997
Human cell line THAI DCH023 MHC class I HLA-B gene (allele
HIA-8+1525), exon 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 243)
                                                                                                                                                                                                                                                                                                    Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases I to 24)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
Rungroung, E., Belchandra, S., Juji, T., Tokunaga, K. and
Grosse-Wilde, H.
B15 alleles (8*1525)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 243)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and
Grosse-Wilde, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .243
Acronalsm="Homo sapiens"
Ab_xref="taxon:9606"
Abromosome="6"
Amap="6p21"
Acell_type="lymphoblastcid"
Acell_line="THAI DCH023"
J. .243
Jene="HLA-B"
Acronalsm="1. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dercent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: HSHLABM1 from: 1
                                                                                                                                                                                            U91334.1 GI:1906675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-35 x HSHLABM1
seq_name: gb_pr2:HSHLABM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pr2:HSHLABO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg_documentation_block:
LOCUS HSHLABO1
DEFINITION Human cell 11
                                                    seq_documentation_block:
LOCUS HSHLABM1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 of 2
                                                                                                                                                                                                                                                   1 of 2
                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SEGMENT
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                    LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                            VERSION
KEYWORDS
SEGMENT
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eutheria: Primates; Catarrhini; Hominidae; Homo.

Entered: Catarrhini; Hominidae; Homo.

Rungroung, E. and Bejchandra, S.

Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,

Rungroung, E. and Bejchandra, S.

Direct Submission

L. Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700, Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSHLABKI 243 bp DNA PRI 26-MAR-1997 Human cell line THAI DCH022 MHC class I HLA-B gene (allele HLA-B1521), exon 2. U91332 U91332.1 GI:1906671
                                                                                                                                                                                                                                                                                                                1 TyrGlyArgLeuAsnArgLeuSerGluArgArgGluSer......Le 14
                                                                                                                                                                                                                            to: 203273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dercent Identity: 100.000
                                                         Gaps: 1
Percent Identity: 52.174
                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AC010932 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cell_line="rHAI DCH022"
/cell_type="lymphoblastoid"
<1. .243
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. 243
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 CGAGAGACCTGCGGAACCTGCGCGGCTAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: HSHLABK1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83
                                                                                                                                                                                                                                                                                                                                                                                                                        14808 CAAAAATCTCAGAGGCTAC 24790
                                                                                                                                     alignment_block:
US-08-653-294-35 x AC010932/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /map="6p21"
                                                                                                                                                                                                                                                                                                                                                                                              14 uArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=2
79 c
                          51.50
2.861
78.261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-35 x HSHLABK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pr2:HSHLABK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS HSHLABK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                 Ratio:
Percent Similarity:
                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 of 2
human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
alignment_scores
```

DEFINITION

ACCESSION

VERSION KEYWORDS SEGMENT SOURCE

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE

AUTHORS

TITLE JOURNAL

FEATURES

BASE COUNT ORIGIN

exon

```
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 246)

2 (bases 1 to 246)

3 (bases 1 to 246)

4 (bases 1 to 246)

5 Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Bl5 alleles (B*1502)

6 (bases 1 to 246)

7 (bases 1 to 246)

8 Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

8 Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

8 Siriraj, Hospital, Mahidol University, Prannok Road, Bangkok 10700, Siriraj, Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                          /product="MHC class I antigen HLA-B"
/protein_id="AaB67807.1"
/db_xref="G1:2345104"
/translation="TampregepreiavgyvDDTQFVRFDSDAASPRWAPRAPHIE
/cranslation="TampregepreiavgyvDDTQFVRFDSDAASPRWAPRAPHIE
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPRAPHIE
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPRAPHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPPAHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPPAHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPPAHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPPAHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPPAHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPPAHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASPRWAPPAHIE"
/cranslation="TampregepreiavgyvDTQFVRFDSDAASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), a mon partial cds.

AF014771 GI:2345107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="6p21"
/cell_type="lymphoblastoid"
<1. .>246
/gene="HLA-B"
/allele="HLA-B*1502"
1. .246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH4061"
/chromosome="6"
                                                   /cell_type="lymphoblastoid"
<1. .>246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HLA-B"
/allele="HLA-B*1502'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: AF014769 from: 1
   /chromosome="6"
/map="6p21"
                                                                                                                                                                                                                                                                                                                       /gene="HLA-B"
/codon_start=3
                                                                                                                                                                         1. .246
/gene="HLA-B"
/note="2"
                                                                                                                                                                                                                                                                /number=2
                                                                                                                                                                                                                                                                                               <1. .>246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-35 x AF014769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_pr2:AF014771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AF014771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rhailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                          gene
                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                            BIS alleles (8*1525)
BIS alleles (8*1525)
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, K.,
Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and
Grosse-Wilde, H.
Direct Submission
Submitted (26-FEB-1997) Transfusion Medicine, Faculty of Medicine,
Slriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine,
Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_line="THAI DCH012"
/cell_type="lymphoblastoid"
l. .24
/gene="HLA-B"
/note="Allele: HLA-B*1525; similar to exon 2 of B*1501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AF014769 246 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
AF014769 GI:2345103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
B15 alleles (B*1502)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 246)
Chandnayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D.,
Rungroung, E. and Bejchandra,S.
Direct Submission
Chandanayingyong, D., Sirikong, M., Srinak, D., Longta, R., Rungroung, E., Bejchandra, S., Juji, T., Tokunaga, K. and Grosse-Wilde, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                        1. 243
'Ocganism"Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
/map="6p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .246 // Organism="Homo sapiens" /db_xref="taxon:9606" /cell_line="Thai DCH4060"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 CGAGAGACCTGCGGAACCTGCGCGCGTAC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: HSHLABO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .lignment_block:
US-08-653-294-35 x HSHLABO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_pr2:AF014769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AF014769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                    TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

```
/protein_id="Aab67811.1"
/db_xref="G1:2245112"
/tb_xref="G1:2245112"
/translation="TamSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPWIE
/translation="TamSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPWIE
/translation="TamSRPGRGEPRFIAVGYNDSEA"
/translation="TamSRPGRGEPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Sungroung, E. and Bejchandra, S.
Direct Submission Hedicine, Faculty of Medicine, Submitted (18-UUL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFU14775 246 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)
Chandanayingyong,D., Sirikong,M., Luangtrakool,K., Srinak,D., Bustroung,E. and Bejchandra,S.
Bustroung,E. and Estenandra,S.
Unpublished
                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ceil_type="lymphoblastoid"
<1. .>246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1. 246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH018"
/chromosome="6"
/map="6p21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 CGAGAGAGCCIGCGGAACCIGCGCGGCIAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /allele-"HLA-B*1502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF014775.1 GI:2345115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene-"HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene-"HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number=2
                                                                                                                                                                                                                                                                                                              Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: AF014773
                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-35 x AF014773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_pr2:AF014775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AF014775
                                                                                                                                              ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rhailand
                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Eucheria; Chandara; Eutheria; Euth
                                                                                                                                                                                                                                                                                                                      /translation="TAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPWIE
QEGEEWWRNTOISKTUTYRRESIBNIRGYYNQSEA"
81 c 92 d 28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF014773 246 bp DNA PRI 27-AUG-1997 Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele), exon 2 and partial cds. AF014773 GI:2345111
                                                                                                      <1. .>246
/gene="HLA-B"
/codon_start="
/product="MHC class I antigen HLA-B"
/protein_id="AAB67809.1"
/db_xref="GI:2345108".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=3
/product="MHC class I antigen HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 10 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. 246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH3086"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="6p21"
/cell_type="lymphoblastoid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 CGAGAGGCTGCGGGAACCTGCGGGGGTAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /allele="HLA-B*1502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .246
gene="HLA-B"
/gene="HLA-B"
/note="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                               81 c
                                                                        /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-35 x AF014771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AF014771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_pr2:AF014773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rhailand
                                                                                                                                                                                                                                                                                                                                                                                               22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
```

20

from: 1

```
seq_documentation_block:

LOCUS AF014779 246 bp DNA PRI 27-AUG-1997

DEFINITION Homo saptens MHC class I antigen HLA-B gene (HLA-B*1502 allele),

exon 2 and partial cds.

ACCESSION AF014779

VERSION AF014779 GI:2345123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="myhai DCH002"
/chromosome="6"
/map="fop1"
/cell_type="lymphoblastoid"
<1. .246
/allele="HLA-B*1502"
1. .246
/gene="HLA-B*1502"
                                                                             198 CGAGAGCCTGCGGAACCTGCGCGCTAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                           11 ArgGluSerLeuArgAsnLeuArgGlyTyr
                             to: AF014777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-35 x AF014779
US-08-653-294-35 x AF014777
                                                                                                                      seq_name: gb_pr2:AF014779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rhailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                               ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="MMC class I antigen HLA-B"
/protein_id="AAB67815.1"
/protein_id="AAB67815.1"
/db_xref="G1:2345120"
/translation="TAMSRPGGEPRFIAVGYVDDTQFVRFDSDAASPRWAPRAPWIE
QEGPEYWDRWGISKTRYTGTRESLRNLRGYYNQSEA"
81 c 82 g 18 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Brungroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                  AF014777 246 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 246)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.
Englalleles (8*1502)
Unpublished
                           Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="lymphoblastoid"
<1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH017"
/chromosome="6"
/map="6p21"
                                                                                                                                      to: 246
                                                                                                                                                                 /allele="HLA-B*1502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualiflers
                                                                                                                                        from: 1

    .246
    /gene="HLA-B"

                                                                                                                                                                                                                                                                                                                                        AF014777.1 GI:2345119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <1. .>246
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number=2
                           Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                    Align seg 1/1 to: AF014775
                                                                                     alignment_block:
US-08-653-294-35 x AF014775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                               seq_name: gb_pr2:AF014777
                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AF014777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55
                                                                                                                                                                                                                                                                                                                                                                          human.
              alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
```

```
/"...246
/gene="HLA-B"
/goodo__start=3
/product="MHC class I antigen HLA-B"
/translation="TAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPWIE
/product="MHC class I antigen HLA-B"
/product="MHC class I an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AF014779 from: 1
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.00
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 246)

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Begichandra, S.

L Unpublished

E 2 (bases 1 to 246)

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Direct Submission

E Submitted (18-0UL-1997) Transfusion Medicine, Faculty of Medicine, Sirital, Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="TAMSRPGRGEPRFIAVGYUDTOFVRFDSDAASPRMAPRAPWIE
QEGPEYWDRNTQISKINTQTYRESLRNLRGYYNQSEA"
81 c 82 g 28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AF014785 250 bp DNA PRI 27-AUG-1997
LOCUS AF014785 allele),
DEFINITION Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
ACCESSION AF014785
VERSION AF014785 GI:2345135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=3
/product="MHC class I antigen HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="6p21"
/cell_type="lymphoblastoid"
<1. .>246
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
1. 246
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH016"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAB67821.1"
/db_xref="GI:2345132"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 CGAGAGGCTGCGGAACCTGCGCGGCTAC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="HLA-B"
/allele="HLA-B*1502"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AF014783 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <1. .>246
/gene="HLA-B"
  AF014783
AF014783.1 GI:2345131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="2"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-35 x AF014783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_pr2:AF014785
                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                     rhailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55
                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                     KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
ACCESSION
VERSION
                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                     TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene- ..... /
/codon_start=3
/producf_MHC class I antigen HLA-B"
/protein_id="AAB67819.1"
/db_xref="GI:2345128"
/translation="TAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRWAPRAPWIE
OEGPEYWDRNTQISRTUTQTYRESIRRIRGYYNQSEA"
82 g 2 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Faculty of Medicine, Road, Bangkok 10700,
                                                                                                                                                                                                                      Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eukaryota: Metazoa: Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 246)

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

L Unpublished

E 2 (bases 1 to 246)

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Rungroung, E. and Bejchandra, S.

S Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Sungroung, E. and Bejchandra, S.

Direct Submission

L Submitted (18-70L-1997) Transfusion Medicine, Faculty of Medicine Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700
                                                    seq_documentation_block:
LOCUS AF014781 246 bp DNA PRI 27-AUG-1997
DEFINITION Homo saptens MHC class I antigen HLA-B gene (HLA-B*1502 allele),
exon 2 and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. 246
7. Cardanis="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="That DCH003"
/chromosome="6"
/map="6p21"="f"
/cell_type="lymphoblastoid"
/cell_type="lymphoblastoid"
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /allele="HLA-B*1502"
1. .246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <1. .>246
/gene="HLA-B"
                                                                                                                                                               AF014781.1 GI:2345127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AF014781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-35 x AF014781
                     seq_name: gb_pr2:AF014781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr2:AF014783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
                                                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores
                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGIN
```

```
/product="MHC class I antigen HLA-B"
/product="MHC class I antigen HLA-B"
/protein_id="AAB67823.1"
/db_xref="G1:2345136"
/translation="FYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRWAPRAPW
IEQGEPEYWDRETQLSKINTCTYREGIRNLRGYYNQSEA"
81 c 84 g 31 t
                                                                                                    Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Chandanayingyong, D., and Bejchandra, S.
Bingroung, E. and Bejchandra, S.
Direct Submission
Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF014787 250 bp DNA PRI 27-AUG-1997
Homo sapiens MHC class I antigen HLA-B gene (HLA-B*1525 allele),
excon 2 and partial cds.
AF014787 GI:2345139
l (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
Rungroung, E. and Bejchandra, S.
B15 alleles (B*1525)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 250)

Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D., Rungroung, E. and Bejchandra, S.

Bl5 alleles (B*1525)

Unphilished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 250)
Chandanayingyong, D., Sirikong, M., Luangtrakool, K., Srinak, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                     /map="6p21"
/cell_type="lymphoblastoid"
1. 250
/gene="HLA-B"
/allele="HLA-B*1525"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                 Location/Qualifiers
1. .250
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="That DCH1109"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AF014785 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="HLA-B"
/note="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <1. .>250
/gene="HLA-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-35 x AF014785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_pr2:AF014787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS
                                                                                                                                                                                                                        Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                  TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
```

```
/product="MHC class I antigen HLA-B"
/protein_id="AAB67825.1"
/db_xref="G1:2345140"
/translation="FYTAMSRPGRGEPRFIAVGYVDDTQFVRFDSDAASPRMAPRAPW
IEGGEPEWDRETQISKINTQTYRESIRNLRGYYNQSEA"
81 c 84 g 31 t
Rungroung, E. and Bejchandra, S. Blreet Submission Blreet Submission Submitted (18-JUL-1997) Transfusion Medicine, Faculty of Medicine, Siriraj Hospital, Mahidol University, Prannok Road, Bangkok 10700,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                   /map="6p21"
/cell type="lymphoblastoid"
1. .250
/gene="HIA-B"
/allele="HIA-B*1525"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                  1. .250 /
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="Thai DCH3258"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AF014787 from: 1
                                                                                                                                                                                                                                                                                                                                         <1. .>250
/gene="HLA-B"
/codon_start=1
                                                                                                                                                                                                                                                                                       /gene="HLA-B"
/note="2"
                                                                                                                                                                                                                                                                                                                          /number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-35 x AF014787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
                                                                    Thailand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                   TITLE
JOURNAL
                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                          CDS
                                                                                  FEATURES
```

THIS PAGE BLANK (USPTO)

```
| Human secreted protein 5' ES | Sequence of Optine synthase | Complete nucleotide sequen | Saccharothrix australiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-40G-1995 (first entry)
pHLA-B7 expression vector.
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
expression vector; pHLA-B7; heavy human HLA-B7; bicistronic mRNA;
light beta-2 microglobulin; class I major histocompatibility complex;
MHC; human leukocyte antigen; HLA; covalently closed circular DNA; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualiflers
1. .354
/*tag= a
//rtag= a
//rtag= a
//note= "PBR322 backbone contg. bacterial origin of replication"
355. .1170
/*tag= b
//note= "kanamycin resistance gene open reading fram the gene is taken from the transposable element rn903"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F 22-SEP-1999:

R 22-SEP-1999;
22-SEP-1999;
22-SEP-1999;
22-SEP-1999;
22-SEP-1999;
22-SEP-1999;
22-SEP-1999;
32-SEP-1999;
33-SEP-1999;
33-SEP-1999;
35-SEP-1999;
36-SEP-1999;

                                                                                                                                                                                                                                                                                                        HLA-B35 exon. Haman leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss. Homo saplens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 100.000
     416 1
24593
24596
1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/note= "SV40 polyA signal sequence"
40.82
6.4e+03
6.4e+03
237.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1410. .1177)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. 1089
/*tag= a
120.57
81.18
81.18
106.84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: 012115 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВЪ.
                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q75974 standard; cDNA; 4059
Q75974;
                                                                                                                                                                                             seq_documentation_block:
1D Q12115 standard; DNA; 1089
AC Q12115;
DT 29-AUG-1991 (first entry)
  42.50
42.50
42.50
42.00
                                                                                                                                        seq_name: N_Geneseq_36:Q12115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seg_name: N_Geneseg_36:Q75974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-35 x Q12115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
Quality:
Ratio:
     N_Geneseq_36:X41493
N_Geneseq_36:N50226
N_Geneseq_36:N50182
N_Geneseq_36:X07410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J03112486-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                Documentation ...

| HIA-835 exon. HIA-835 gene - u | PHIA-87 expression vector. New | PHIA-87/beta-2 microglobulin e | PHIA-87/beta-2 microglobulin e | Human CRIPPO-related gene CR-3 | DNA encoding human CRIPTO-related gene (CR-1 Extractor) | Coding sequence for the alpha | Extractor | Extractor | Iquand 3 |
| Mouse TIE-2 receptor ligand 3 | Tumour rejection antigen prec | Sequence of amylase gene and u | Coding sequence for the alpha' | EST clone CE242. New polynucled | Coding sequence for the alpha' | EST clone CE242. New polynucled | HIA-C exon Cb-1. HIA-C gene, | HIA-C exon Cb-1. HIA-C exon Cb-1. HIA-C gene, | HIA-C exon Cb-1. HIA-C gene, | HIA-C exon Cb-1. HIA-C g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expression vector pNF2222. New Streptococcus pneumoniae genom Expression vector pNF2156. New Mutagenic plasmid pNF2216. New Mutagenic plasmid pNF22176. New Promoter probe vector pNF2214. New Human protein tyrosine phospha! Polynucleotide sequence from Synthetic glyphosate oxidoredu Manipulated glyphosate oxidoredu Manipulated glyphosate oxidoredu CPT1-GOX gene fusion. Chemical Glyphosate oxidoreducies proposate oxidoreducies proposate oxidoreducies proposate oxidoreducies (Glyphosate oxidoreducias) streptococcus pneumoniae genom is Bacterial artificial chromosocius continuation (7 of 10) of 19 Enterococcus faecalis genome 1000 i Continuation (7 of 10) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human growth regulator proteir
                                                                                                                                                                                       Command line parameters:
-WODEL_frame+_p2n.model -DEV=xlp
-0=/cgn1_1/GFPOL_p2n.model -DEV=xlp
-0=/cgn1_1/GFPOL_p2n.model -DEV=xlp
-0=/cgn1_1/GFPOL_p2n01/USOB653294/runat_04022000_160701_15807/app_query.fasta.2
-DB=N.Geneseq_36 -QFPT=fastap -SUFFIX=rng -GAPOP=12.000
-GAPOTT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -PGLEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE=LOCAL -OUTFNT=Pfs -NORM=ext -MINLEN=0
-MAXLEN=1000000 -USER=USOB653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ! Documentation
                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
        out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 4.60

.988 23.45

.62 46.11

.62 46.11

.62 46.11

.62 46.11

.62 46.11

.62 46.11

.62 46.11

.62 46.11

.63 4.65

.93 .94

.94 .95

.95 .94

.95 .94

.95 .95

.95 .94

.96 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .95

.97 .97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EScore
  Om of: US-08-653-294-35 to: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.81
86.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68.2
68.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
551.00
55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000
                                                          Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search information block:
Query: US-08-653-294-35
Query length: 20
Database: N_Geneseq_36:*
                                                          Date: Feb 8, 2000 7:31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36:X20248_06
N_Geneseq_36:X20250 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:V69920
N_Geneseq_36:Q85924
N_Geneseq_36:X20556
N_Geneseq_36:Q20835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:Q12115
N_Geneseq_36:Q75974
N_Geneseq_36:Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:022494
N_Geneseq_36:T71145
N_Geneseq_36:T80987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:V83924
N_Geneseq_36:Q22495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Geneseq_36:V83923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:V17562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geneseq_36:X12977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Geneseq_36:V89291
N_Geneseq_36:V82783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T11549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .V69919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N_Geneseq_36:T99594
N_Geneseq_36:T11549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_36:V90017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _Geneseq_36:V1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_36:V
N_Geneseq_36:V
N_Geneseq_36:V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _Geneseq_36:7
_Geneseq_36:7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:
N_Geneseq_36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genesed_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Genesed_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genesed_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score_list:
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_3
N_Geneseq_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Genesed_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genesed_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Genesed_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genesed"
```

```
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9429469-A.
                                                                                misc_signal
                                                                                                                                                                                                                                               mat_peptide
                                                                                                                                                                                                                                                                                                              3'utr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3'utr
                                                                                                                                 cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rbs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cds
 /*tag= a
/note= Rous sarcoma virus LTR promoter domain, derived
for the Schmidt-Rupin strain nucleotides
8673-9146. This region also includes a 56 bp
region of a synthetic oligonucleotide which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-AuG-1995 (first entry)
pHLA-B7/beta-2 microglobulin expression vector.
expression vector; pHLA-B7/beta-2 microglobulin; heavy human HLA-B7;
light beta-2 microglobulin; class I major histocompatibility complex;
mHC; bicistronic mRNA; human leukocyte antigen; HLA;
covalently closed circular DNA; ds.
                                                                                                                                                                               /*tag= g
/note= "Rous sarcoma virus 3' LTR promoter region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1000 T;
                                                               /*tag= e
/note= "3' untranslated region of HLA-B7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 4059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1033 G;
                                                                                                                                 /*tag= .f
/note= "HLA-B7 open reading frame"
                           /note= "SV40 small t intron"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: Q75974 from: 1
 complement (1412. .1560)
                                                                                               heavy chain mRNA"
complement (1795. .2880)
                                                                                                                                                                                                            3416. 4059
/*tag= h
/note= "pBR322 backbone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1051 C;
                                                 complement (1561. .1794)
                                                                                                                                                              complement (2886. .3415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2589 CGAGAGACCTGCGGAACCTGCGCGCCTAC 2560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:

AC 075973 standard; CDNA; 4965 BP.
AC 075973;
DT 23-AUG-1995 (first entry)
DE pHLA-B7/beta-2 microglobulin expression vector; pHLA-B7/beta-2 KW ight beta-2 microglobulin; class KW ight beta-2 microglobulin; class KW ight beta-2 microglobulin; class KW covalently closed circular DNA; ds CS Synthetic.

FT Key Location/Qualifler FT Itr /*tag* a /*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             975 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-35 x Q75974/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:Q75973
                                                                                                                                                                                                                                                                                             27-MAY-1994; U06069.
07-JUN-1993; US-074344.
                                                                                                                                                                                                                                                                                                                           (UNMI ) UNIV MICHIGAN. (VICA-) VICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4059 BP;
                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                WO9429469-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
 intron
                                                 3'utr
                                                                                                              cds
                                                                                                                                                                ltr
```

```
/note- "bovine growth hormone 3'UTR and transcriptional terminator; it starts at a blunt-ended BglI site within the 3'UTR of the mRNA coding sequence" 2979. 2984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ncte- "murine encephalomyocarditis CAP-independent translational enhancer (EMCV-CITE); taken from nucleotides 255-843 of cloned EMCV genomic DNA. It is a non-coding regulatory sequence functioning as an internal entry point for the eukaryotic ribosomal subunits when located within a mRNA mol. It enables the translational start codon of the beta-2 microglobulin, downstream of the HLA-B7 scopnised by the ribosome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= o
/note= "kanamycin resistance gene open reading frame;
the gene is taken from the transposable element
T1903.*
                                                                                                                                                                                                                                                                                                                                                                                                         /*tag- e
/note= "encodes putative HLA-B7 heavy chain mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note- "encodes beta-2 microglobulin; this cDNA is defarty. from chimpanzee (differs to the human cDNA by only 4 bases)"
2840. .2846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note- "pBR322 backbone contg. bacterial origin of replication, it represents nucleotides 2244-3193"
modifies this regulatory sequence to effect a
higher level of expression of downstream
sequences. The oligonucleotide removes a
polyadenylation signal sequence originally found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note- "3' untranslated sequence of HLA-B7 heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= g // Arag= multiple cloning site, forms a junction // note= "multiple cloning site, forms a junction between the HIA-B7 sequence and the EMCV-CITE sequence, and is used to facilitate subcloning" 1889. .2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag* n
/note= "synthetic linker to facilitate cloning"
complement (3151. .3967)
                                                                                                                                               /*tag= b
/label= consensus_Kozak_signal_sequence
/sis. .1620
/*tag= c
/note= "HLA-B7 heavy chain open reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= j
/note= "3' untranslated region of the beta-2
microglobulin mRNA"
                                                                                                                                                                                                                                                                                                                         / note= "encodes putative signal peptide of HIA-B7 heavy chain" 607. .1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note- "synthetic linker" 'vurk
                                                                                                  in the RSV DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1621. .1853
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .2839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1854. .1888
                                                                                                                                                                                                                                                                         535. .606
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag- h
                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
3112.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                 signal_peptide
```

```
Key
 888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Marquet M. Nabel EG, Nabel GJ;

National Marquet M. Nabel EG, Nabel GJ;

New vectors for gene therapy, partic for tumours - comprising

New vectors for gene therapy, partic for tumours - comprising

The partic material encoding one or more cistron(s) which express

For immunogenic or therapeutic peptide(s)

The partic marginal sequence gene, contains the plasmid bNA encoding the chart with man MIA-BY and light (beta-2 microglobulin) proteins of a class I major hisococompatibility complex (MHC) antigen. The plasmid is designed to express these two proteins via a bicistronic mRNA in class I major hisococompatibility complex (MHC) antigen. The plasmid is designed to express these two proteins via a bicistronic mRNA in class I major hisococompatibility complex (MHC) antigen of the plasmid is charinal repeat. Termination of transcription of the mRNA is dependent on a Rous Sarcoma Virus (RSV) promoter sequence deriv. from the 3' long terminal repeat. Termination of the heavy chain is regulated by the CTE. Finally the replication of the plasmid in controlled by the CTE. Finally the replication of the plasmid in bacterial cells is controlled by the presence of a bacterial origin of replication. The vector is used partic. for the treatment of neoplastic for the classes, eg. melanoma, and provides enhanced gene delivery and expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New CRIPTO gene CR-1 and CRIPTO-related gene CR-3 genomic DNA - CR-3 protein and anti-CR-3 antibodies, useful in immunoassay to detect CR-3 as tumnour specific marker

Disclosure: Page 29: 44pp; English.

The CR-3 nucleotide sequence was isolated from a human genomic library using a labelled DNA fragment containing 800bp upstream of the translation initiation site of CR-1. Clones were isolated which contained the 5' CDNA non-coding region of CR-3. One clone was
                                                                                                                                                                                                                                                                                                                                                                                          1163 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-AUG-1992 (first entry)
Human CR.PPO-related gene CR-3.
cell proliferation; tumour; CR-1; transforming growth factor; epidermal growth factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                          1338 G;
                                                                                                                                                                                                                                                                                                                                                                                          1293 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: Q75973 from: 1 to: 4965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      829 CGAGAGACCTGCGGAACCTGCGCGGCTAC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
809. .1375
/*tag= a
/product= CR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1992.
23-AUG-1991; 749001.
23-AUG-1991; US-749001.
(USSH ) US DEPT HEALTH & HUMAN.
Salomom D, Persico M;
WPI; 92-123675/15.
P-PSDB; R22547.
                                                                                                                                                                                                                                                                                                                                                                                          1171 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID Q22494 standard; DNA; 2675 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: N_Geneseq_36:022494
27-MAY-1994; U06069.
07-JUN-1993; US-074344.
(UNMI ) UNIV MICHIGAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-35 x Q75973
                                                                                                                                                                                                                                                                                                                                                                                          4965 BP;
                                             (VICA-) VICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US7749001-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              022494;
```

```
sequenced and found to include a complete CRIPTO CDNA lacking introns and containing a poly(A) tract at the 3' end. Seven single base pair substitutions were observed in the coding region (c.f., CR-1 sequence in Ciccodicola A. et al., EMBO J.81.987-1991(1989)), six of which gave rise to amino acid changes. The 3' non-coding sequence is less similar (97% identical) to CR-1. Most of the differences occur in the inverted Alu sequence. The unusual poly(A) addition site AGTAAA found in the CR-1 gene is also conserved in CR-3. The similarity between CR-1 and CR-3 extends for 697 nucleotides upstream of the initiator AUG where it is possible to observe 7 base pair substitutions and 6 nucleotide deletions. The 14 "Others" in the sequence represent nucleotides whose clemental of the initiation and continued deletions. The 14 "Others" in the sequence represent nucleotides whose the sequence printed in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:

ID T71145; standard; DNA; 2675 BP.

AC T71145;

DT 19-AUG-1997 (first entry)

DT DN encoding human CRIPTO-related gene product, CR-3.

KW CRIPTO; CR1; CR3; epidermal growth factor superfamily; EGF; mitogen; KW tumour marker; epithelium; mesenchyme; diagnosis; prognosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New DNA encoding the human CRIPTO-related gene product CR-3 - used to produce recombinant protein, useful for preparation of diagnostic antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tills encodes a human CRIPTO-related gene product CR-3. CR-3 is thought to be a tumour-specific marker and as such DNA and amino acid sequences of CR-3 and derivatives can be used in the diagnosis, prognosis and possibly treatment of some types of cancer. CR-3 includes a region homologous to products of the epidermal growth factor superfamily of genes and it may be a mitogen involved in regulating proliferation, differentiation and transformation of sequence 2675 BP; 618 C; 555 G; 763 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.00 Length: 21
3.200 Gaps: 1
71.429 Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 2675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-AUG-1991; 749001.
23-AUG-1991; 02-74901.
17-NOV-1993; US-744901.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PEFZISOO MG, SALOMON DS;
PPESJEO, MG, SALOMON DS;
P-PSDB; W19980.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
809. .1375
/*tag= a
/product= CR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Column 17-20; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: Q22494 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:T71145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2211 CAAAATGGGTTAC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-35 x Q22494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 nLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS5620866-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1997
```

```
04-NOV-1997 (first entry)
CRIPTO-related gene, CR-3.
CRIPTO-related gene; CR-3; epidermal growth factor; EGF; TGF-alpha; amphiregulin; tumour specific marker; colon cancer cell line; colorectal tumour; mesenchyme; epithelial cell; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= i
/note= "C>T mutation from CR-1 sequence, causes
Ala>Val mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= m
/note= "C>T mutation from CR-1 sequence, causes
Pro>Leu mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  causes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            causes
                                                                                                                                                                                               2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= j
/note= "T>C mutation from CR-1 sequence,
val>Ala mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= 1
/note= "T>G mutation from CR-1 sequence,
Tyr>Asp mutation"
1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ^*tag= k
note= "G>A mutation from CR-1 sequence"
                Length: 21
Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153. .162

/*tag= e

/*tag= "Pyrimidine rich stretch"

371. .395

/*tag= f

/note= "Pyrimidine rich stretch"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note "yrimidine rich stretch"
[641] 1931
*tag h
                                                                                                                                           to: 2675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualiflers

809. .1375

**tag= a

/*tag= b

/*tag= b

511. .516

/*tag= c

/*bound_moeity= SPI

/*tag= d

/*tag= d

/*pound_moeity= SPI

/*tag= d

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Alu_sequence
                                                                                                                                          Align seg 1/1 to: T71145 from: 1
                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID T80987 standard; DNA; 2675 BP.
AC T80987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473. .482
/*tag= 9
            48.00
3.200
71.429
                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:T80987
                                                                                                                                                                                                                                                                                    2211 CAAAATGGGTTAC 2223
                                                                                        alignment_block:
US-08-653-294-35 x T71145
                                                                                                                                                                                                                                                    16 nLeuArgGlyTyr 20
                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein_bind
 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
```

```
This sequence represents the CRPTO-related gene, CR-3. The CR-3 gene sequence is identical to the human CRIPTO gene with the exception of eight base pair substitutions that give rise to six amino acid changes. GR-3 exhibits partial amino acid sequence homology and a tertiary structure within a 38 amino acid sequence homology and a tertiary structure within a 38 amino acid region similar to the epidermal growth factor (EGF) supergens family that includes EGF, TGF-alpha and amphirequilm. Expression of CR-3 may serve as a tumour specific marker as it is expressed in several human colon cancer cell lines and possibly in human colorectal tumours. The assay of the amount of CR-3 in a sample can be used in studies on the regulation of the proliferation, differentiation, and transformation of various mesenchymal and epithelial cells. Study of the expression of CR-3 may also be used in the diagnosis, prognosis and treatment of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assays for CRIPTO-related gene product CR-3 - used in studies on the regulation of the proliferation, differentiation and transformation of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human CRIPTO-related gene(CR-3).
human CRIPTO-related protein; CR-1; antibody; CR-3; proliferation;
differentiation; transformation; mesenchymal cell; epithelial cell;
tumour specific marker; cancer; ds.
Homo sapiens.
                                                                              /*tag" o
/note= "G>A mutation from CR-1 sequence, causes
G1y>Glu mutation"
1341
                                                                                                                                                                                      /*tag= p
/note= "T>C mutation from CR-1 sequence, causes
Val>Ala mutation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   n
"G>A mutation from CR-1 sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 21
Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                           22-JUL-1997.
23-AUG-1991; 74-9001.
23-AUG-1991; US-74-9001.
17-NOV-1993; US-154-198.
05-JUN-1995; US-154-198.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
PETSICA MC, SALOMON DS;
P-PSDB; W25-667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 2675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
809. .1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Fig 2; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= CR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID V83924 standard; DNA; 2675 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V83924;
03-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.00
3.200
71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:V83924
/*tag=
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2211 CAAAATGGGTTAC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: T80987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-35 x T80987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16 nLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                     mutation
                                                                                                                                                             mutation
```

```
03-MAR-1999 (first entry)
Human CRIPTO-related gene (CR-1).
human CRIPTO-related protein; CR-1; antibody; CR-3; proliferation;
differentiation; transformation; mesenchymal cell; epithelial cell;
tumour specific marker; cancer; ds.
                                                                                                                                                                                                                                             2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
                          Length: 21
Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
887. .4167
/*tag= a
/note="contains introns"
887. .921
/*tag= b
                                                                                                                                                                          to: 5761
                                                                                                                                                                          Align seg 1/1 to: Q22495 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID V83923 standard; DNA; 5761 BP.
AC V83923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /number 1
2011. .2063
/*tag d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number= 4
2865. .2974
/*tag= j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number= 5
2975. .4048
/*tag= k
/number= 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number= 3
2652. .2766
/*tag= h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2767. .2864
/*tag= 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4049. .4167
/*tag= 1
/number= 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /number= 2
2064. .2146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2147. .2281
/*tag- f
/number- 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2282. .2651
/*tag= g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /number= 1
921. .2010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= c
                          48.00
3.200
71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'number-
                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:V83923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-DEC-1998.
05-JUN-1995; 464023.
23-AUG-1991; US-749001.
17-WOV-1995; US-464023.
05-JUN-1995; US-464023.
(USSH ) US DEPT HEALTH &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                   5010 CAAAATGGGTTAC 5022
                                                                                                              alignment_block:
US-08-653-294-35 x Q22495
                                                                                                                                                                                                                                                                                                           16 nLeuArgGlyTyr 20
                                                Ratio:
Percent Similarity:
                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5854399-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AND PROPERTIONS OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                  Example 3; Columns 17-22; 26pp; English.

The present sequence encodes a human CRIPTO-related protein CR-3. The present sequence encodes a human CRIPTO-related protein CR-3. The specification describes an antibody which has binding affining to CR-3 and not to CR-1. The antibodies can be used for the detection of CR-3. CR-3 is a regulatory molecule involved in regulating the proliferation, calliferentiation, and transformation of various mesenchymal and epithelial cells. In addition expression of CR-3 may serve as a tumour specific marker that may have applicability in the diagnosis, prognosis and possible treatment of specific types of cancer.

Sequence 2675 BP; 739 A; 618 C; 555 G; 763 T;
                                                                                                                                                                                                                New antibody to human CRIPTO-related polypeptide-3 - used for the detection of CRIPTO-related polypeptide-3 which is involved in the regulation of the proliferation, differentiation and transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New CRIPTO gene CR-1 and CRIPTO-related gene CR-3 genomic DNA - CR-3 protein and anti-CR-3 antibodies, useful in immunoassay to detect CR-3 as tumour specific marker
Disclosure: Page 22: 44pp; English.
The CR-1 genomic clone can be used in transgenic animals to examine the effects of overexpression of this gene on development and tumorigenicity and to study regulation of CR-1 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1699 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-1992 (first entry)
Human CRIPTO gene CR-1.
cell proliferation; tumour; CR-3; transforming growth factor; epidermal growth factor; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1227 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
US5854399-A.
29-DEC-1998.
29-DEC-1998.
35-JUN-1999.
17-NOV-1993. US-749001.
17-NOV-1993. US-154198.
05-JUN-1995. US-464023.
(USSH) US DEPT HEALTH & HUMAN SERVICES.
PERSIGN MG, Salomon DS;
WPI; 99-095001/08.
P-PSDB; W87631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1306 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: V83924 from: 1 to: 2675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-AUG-1991; 749001.
23-AUG-1991; US-749001.
(USSH) US DEPT HEALTH & HUMAN.
SALOMOM D. PERSICO M;
WPI; 92-123675/15.
P-PSDB; R22548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1529 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID Q22495 standard; DNA; 5761 BP.
AC Q22495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.00
3.200
71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:022495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2211 CAAATGGGTTAC 2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-35 x V83924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 nLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5761 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
US7749001-A.
25-FEB-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                       of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
```

HEALTH & HUMAN SERVICES

ဖ

```
alignment_block:
US-08-653-294-35 x x12977/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infection
88888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taugh 198-052298/05.

Suppression of specific classes of soybean seed protein genes - useful to change seed storage protein profiles of transgenic plants bisclosure; Page 29-30; Sapp: English.

This sequence represents the coding sequence for the alpha subunit of the soybean seed protein beta-conglycinin. The method of the invention is for reducing the quantity of a soybean seed storage protein (A), such as beta-conglycinin, in soybeans. It comprises: (a) constructing a chimeric gene comprising: (i) a nucleic acid fragment encoding all or a portion of (A) placed in sense or antisense orientation region; (b) creating a transgenic soybean cell the chimeric gene of (1); and (ill) a transcriptional termination region; (b) creating a transgenic soybean cell the chimeric gene of (a); and (c) growing the transgenic soybean cell the chimeric gene of (a); and (c) growing the transgenic conditions that result in expression of the chimeric gene of (a); where the quantity of one or more members of a class of (A) subunits is reduced when compared to soybeans not containing the chimeric gene of (a); the method is used to construct transgenic soybean lines where the expression of genes encoding (A) are modulated to effect a change in seed storage protein profile of transgenic plants.
                                                                                                                                    The present sequence encodes a human CRIPTO-related protein CR-1. The specification describes an antibody which has binding affinity to CR-3 and not to CR-1. The antibodies can be used for the detection of CR-3. CR-3 is a regulatory molecule involved in regulating the proliferation, differentiation, and transformation of various mesenchymal and epithelial cells. In addition expression of CR-3 may serve as a tumour specific marker that may have applicability in the diagnosis, prognosis and possible treatment of specific types of cancer. Sequence 5761 BP; 1529 A; 1304 C; 1229 G; 1699 T;
                                                 New antibody to human CRIPTO-related polypeptide-3 - used for the detection of CRIPTO-related polypeptide-3 which is involved in the regulation of the proliferation, differentiation and transformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1998 (first entry)
Coding sequence for the alpha subunit of beta-conglycinin.
Beta-conglycinin; soybean seed protein; transgenic plant; seed storage protein profile; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GlyArgLeuAsnArgLeuSerGlu.....ArgArgGluSerLeuArgAs
                                                                                                                                                                                                                                                                                                                                                 Caps: 21 Gaps: 1 Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: V83923 from: 1 to: 5761
                                                                                                                       Example 2; Columns 9-16; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-DEC-1997.
10-UUN-1997.
14-JUN-1995. US-019940.
(DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID V17562 standard; cDNA; 1818 BP.
                                                                                                                                                                                                                                                                                                                                                                     3.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:V17562
                                                                                                                                                                                                                                                                                                                                                       48.00
Persica MG, Salomon DS;
WPI; 99-095001/08.
P-PSDB; W87630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5010 CAAAATGGGTTAC 5022
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-653-294-35 x V83923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GM, Kinney AJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 nLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycine max.
WO9747731-A2.
                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
                                                                                                          cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fader
```

```
Claim 1) Page 412-413; 2084pp; English.

A computer readable medium has been developed which has recorded on it
A computer readable medium has been developed which has recorded on it
922 nucleotide sequences isolated from the Enterococcus faecalis genome.
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences, also known as contigs. The computer-based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
diagnosing Enterococcus infection in an animal and monitoring
progression of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
another related organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus faecalis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1998.

14-NOV-1997: US-066009.

16-MAY-1997: US-044031.

16-MAY-1997; US-044031.

16-MAY-1997; US-046655.

16-MAY-1997; US-046655.

BATASh SC, Dillon PJ, Kunsch CA;

WPI: 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides

used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
Modification of the seed storage protein profile can result in the production of novel soy protein products with unique and valuable functional characteristics.

Sequence 1818 BP: 881 A; 424 C; 427 G; 386 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-1999 (first entry) anterococus faccalis genome contig SEQ ID NO:40. Enterococcus faccalis; contig; detection; Enterococcus infection; vaccine; attenuation; computer readable medium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    395 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                631 TATGGTCGCATTCGCGTCCTCCAGAGGTTCAACCAACGCTCCCCACAACT 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TyrGlyArg.....LeuAsnArgLeuSerGluArgArgGluSerLe 14
                                                                                                                                                                                                                                                                    47.50 Length: 23
2.794 Gaps: 1
73.913 Percent Identity: 47.826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: V17562 from: 1 to: 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        269 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X12977 standard; DNA; 1346 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            395 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    681 TCAGAATCTCCGAGACTAC 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 uArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: N_Geneseq_36:X12977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterococcus faecalis. WO9850555-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-35 x V17562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1346 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seg_documentation_block:
                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                        alignment_scores;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
```

Length: 19 Gaps: 0 Percent Identity: 42.105

47.00 2.938 84.211

```
The present sequence encodes a secreted protein. The polynucleotide and secreted protein are predicted to have biological activities which would make them suitable for treating, preventing medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune stimulating activity, issue growth activity, activity, haematopolesis regulating activity, tissue growth activity, activity,inhibin activity, chemotactic/chemokinetic activity, activity,inhibin activity, receptor/ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity (no data is given in the specification to support these activities). The polynucleotide is also stated to be useful for gene therapy.

Sequence 745 BP; 179 A; 229 C; 176 G; 161 T;
  chemokinetic activity; haemostasis; thrombolytic activity; receptor; ligand; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding TIE ligands 3 and 4 - useful for, e.g. blocking blood vessel growth and promoting neovascularisation, etc.
                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding secreted human proteins - derived fro human foetal brain, adult brain, foetal kidney, placenta or adult pineal gland cDNA 11braties. Claim 26; Page 80; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tyrosine kinase; mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-1998 (first entry)
Mouse TIE-2 receptor 11gand 3 cDNA.
Mouse TIE-2 receptor 11gand; TIE 11gand 3; tyrosine kinase; mouse, anglogenesis; vascularisation; blood vessel growth; tumour;
                                                                                                                                  20-MAR-1998; U05653.
21-MAR-1998; US-044466.
21-MAR-1997; US-044466.
(GMA ) GENETICS INST INC.
AGOSTINO MJ, Jacobs K, Lavallie ER, MCCOY JM, Merberg D, Racie LA, Spaulding V, Treacy M; P-PSDB; W85461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 ArgLeuAsnArgLeuSerGluArgArgGluSerLeuArg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AGAGTCAACAGGCTAAGTGAGAGGAGGGATGCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: V82783 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-DEC-1997.
19-JUN-1997; U10728.
02-JUN-1996; US-022999.
19-JUN-1996; US-655926.
02-JUL-1996; US-021087.
(REGE-) REGENERON PHARM INC.
JONES PF, VALENZUELA DM, Yancopoulos GD;
WPI; 98-063143/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
ID T99594 standard; cDNA; 1849 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-35 x V82783/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; receptorbody; ss.
Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46.00
4.182
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:T99594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                         WO9842739-A2.
                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9748804-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T99594;
22-JUN-1998
                                                                                                                   01-OCT-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Key
  EST clone CG336. Indiana: expressed sequence tag; EST; haematopoiesis; tissue growth; activin; inhibin; chemotaxis; chemokinesis; haemostatic; receptor; ligand; thrombolytic; anti-inflammatory; cadherin; anti-tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polynucleotides encoding human secreted proteins - derived from
e.g. human blood, kidney, foetal lung, placenta, testes, brain,
ovary, pituitary, retina and colon cDNA libraries.
To Claim 1: Page 171; 618pp: English.
The present sequence represents a human expressed sequence tag (EST).
The polynucleotide, which is a secreted EST, and the encoded protein
are predicted to have useful biological activities which would make
them suitable for treating, preventing or ameliorating medical
conditions in humans and animals, although no supporting data is
given. Suggested activities include nutritional activity, immune
stivity, tissue growth activity, activin/inhibin activity,
chemotactic/chemokinetic activity, haematopolesis regulating
activity, receptor/ligand activity, anti-inflammatory activity,
catherin/tumour invasion suppressor activity, tumour inhibition
activity. The polynucleotide may also be useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-1999 (first entry)
Clone dn809_5 isolated from human foetal brain cDNA library.
Secreted protein; nutritional activity; immune stimulating; vaccine; suppressing activity; hamatopolesis regulating activity; tissue growth activity; activin; inhibin activity; chemotactaxis;
                                                                     1111111111111:::::: ::: :::::!|| |||||||:: 153
                                           1 TyrGlyArgLeuAsnArgLeuSerGluArgArgGluSerLeuArgAsnLe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; 99-070077/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100
to: 1346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 AGAGTCAACAGGCTAAGTGAGAGGAGAGGGATGCTACGC 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ArgLeuAsnArgLeuSerGluArgArgGluSerLeuArg 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 G;
  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 C;
Align seg 1/1 to reverse of: X12977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: V89291 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID V82783 standard; cDNA; 745 BP.
AC V82783;
                                                                                                                                                                                                                                                                                                   V89291 standard; cDNA; 289 BP.
V89291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 A;
                                                                                                                                                                                                                                                                                                                                            5-FEB-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.00
4.182
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                seq_name: N_Geneseq_36:V89291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:V82783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-OCT-1998.
10-APR-1998; U06955.
10-APR-1997; US-838821.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-35 x V89291
                                                                                                                                                                                                                                                                           seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy; ss.
Homo sapiens.
WO9845436-A2.
                                                                                                                                                                             1152 TAAAGGC 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                  17 uArgGly 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
```

K K K E B G G G G G

ω

us-08-653-294-35.rng

```
Claim 23; Fig 6A-B; 86pp; English.

This cDNA sequence includes a coding region for novel mouse TIE ligand-3 (mTL-4, see W26792), a TIE-2 receptor ligand that is a tyrosine kinase with immunoglobulin and epidermal growth factor homology domains. It was obtained by PCR amplification of CDNA derived from mouse cell lines C2012ras and M687 using primars (see 19959-96) specific for mTL3. A host-vector system for the production of mTL-3 is claimed, as well as an antibody which precifically binds mTL-3, a receptorbody which specifically binds mTL-3, a conjugate comprising mTL-3 and a cytotoxic agent, and an isolated nucleic acid (see T99593) coding for human TIE ligand (see W26791). TL3, TL4, their antagonists, etc. are useful for blocking blood vessel growth, promoting neovascularisation promoting or blocking the growth or differentiation of a cell expressing the TIE receptor and attenuating or preventing tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "This region is 4.7-5.3 kilobases in length
/note= "This region has not been
deduced."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumour rejection antigen precursor coding sequence.
Tumour rejection antigen precursor; TRAP, TRA, melanoma; cancer;
tumour; treatment; detection; vaccine; HLA-A2; adoptive transfer;
T cell; T lymphocyte; human leukocyte antigen; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genomic DNA encoding a tumour rejection antigen precursor processed to antigen presented by HLA-A2, useful for treating or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      707 CAGCTTAACAGCCTCCAAGAGAAGAGGAACAACTGCACAGTCTCCTGGG 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 18
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag- a
/note= "Unidentified nucleotide."
9422. .9456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 De PLAEN
                                                                                                                                                                                                                                                                                                                                                                                    507 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11539
/*tag= c
/note= "Unidentified nucleotide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: T99594 from: 1 to: 1849
                                                                                                                                                                                                                                                                                                                                                                                      549 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Coulie P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wolfel T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosing melanoma
Claim 3; Page 18–22; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1994; US-272351.
10-JAN-1995; US-370319.
(LUDW-) LUDWIG INST CANCER RES.
Boon-falleur T, Brichard V, C
Traversari C, Van PEL A, Wolf.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID T11549 standard; DNA; 13585 BP.
AC T11549;
                                                                                                                                                                                                                                                                                                                                                                                      451 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:T11549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-35 x T99594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -JUN-1995; U08153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9601557-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  757 CCAT 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19 yTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                        Sequence
```

```
The tumour rejection antigen precursor (TRAP) is processed to a tumour rejection antigen (TRA) presented by HLA-A2 molecules. TRA is used to generate cytotoxic I lymphocytes for treating cancer (espimelanoma). It can also be used to raise specific antibodies, and when complexed with HLA-A2, it can be used to prduce vaccines. Cytotoxic I lymphocytes so generated can be used in adoptive transfer or generated, or they can be generated in vivo by using a vector containing the appropriate gene or using TRA or TRAP together with an adjuvant that facilitates entry into HLA-A2 presenting cells. Diagnostic methods involving the detection of expression of TRAP sequence 13585 BP; 3827 A; 2859 C; 2968 G; 3894 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LeuAsnArgLeuSerGluArgArgGluSerLeuArgAsnLeuArgGly 19
                                                                                                                                                                                                                                                                                                                                                                                      46.00 Length: 16
3.538 Gaps: 0
81.250 Percent Identity: 56.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: T11549 from: 1 to: 13585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-35 x T11549
                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
     88888888888888
```

```
AI794877 sb72h01.yl Gm-c1010
AI795011 sb75a10.yl Gm-c1010
AQ873097 v59C8 mIn-3xHA/lacz
                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherita; Primates; Catarrhini; Hominidae; Homo.

Eutherita; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 103)

8 Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Man-Wai,C., Man-Wai,C., Clayton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A., Gnehm.C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.J., Kelley,J.M., McDonald,L.A., Nguyen,D.T., Phillipps,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R., Small,K.V., Spriggs,T.A., Utterback,T.R., Weldman,J.E., Li,Y., Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J., Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W., Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Coleman,T.A., Welly, M., Gruber,J., Hudson,P., Kim,A.K., Dillion,P.J., Fannon,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M., and Vonter,J.C.

Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: MI3 Reverse
                                                                                                                                                                                        2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AA319533 103 bp mRNA EST 19-APR-1997
DEFINITION EST21772 Adrenal gland tumor Homo sapiens CDNA 5' end similar is similar to major histocompatibility complex, class I, B (GB:M16102), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 12, 1996 this sequence version replaced gi:1393672 Other_ESTs: THC169519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioinformatics
The Institute for Genomic Research
The Madical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 100.000
  527
197.12
197.12
207.84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
1. .103
129.22
129.22
128.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                       AA319533
AA319533.1 GI:1971860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
47.50
47.50
47.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-35 x AA319533
                                                                                           seq_name: gb_est12:AA319533
                                                                                                                                                                                                                                                                                                                               human.
gb_est34:AI794877
gb_est34:AI795011
gb_gss6:AQ873097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Documentation
| AA319533 EST21772 Adrenal gland
| AA319533 EST21772 Adrenal gland
| AA319533 EST21775 Adrenal gland
| AA319533 EST50621 Activated T-C
| AA524961 EST60621 Activated T-C
| AA524961 EST160074 Pancreas tum
| AA324960 EST6101 Activated T-C
| AA058454 2167407.x1 Stratagene
| AA160317 2c56c07.x1 Stratagene
| AA160317 2c56c07.x1 Stratagene
| AA31080 EST815153 Jurkat T-cel
| AA31080 EST815153 Jurkat T-cel
| C18310 C18310 Human placenta cC
| AA663896 ac74401.s1 Stratagene
| AA1039796 DKF2P44481912.x1 Ac1
| AA5732 th12903.x1 NCT_CGAP_CG
| AA663896 ac74601.s1 Stratagene
| AA53135 PWYS605.x1 NCT_CGAP_CG
| AA663896 CETT-HSP-2173M11.TF CT
| AA077514 RPCI-11-162P10.TJ RPCI
| AA077514 RPCI-11-162P10.TJ RPCI
| AA077514 RPCI-11-162P10.TJ RPCI
| AA31579 EST35512 Embryo, 8 wee
| AM184423 fj14403.x1 Stratagene
| AA13579 EST35512 Embryo, 8 wee
| AA13579 EST35512 Embryo, 8 wee
| AA13579 EST35512 Embryo, 8 wee
| AA31579 RST35512 Embryo, 8 wee
| AA31579 AA31579 EST35512 Embryo, 8 wee
| AA31579 RST35512 Embryo, 8 wee
| AA31579 AA31579 AA31579 AA31577 A
                                                                                                                                                    Command line parameters:
-MODEL_frane+_p2n.model_DEV=x1p
-V_Cgn1_1/WSPTO_spool/WS0853294/runat_04022000_160700_15770/app_query.fasta.2
-V_CGG1_1/WSPTO_spool/WS08653294/runat_04.040.-160700_15770/app_query.fasta.2
-DB=EST .QFMT=fastap -SUFFIX=rst .GAPOP=12.000 -GAPDXT=4.000
-MINAATCH=0.100 -LOOPCIL=0.000 -LOOPEXT=0.000 -GGAPOP=4.500
-GGAPDXT=0.050 -XGAPOP=10.000 -XGAPDXT=0.500 -FGAPOP=6.000
-FGAPDXT=7.000 -YGAPOP=10.000 -YGAPDXT=0.500 -DELOP=6.000
-DELEXT=7.000 -YGAPOP=10.000 -YGAPDXT=0.500 -DELOP=6.001
-LIST=45 -DOCALIGN=200 -THR_SCORE-pct -ALIGN=15 -MODE-LOCAL
-UNCPU=F6 - NORM-ext -MINIEN-0 -MAXLEN-1000000 -USER-US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                      About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.30
113.08
113.08
120.08
120.08
131.38
331.38
331.39
34.11
44.11
131.38
101.38
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
101.39
  out_format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28500e
1148.49
1148.49
1148.49
1141.30
1141.30
1141.30
1141.30
1141.30
1141.30
1141.30
1141.30
1141.30
1141.30
1131.50
1131.50
1131.50
1131.50
1130.27
1130.27
1130.27
1130.27
1130.27
1130.27
1130.27
1130.27
1130.27
1130.27
1130.27
OM of: US-08-653-294-35 to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 7600.090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$51.00
$5
                                                Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                      Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strd
                                           Date: Feb 8, 2000 6:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query: US-08-653-294-35
Query length: 20
Database: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est13:AA351477
gb_est13:AA352603
gb_est12:AA294911
gb_est12:AA29401
gb_est13:AA2966
gb_est13:AA24068
gb_est10:AA160317
gb_est10:AA100680
gb_est7:W40489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est35:AL039796
gb_est28:AL524732
gb_est37:AW008453
gb_est11:AA263135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est11:AA205710
gb_est34:AI795124
gb_est13:AA331579
gb_est44:AM184423
gb_est15:AA129456
gb_est10:AA129456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est12:AA310808
gb_est9:C18310
gb_est17:AA663896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est21:AA915979
gb_est11:AA216757
gb_est44:AW187318
gb_est15:AA526987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_gss10:AQ248102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss13:AQ475632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_gss13:AQ475628
gb_gss12:AQ377514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est5:D73898
gb_est9:AA063950
gb_gss11:AQ299878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_gss11:AQ295324
gb_gss15:AQ641860
gb_est34:AI794913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_gss8:AQ009853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_gss3:B20346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss3:B90159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_gss3:B50728
```

```
Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12140200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukaryota; Metazoa; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Sadams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J.D.,

Kelley, J.M., Kelley, M.M., Fritchman, J.L., Geoghaqen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.Jr.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Sprigs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Caco, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dimke, D., Ferrie, A., Fischer, C., Hastings, G.A.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,

Raymond, L., Weil Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Pillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                     seq_documentation_block:
LOCUS
LOCUS
AA561477
189 bp mRNA EST
LOCUS
DEFINITION EST70761 T-cell lymphoma Homo sapiens cDNA 5' end similar to
similar to major histocompatibility complex, class I, Bw62.3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: arkerlav@tigr.org
Email: arkerlav@tigr.org
Information and argument and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 12, 1996 this sequence version replaced gi:1404737.
Other_ESTs: THC169519
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="ATCC (inhost):165623"
/db_xref="taxon:9606"
/clone_lib="T-cell lymphoma"
/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
to: 103
                                                 11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 g
  from: 1
                                                                                                                                                                                                                                                                                                                           AA361477.1 GI:2013795
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o 09
Align seg 1/1 to: AA319533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                   seq_name: gb_est13:AA361477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12140200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45
                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
```

```
Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eutheria; Cataroa; Eria; Balacia; Primates; Primaria; Primaria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cione_lib="Activated T-cells XX"
/cell_type="T-lymphocyte"
/dev_stage="adult"
/note="Yector: pBluescript SK-; Site_l: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On May 8, 1995 this sequence version replaced g1:800964.
Other_ESTs: THC172938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
Bioinformatics
Bioinformatics of Genomic Research
7712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056

    .218
    ^corganism="Homo sapiens"
    /db_xref="khTCC" (inhost):152802"
    /db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28 t
                                                                                                  to: 189
                                                                                                                                                                                     Location/Qualifiers
                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA352603
AA352603.1 GI:2004923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 C
                                                                                             Align seg 1/1 to: AA361477
US-08-653-294-35 x AA361477
                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est13:AA352603
```

```
Align seg 1/1 to: AA294911
                                                                                                  Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                        alignment_block:
US-08-653-294-35 x AA294911
                                                                                                                                                                                                                                                                                                                                                                                                                                   seg_name: gb_est13:AA352960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12140200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uman.
                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lutheria, Primates; Catarinii; Hominidae; Homo.

Butheria, Primates; Catarinii; Hominidae; Homo.

Radams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,

Buli, C.J., Lee, N.H.; Kirkness, E.F., Weinstock, G., Goodayne, J.D.,

White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.

Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,

Flizgerald, L.M., Flizthugh, W.M., Fritchman, J.L., Geophagen, N.S.,

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., T.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saddek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weddman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Low, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hunglun, J., Li, H., Meissner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Ming, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fennon, R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of CDNA sequence

Nature 377 (6547 Suppl), 3-174 (1995)

On Nov 29, 1993 this sequence version replaced gi:430148.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AA294911 259 bp mRNA EST 18-APR-1997 EST100074 Pancreas tumor I Homo sapiens cDNA 5' end similar to similar to major histocompatibility complex, class I, Bw62.3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tlgr.org/tdb/hgi/hgi.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: pancreas; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI"
87 c 75 q 30 t 7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7712 Medical Center Drive, Rockville, MD 20850 USA
el: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 others
                  Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="AtrCc (inhost):190413"
/db_xref="taxon:9606"
/clone_lib="Pencreas tumor I"
/dev_stage="adult"
                                                                                                                                                                                                        to: 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              he Institute for Genomic Research
                                                                                                                                                                                                                                                                                11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: arkerlav@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence.
AA294911
AA294911.1 GI:1947266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Kerlavage, AR
                  Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                   to: AA352603
                                                                                                                        alignment_block:
US-08-653-294-35 x AA352603
                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est12:AA294911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [e]:
                                                                                                                                                                                                        Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
```

```
Alignment_Scores 17.

Percent Similarity: 100.000 Percent Identity: 100.000

Alignment_block:

U. Align seg 1/1 to: AA294911 ...

Align seg 1/1 to: AA294911 i...

AA32960 i...

A
```

57

```
113
                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est11:AA224068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Marra, M.
      ಥ
    73
                                                                                 alignment_scores
                                                                                                                                                                                                                                             Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homosapiens
Homosapiens
Homosapiens

Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 373)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., Dubuque,T., Favello,A., Gish,W.,

Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,

Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,

Trevaskis,E., Underwood,K., Wohldmann,P., Materston,R., Wilson,R.,

and Mara,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ~3' adaptor sequence: 5'
                      Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1592 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 268.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="Solk cells (kanamycin resistant)"
/note="Organ: colon; Vector: pBluescript SK-; Site_1:
EcoR; Site_2: XhoI; Cloned unidirectionally. Primer:
ologo dr. T-84 colonic epithelial cell line. Average
insert size: 1.0 kb; Uni_ZAP XR Vector; -5' adaptor
sequence: 5' GAATTCGGCACGAG 3' -3' adaptor sequence: 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Sep 12, 1996 this sequence version replaced gi:1393357 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'clone_lib="Stratagene colon (#937204)"
                                                                                                                                                            Gaps: 0 Caps: 0 Percent Identity: 100.000
                                                              'n
/dev_stage="adult"
/note="Vector: pBluescript SK-;
xhol"
                                                              ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 373
/organism="Homo sapiens"
/db_xref="GDB:3813009"
/db_xref="taxon:9606"
/clone="IMAGE:509677"
                                                              35
                                                                                                                                                                                                                                                                                                         to: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCGAGTTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                     182 CGAGAGGCCTNCGGAACCTTCGCGGCTAC 211
                                                                                                                                                                                                                                                                                                                                              11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                p
                                                              88
                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA058454
AA058454.1 GI:1551280
                                                              80
C
                                                                                                                                                              Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AA352960
                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-35 x AA352960
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est8:AA058454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sednence.
                                                              62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uman.
                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
```

```
seq_documentation_block:
19-FEB-1997
LOCUS AA224068 397 bp mRNA EST 19-FEB-1997
LOCUS XA11f02.1: Strategene hNT nuron (#937233) Homo sapiens cDNA clone
LIMAGE:648507 5' similar to 9b:L22549_cds1 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, B-39 B*3901 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:648507"
/clone_lib="Stratagene hNT neuron (#937233)"
/do_stage="hNT neurons"
/lab_host="Solk (kanamycin resistant)"
/lab_host="Solk (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: CoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript Stranger Site_2: Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

11 (bases 1 to 397)

11 (lasse; Lo 397)

11 (lassoe, S., Dietrich, N., DuBuque, T., Favello, M., Gish, W., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Markins, M., Hulkman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Thierry-Meg, J., Rohliting, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J., Trevsskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This close is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28m13 revl ET from Amersham High quality sequence stop: 295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Nov 29, 1993 this sequence version replaced gi:430429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
others
                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTCGAGTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229 CGAGAGCCTGCGGAACCTGCGCGCCTAC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref-"GDB:5588245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 ArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref-"taxon:9606"
      þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA224068.1 GI:1844610
      O
                                                                                                                                                                                                                                                                         Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: AA058454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-35 x AA058454
```

from: 1

to: AA160317

ē,

```
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .405

/organism="Homo sapiens"
/db_xref="top8.462278"
/db_xref="taxon:9606"
/clone="IMAGE:590892"
/clone=lib="Stratagene pancreas (#937208)"
/clone=lib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:

LOCUS AAA60317

AA560317

DEFINITION 2056c07.r1 Stratagene pancreas (#937208) Homo sapiens CDNA clone
IMAGE:590892 5' similar to gb:011265 HIA CLASS I HISTOCOMPATIBILITY
ANTIGEN, B-35 B*3501 ALPHA (HUMAN);, mRNA sequence.

VERSION AA160317.1 GI:1734956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length. 1671 Std Error: 0.00
Seg primer: -28M13 rev2 from Amersham
High quality sequence stop: 332.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homosapiens
Eukaryota: Metazoa: Chordata: Craniata: Vertebrata; Mammalia;
Eukaryota: Metazoa: Chordata: Craniata: Nominidae; Homo.

1 (bases 1 to 405)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1406818.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 others
                                        Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                         to: 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297 CGAGAGGCCTGCGNAACCTGCGCGCGTAC 326
                                                                                                                                                                                                                                                                                                                                                                                                                                           11 ArgGluSerLeuArgAsnLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                         from: 1
                                             Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AA224068
                                                                                                                                                                                                                 alignment_block:
US-08-653-294-35 x AA224068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-35 x AA160317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_est10:AA160317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
    alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
```

```
Eukaryotta.

Eukaryotta.

Eukaryotta.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Hiller, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,

Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N.,

Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L.,

Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J.,

Treyaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Marra,M.
Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1534 Std Error: 0.00
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 275.
Location/Qualifiers
                                                                                                                                                         AA100680 419 bp mRNA EST 31-JUL-1997 21980b2.r1 Strategene colon (#937204) Homo sapiens CDNA clone ILMAGE:511851 5' SIMILAR to gb:NZ4039.cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-18 B*1801 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Wilson RK Washington University School of Medicine Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AsnArgLeuSerGluArgArgGluSerLeuArgAsnLeuArgGlyTyr 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 1
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AA100680 from: 1 to: 419

    .419
    /organ1sm="Homo sapiens"
    /db_xref="GDB:3844346"

                 281 CGAGAGAGCCTGCGGAACCTGCGCGGCTAC 310
11 ArgGluSerLeuArgAsnLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 9
                                                                                                                                                                                                                                                                            AA100680
AA100680.1 GI:1646981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51.00
3.643
87.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-35 x AA100680
                                                                                       seq_name: gb_est9:AA100680
                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                           Homo saptens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85
                                                                                                                                                                                                                                                                                                                                                       human .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                              LOCUS
DEFINITION
                                                                                                                                                                                                                                                                            ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
```

seq\_documentation\_block: LOCUS W40489

DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

Homo sapiens

ORGANISM

REFERENCE AUTHORS

human.

seq\_name: gb\_est7:W40489

```
Ladragia Frinances, Catarinin; Hominidae, Homo.

Butherly Frinances, Catarinin; Hominidae, Homo.

Butherly Frinances, E., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,

Ritzgerald, E.M., Fitzhugh, W.M., Fritchman, J.L., Geoglagen, N.S.,

Glodek, A., Gnehm, C.L., Hane, M.C., Hedblom, E., Hinkle, P.S.Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., WcDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

Dinke, D., Ferrie, A., Fischer, C., Hastings, G.A.,

Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Melssner, P.S., Olsen, H.,

Raymond, L., Wei, Y.F., Wing, J., Li, H., Melssner, P.S., Olsen, H.,

Fraser, C.M., and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cons agenere
Email: arkerlav@tigr.org

Email: arkerlav@tigr.org

Email: arkerlav@tigr.org

Information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Incation/Qualifiers

1. 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Jurkat T-cells V"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI"
                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced gi:1397854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="ATCC (inhost):156811"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292 CGAGAGAGCCTTCGGAACCTGCGCGCGCTAC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ArgGluSerLeuArgAsnLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerlavage, AR
                                                                                                             AA310808
AA310808.1 GI:1963136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: THC180721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-35 x AA310808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AA310808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.00
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     অ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12140200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                      ORGANISM
                                                                                                             ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
COMMENT
                                                                                                                                                          KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE
                                                                                                                                                     zc84b01.rl Pancreatic Islet Homo sapiens cDNA clone IMAGE:328969 5' similar to gb:U11265 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, B-35 B*3501 ALPHA (HUMAN);, mRNA sequence. W40489 U3:1324496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          On Jan 25, 1995 this sequence version replaced gi:637865.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REGA+FT
High quality sequence stop: 397.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 others
....AGCCTGCGGAACCTGCGCGGCTAC 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:1263173"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             279 CGAGAGACCTGCGAAACCTGCGCGGCTAC 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/clone="IMAGE:328969"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 ArgGluSerLeuArgAsnLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .427
/organism="Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: W40489 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio: 5.100
Percent Similarity: 100.000
225 CACAGACTTACCGAGAGA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-35 x W40489
```

and Marra, M.

97044478

TITLE JOURNAL MEDLINE COMMENT

FEATURES

seq\_name: gb\_est12:AA310808

Align seg 1/1

Quality:

alignment\_scores:

87

BASE COUNT ORIGIN

LOCUS

ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

```
/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/dev_stage="34 years old"
/lobe_host="SolR (kanamycin resistant)"
/note="Vector: Bluescript SR.; Site_1: EcoRI: Library
/solk aleutian. Schizophrenic suicide.
/sandom primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N.; Torrey, E.F.; Volken R.,
and the Stanley Neuropathology Consortium - Analysis of
/note RNAs from the Brains of Individuals with Psychiatric
/solns Hopkins School of Medicine, Baltimore MD."
/solns Hopkins School of Medicine, Baltimore MD."
                                                                       Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortum (info@image.llnl.gov) for further information.
Fossible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
High quality, sequence stop: 430.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL039796 503 bp mRNA EST 29-SEP-1999
DKF2p434B1912_r1 434 (synonym: htes3) Homo sapiens cDNA clone
DKF2p434B1912_5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duesterhoeft, A., Lauber, J., Mewes, H.W., Gassenhuber, J. and
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1394858.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST (Duesterhoeft, et al.)
Unpublished (1999)
On Jun 2, 1999 this sequence version replaced gi:4967270.
Contact: Duesterhoeft A
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:969889"
/clone_11b="Stratagene schizo brain Sll"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AA663896 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL039796.1 GI:5408804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                               1. .479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-35 x AA663896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est35:AL039796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AL039796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wiemann, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                       Libbases 1 to 475)
Fujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kujiwara,T., Hirano,H., Hishigaki,H., Horie,M., Kawai,A., Kuga,Y., Kyushiki,H., Nagata,M., Okuno,S., Ozaki,K., Shimizu,F., Shimda,Y., Shinomiya,H., Nakamura,Y. and Takahashi,E.
Askawa,H., Nakamura,Y. and Takahashi,E.
Otsuka cDNA project
Contact: T996 this sequence version replaced gi:1393837.
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10, kagssuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AA663896 479 bp mRNA EST 15-DEC-1997

DEFINITION a274001.s1 Strategene schizo brain S11 Homo sapiens cDNA clone
IMAGE:969889 3' similar to gb:M28203 HLA CLASS I HISTOCOMPATIBILITY
ANTIGEN, B-62 B*1504 ALPHA (HUMAN):, mRNA sequence.

ACCESSION AA663896.1 GI:2617887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 479)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Morte, E., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylle,T., Waterston,R. and Wilson,R. WashU-NCI human EST Project
                                                                                                   C18310 475 bp mRNA EST 02-OCT-1996 C18310 Human placenta CDNA (TFujiwara) Homo sapiens CDNA clone GEN-560D07 5', mRNA sequence.
C18310 G1:1579912
                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .475
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_orne=18b=18b0507"
/clone=1ib="Human placenta cDNA (TFujiwara)"
/tissue_type="placenta"
a 161 c 154 g 68 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: C18310 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 0886-65-2888
Fax: 0886-37-1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est17:AA663896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-35 x C18310
                                                                            seg_documentation_block:
                         seq_name: gb_est9:C18310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
```

source

FEATURES

TITLE JOURNAL COMMENT

BASE COUNT

ORIGIN

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE

```
572 GGGA 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 gGly 19
                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.nobi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.nobi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Tumor Gene Index

Tumor Gene Index

Unpublished (1997)
On May 7, 1998 this sequence version replaced gi:3121511.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausbergenih.gov
Tissue Procurement: Ash Alizadeh, John Byrd, M.D., Mike Grever,
M.D., Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             th129313.X NCI_CGAP_CLLI Homo sapiens cDNA clone IMAGE:2118100 3/
similar to SW:MY16_MOUSE P17564 MYELOID DIFFERENTIATION PRIMARY
RESPONSE PROTEIN MYD116. ;, mRNA sequence.
A1524732. GI:4438867
               Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de; sequenced by Qiagen within the cDNA sequencing consortium of the
                                                                                           German Genome Project.

No s1 sequence available at the RZPD in Berlin.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: pSport1; Site_1: Not1; Site_2: Sal1"
165 g 68 t 2 others
                                                                                                                                                                                                                                                                   /organism="Homo saplens"
/db_xref="taxon:9606"
/clone="Dkr2p434B1912"
/clone_lib="434 (synonym: htes3)"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 100.000
This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ww-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -400P from Gibco
High quality sequence stop: 422.
Location/Qualifiers
1. .583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                            1. .503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AL039796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-35 x AL039796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est28:AI524732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AI524732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
```

)

į

```
Immunomodulating d
HLA-B2702 CTL modu
HLA-B2702 GTL modu
HLA-B2702 CTL modu
HLA-B2702 CTL modu
Peptide B2702.84-7
HLA-B2702 84-75T/7
HLA-B2702 84-75T/7
HUAND MHC 1 alpha
HUAND HUA-D2702 CTL modu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chloroperoxidase.
Heptitis GB virus
Xanthosine N7 meth
Coffee xanthosine
Coffee XMT protein
Corn p-hydroxyphen
Neuronal nicotinic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunomodulating d
HLA-B2702 CTL modu
Peptide B2702.84-7
Human DNAX toll-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curvularia verrucu
Curvularia verrucu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human neuronal nic
                                                                                                                                                                                                                                                                                                                                                                                                                                           HLA-B2702 84-79-84
Peptide B2702.84-7
                                                                  February 8, 2000, 04:05:44; Search time 133.56 Seconds (without alignments) 2.128 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                       Description
                                                                                                                                                                                                                        188963
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                188963 segs, 23686106 residues
                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                           R95429
W33798
W33799
R92907
R92909
R33778
W33778
W33791
W33792
R9110
R9117
R9117
R9117
R9117
R9117
R9117
R9117
R9117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W33779
R92910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W36351
W86351
W12037
W12042
W44152
R82249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R81449
                                                                                                                                      1 YRLAIRRIALRY 12
                                                                                                          US-08-653-294-36
58
                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match Length DB
                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                                A_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                       Score
```

Database :

Result

۶ ک

Searched:

Run on:

hhib Sing C C Sing C Sing Sing C Sing Sing C Sing C Sing C Sing Sing Sing Sing Sing Sing Sing Sing			6	
growth in cytostatin strain SE strain SE strain SE sa truncate sa front be sa fourth telomeras nanodulator modulator modulator see il used see il used see see see see see see see see see		The state of the s	0; Gaps	
Human g Human c HSV-2 s HSV-2 s M. rosa M. rosa Human t Immunom Immunom		### 189429 standard; peptide; 12 AA. ### 1295. ### 1207.1996 (first entry) ### 1270.9 ### 1270.9 ### 1270.9 ### 1270.9 ### 12.8 ### 1270.9 ### 12.8 ### 1270.9 ### 12.8 ### 12.8 ### 1270.9 ### 12.8 ###	Length 12; ; Indels	
	MENTS	SULT 1  12-NOV-1996 (first entry)  12-NOV-1996 (first entry)  112-NOV-1996 (first entry)  112-NOV-1996 (first entry)  112-NOV-1996 (first entry)  114. PAT-1 alphal-helix; human-leucocyte-associated  T-cell lysate; membrane protein; mammal; heat shock  12 calcium influx; cytotoxic T lymphocyte; CTI  13 calcium influx; cytotoxic T lymphocyte; CTI  14 calcium influx; cytotoxic T lymphocyte; CTI  15 synthetic.  16 NOV-1993; US-150493.  17 NOV-1994; U12985.  18 NAV-1995  18 NAV-1995  19 NOVIV LELAND STANFORD JUNIOR.  Clayberger C, Krensky AM;  WPI; 95-194027/25.  18 NAV-1994; U12985.  19 NOV-1994; U12985.  10 NOV-1994; U12985.  10 NOV-1994; U12985.  10 NOV-1994; U12985.  11 NOV-1994; U12985.  12 NOV-1994; U12985.  13 NOV-1994; U12985.  14 NOV-1994; U12985.  15 STAD JUNIV LELAND STANFORD JUNIOR.  Clayberger C, Krensky AM;  WPI; 95-194027/25.  18 NOV-1994; U12985.  10 NOV-1994; U12985.  11 NOV-1994; U12985.  12 STAD JUNIV LELAND STANFORD JUNIOR.  CLAYDERS COMPISSING JUNIOR.  The protein Py4 first alphace and the passed column containing a covalently bound Hith-B2702 ball column containing a covalently bound Hith-B2702.  COMPOSITIONS COMPISSING them with the extracellular procompounds can be screened for their effect on the Compounds can be screened for their effect on the Compounds can be screened for their extracellular petermining The amount of binding between the candimal the extracellular portion of Fir and antigen presenting cells (Recontaining T-cells (Recontain	ore 58; DB 1; ed. No. 3.3e-05 Mismatches 0	
W83929 W30891 W72010 W72145 W92336 W92336 W92335 W47263 W47263	ALIGNMENT	2 AA.  me. an leucoc tein; mam otoxic T ng cell. ng cell. d surface and differ epresent antigens. Thes ill lysate ell active reactive can be un ergent, a tly bound ergent, a tly bound extracel) differe of with the inding be can be in gen prese on of p74 the p74 the p74	Sc. Pr.	
аанананана		the first of the f	66.	
1100 1100 1100 100 100 100 100 100 100		st entr 4 palin 4 palin 4 palin 4 palin 4 palin 50493. 50493. 50493. 50493. 75959. 75959. 78959. 78959. 78961.	100.0%; larity 100.0%; Conservative	12
51.7 51.7 51.7 51.7 51.7 50.00 50.00		WESTATE 1  1429 1429 1429 1429 12-NOV-1996 (first entry) 12-NOV-1996 (first entry) 12-NOV-1996 (first entry) 13-NOV-1996 (first entry) 14.5 p74; alphal-helix; human-1 1-cell lysate; membrane protein 15 calcium influx; cytotox 16-NOV-1994; ulsenting cytolysis; antigen presenting clayberger C. Krensky AM; WEI; 95-194027/25. 10-NOV-1994; Ulsensky AM; WEI; 95-194027/25. Compons. comprising lymphoid suinhibit cytolytic activity and thibit cytolytic activity and thibit cytolytic activity and thibit cytolytic activity and thibit cytolytic activity and the protein associated with T-cell also immunologically cross reacyll with an amphoteric detergence in with an amphoteric detergency column containing and antigen modulation of CTL activity can containing T-cells and antigen mix the extracellular portion owith p74 for the binding of the sequence 12 AA;	겉	YRLAIRRIALRY              YRLAIRRIALRY
000000000000000000000000000000000000000		129 12925 12929 12-NOV-199 HLA-B2702 HLA-B2702 HLA-B2702 HLA-B2702 HLA-B2702 HLA-B2702 HLA-B2702 W05913288- 10-NOV-199 10	atch cal	1 YRLAI          YRLAI
00000000000000000000000000000000000000		B 4	Query M Best Lo Matches	
		880 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	ОШХ	S S

W33798 standard; peptide; 12 AA. W33798;

RESULT 2 W33798 ID W33798 AC W33798;

Human ligase IV. M DNA-ligase-III. Ne eryA region polype Human cytostatin I Human cytostatin I

Human secreted pro

W76641 W41940 W09022 W74762 W69561 R95634

```
New immunomodulating dimer peptide(s) - based on a Class I HiA-B
alpha-1 domain, used for preventing rejection of transplants or
treating autoimmune diseases
Example 1; Page 19; 41pp; English.

CC cartivity. A peptide-type compound or variant is claimed which has
the remainal and activity, including the N-terminal acylated and/or
CC-terminal and and examples to esterified forms of up to 60 amino acids, where
CC cartivity and activity, including the N-terminal acylated and/or
CC creminal and and the compound comprises the formula; A-B, where A, B =
CC Small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino
acid. The sequence in the brackets may optionally be absent or truncated
at any peptide type bond within the brackets. The compounds comprise
at any peptide type bond within the brackets. The compounds comprise
at any peptide type bond within the brackets. The compounds comprise
on the capture of thibit cytocoxic T-lymphocytes (CTL) from
cacid. They can be used to inhibit cytocoxic T-lymphocytes (CTL) from
conditionation with antiquic peptides or proteins of interest to
activate CTLS. They can also inhibit the proliferation of T cells in
response to anti-CD3. The peptide can be used for preventing rejection
continuated arthritis and lupus erythematosis. The products can also be
considered to reference of the products can also be
considered to reference of the products can also be
considered to reference of the products can also be
considered to a considered the products can also be
considered to a considered the products can also be
considered to a considered the peptide can be used for preventing or products can also be
considered to a considered the peptide can be used for preventing or products can also be
considered to a considered the peptide can be cased for preventing or products can also be
considered to a con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 98-086530/08.

New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Claim 17: Page 35: 41pp; English.

This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autolimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 58; DB 1; Length 12; 100.0%; Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                       24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1997.
22-MAY-1997.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W33799 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W33799;
19-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLAIRRIALRY 12
                                                                                                                                                                                                         27-NOV-1997.
22-MAY-1997; U08689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9744351-A1.
27-NOV-1997.
                                                                                                                                                           Homo sapiens
                                                                                                        rejection.
                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
```

```
claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (R aaf6-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a represents amino acid; are sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proflicration of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of The peptides are administered to a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administered to administeration for alimited period of time (compared to the lifetime modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-B2702 CTL modulating peptide (B2702.84-75/75-84). Cytotoxic I lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 58; DB 1; Length 12; 100.0%; Pred. No. 3.3e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.9%; Score 44; DB 1;
60.0%; Pred. No. 0.024;
ative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R92907 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||||||
| YRLAIRLNERRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1995; U04349,
05-APR-1994; US-2228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayberger C, Krer
WPI, 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
R92907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME OF THE PROPERTY OF THE PR
           22222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   요
```

```
1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-OCT-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
R92909
ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PT companies comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLs.

Example: Page 12; 29pp: English.

Example: Page 12; 29pp: English.

Example: Page 12; 29pp: English.

CC 895413 and 895415-89541 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the HLA-BZ00 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. p74 is a T-cell surface membrane control associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70.

CC protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein HSC70.

CC protein associated number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by 19sis of a suitable coll with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-BZ702 palindromic peptide.

CC compositions comprising the extracellular fragment of p74 combined with the extracellular portion of p74 induces calcium influx, and inhibits compounds can be screened for their effect on the cytolysis. Candidate compounds them with the extracellular portion of p74 induces calcium influx.

CC containing T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

Sequence 20 AA;
                                                                                                12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
HLA-D2702 84-75-84 palindrome.
The p74: alphal-helix: human-leucocyte-associated antigen; inhibitor;
T-Cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytocoxic T lymphocyte; CTL; differentiation;
cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1998 (first entry)
Immunomodulating dimer peptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
Lansplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.9%; Score 44; DB 1; Length 20; Best Local Similarity 60.0%; Pred. No. 0.024; Matches 12; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
WPP: 98-086530/08.
                                                                                                                                                                                                                                                                                                                                    10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI: 95-194027/25.
                                              R95428 standard; peptide; 20 AA.
R95428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W33778 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-1997.
22-MAY-1997; U08689.
                                                                                                                                                                                                                                                            Synthetic.
WO9513288-A1.
18-MAY-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
RESULT
R95428
                                                                            NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
treating autoimmune diseases

Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
claimed which has immunomodulating activity, including the N-terminal
acylated and/or C-terminal amidated or esterified forms of up to 60
comino acids, where the peptide-type compound comprises the formula; A-B,
where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
V; aa77 = D, S or N; aa79 = R or G; aa80 = 1 or N; aa81, aa81 = E or
Aydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and as
represents amino acid. The sequence in the brackets may optionally be
absent or truncated at any peptide type bond within the brackets. The
compounds comprise amino acid sequences related to a Class I HLA-B
alphal domain (positions 79-84). They can be used to inhibit cytotoxic
T-lymphocytes (CTL) from undesirably attacking cells in a host or in
proteins of interest to activate CTLs. They can also inhibit the
protiferation of reals in response to anti-CD3. The peptide can be
used for preventing rejection of transplants or for treating autoimmune
diseases, e.g. diabetes, rheumatoid atthritis and lupus erythematosis.

The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R829307-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abaltic the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.9%; Score 44; DB 1; Length 20; 60.0%; Pred. No. 0.024; live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.21; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-1995; U04349.
05-ARR-1994; US-222851.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R92909 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAIRLNERRENLRIALRY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-1996 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match (0.0)
Best Local Similarity 60.09
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.0°
Matches 11; Conservative
```

g

```
Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence class I major histocompatibility complex (MHC) antigens. This sequence I san inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HAA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly of the patient.
                                                                                                                  16-MAY-1996 (first entry)

HLA-B2702 CIL modulating peptide (B2702.84-75(T)/75-84).

Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.

Example 1, Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-1998 (first entry)
Peptide B2702.84-75r/75-84 tested for immunomodulating activity.
Immunomodulating dimer: immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                             Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%; Score 39; DB 1;
55.0%; Pred. No. 0.21;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                     05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAY-1996; US-653294.
(STRD) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                     R92908 standard; peptide; 20 AA
W33791 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11; Conservative
                                                                                                                                                                                                                                                                     12-OCT-1995.
05-APR-1995; U04349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-MAY-1997; U08689.
                                                                                                                                                                                                                                                                                                                                         Clayberger C, Kren
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 98-086530/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AA;
                                                                                                                                                                                                                                                  W09526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33791;
                                                                     Φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
```

ò g NAME OF THE PROPERTY OF THE PR

```
PP 22-MAY-1997; U08689.

PP 24-MAY-1997; U08689.

PP 24-MAY-1997; U08689.

PP 24-MAY-1997; U08689.

PR (STRD) UNIV LELAND STANFORD JUNIOR.

PR (STRD) UNIV LELAND STANFORD JUNIOR.

PI 88-086530/08

WPI; 98-086530/08

WPI; 98-086530/08

WPI; 98-086530/08

PP 4-MAY-1996; DEAD TO PREVENTING TEJECTION OF TRANSPLANTS OF TRANSPLAIN OF TRANSPLA
the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-771) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa14 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HIA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, insending atthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1998 (first entry)
Petide B2702.84-75/75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.21; 1. Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W33792 standard; peptide; 20 AA.
W33792;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRLATRINERRENLRIALRY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 67.2
Best Local Similarity 55.0
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
```

DB 1; Length 20;

Score 39;

ä

ò

Gaps

ö

RESULT 11

õ g R95430

```
14-MAY-1998 (first entry)
Human neuronal nicotinic acetylcholine receptor alpha-3 subunit.
Human; neuronal nicotinic acetylcholine receptor; alpha-3 subunit;
brain tissue; screening; NRChR; antibody.
                                                                                                                                                         Example 4: Page 45: 103pp; English.
R71424-R71438 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain derived peptides and peptide mutants, they were used to modulate interactions between MHC 1 and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment
                                                                                                    Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                      Score 35; DB 1; Length 18; Pred. No. 1.1; 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                 of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "encoded by WWC"
240. .265
/label= TWD1
/note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label- TMD4
/note- "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note- "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 327. .458
/label- cytoplasmic_loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "encoded by TGY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label = unspecified
'note = "encoded by AWC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note- "encoded by WWC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tabel unspecified note noted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= unspecified
'note= "encoded by TWC"
                                                                Olsson L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label = unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label unspecified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W44156 standard; Protein; 504 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= signal
Misc_difference 235
                                                                                                                                                                                                                                                                                                                                                                      60.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73. .296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- TMD3
                                                                Goodenow RS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .480
                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
  12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 FRVDLRTLALRY 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-SEP-1994.
08-MAR-1994; U02447.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference 347
                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc_difference 354
                                                                  Goldstein A, Goo
WPI; 95-098577/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9420617-A2.
                                                                                                                                                   receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
W44156
    ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        reri 3-194940/L/20.

Tomposns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp; English.

CC R95413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequences can be used to isolate the protein p74 from a T-cell lyactivation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Exc.

CC membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Exc.

CC modical and in a limited number of cell types, but is a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HLA-B2702 palindromic peptide. Compositions comprising the extracellular fragment of p74 combined with HLA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.

CC andidate compounds can be screened for their effect on the cytolysis.

CC aciivity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by Sequence 20 AA; Ingand.
                       ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                                                             12-NOV-1996 (first entry)
HIA-B2702 84-757/75-84T palindrome.
HIA-B2702 84-757/75-84T palindrome.
HIA: p74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R71429 standard; peptide; 18 AA.
R71429;
12-0027-1995 (first entry)
Human MHC 1 alpha 1 domain peptide [Ala81]-Dk-(69-85).
Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; peptide [Ala81]-Dk-(69-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
                       ю
Э
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ά
ώ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 20;
Pred. No. 0.51;
0; Mismatches 0; Indels
                     1; Indels
Pred. No. 0.21;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        W09513288-A1.
18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                     cytolysis; antigen presenting cell.
                                                                                                                                                                                                           standard; peptide; 20 AA.
                                                             1 YRLAIR-----RIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.8%;
57.9%;
                                                                                                    1 YRLAIRLNERRENLRTALRY 20
  55.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLAIRLNETRENLRIALR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLAIR-----RIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayberger C, Krensky AM; WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 63.8
Best Local Similarity 57.9
Matches 11; Conservative
                       Conservative
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
WO9505189-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-FEB-1995
  Best Local
Matches 1
                                                                                                                                                                                                        R95430 s
```

RESULT 12

ò а R71429

AC DE DOT OS OS DE PN

ä

Gaps

ŝ,

Indels

ö

Mismatches

;

Conservative

<u>ښ</u>

Matches

```
Example 2: Page 72-73; 99pp; English.

The present sequence represents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR.

Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting duraction with one or more receptor subtypes than drugs identified e.g. screening with cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 15; Page 36; 80pp; English.
R83061-R83085, R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is a dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B3702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75).
CYLOCOXIC T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                              Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 504; 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                   (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC. (SIBI-) SIBIA NEUROSCIENCES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.3%; Score 35; 58.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Krensky AM, Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that express a variety of subtypes.
Sequence 504 AA;
                                                           Elliott KJ, Ellis SB, Harpold MM;
WPI; 94-303024/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R92911 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 | | |||::| |
232 YSLXIRRLSLFY 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clayberger C, Kren
WPI; 95-358582/46.
                                                                                                        N-PSDB; V12200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
R92911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
ò
```

```
Nove 1997: Work 1997: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                        Immunomodulating dimer peptide #2.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34.5; DB 1; Length 20; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                       20 AA.
                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                     W33779 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
1 YRLAIR-----RIALR 11
                              |||||||
| YRLAIRLNERYRLAIR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRLAIR-----RIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                       19-JUN-1998
                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                        15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                        RESULT
W33779
  ò
                                             g
                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
```

8, 2000, 04:05:45

Search completed: February Job time: 9362 sec

DB 1; Length 20;

Score 34.5; D. Pred. No. 1.5;

59.5%; 56.2%;

Query Match Best Local Similarity

Ì

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 7, 2000, 18:04:41 Run on:

Search time 111.22 Seconds (without alignments) 5.089 Million cell updates/sec

1 YRLAIRRIALRY 12 US-08-653-294-36 58 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summarles

pirl:\* pir2:\* pir3:\* PIR\_62:\* 1: pir1: 2: pir2: 3: pir3: 4: pir4: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	probable oxidoredu	Na+/H+ antiporter	histocompatibility	ABC-type transport	ند			chetical	protein	strf protein - Str	conserved hypothet	probable fumarate	avy	hypothetical prote	U		thioether S-methyl	beta-glucosidase h	hflx protein - Myc	ä	hypothetical prote	L17 ribosomal prot	-	hypothetical prote	P-glycoprotein - C	hypothetical prote	P-glycoprotein - C	conserved hypothet	hypothetical prote	preprotein translo
SUMMARIES	QI	G70882	34	829990	S74745	S44230	S17776	S15593	D72507	S44228	S44225	C69460	F72691	B54802	S69745	H71504	F70410	S52102	G69760	S72938	A41798	D65032	C72053	S50980	T16542	148120	E75055	148119	F72323	S	BWBSSY
	DB																													7	
	Length	309	313	348	276	281	281	388	178	267	267	469	573	4367	128	141	190	264	477	518	682	1124	142	203	215	252	253	259	306	339	431
di	Query Match	6	•	62.1	ö	60.3	60.3	ö	ω.	ω.	ω.	ω.	æ.	œ.	ė.	ė.	ė,	ů.	ŝ.	ė	œ.	Ġ.	δ.	'n.	ď.	δ.	ď.	ď.	'n.	55.2	'n
	Score	40	36	36	35	35	35	35	34	34	34	34	34	34	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32
	Result No.	1	7	e	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

hypothetical prote chloride peroxidas	hypothetical prote hypothetical prote	hypothetical prote p-qlycoprotein iso	nonstructural poly	DNA-directed RNA p	3-dehydroquinate d	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote
T04960 S69334	T05172 T00336	T16616 I48123	T08822	F64429	508501	E71567	S76802	S74282	T02119
22	<b>~</b> ~	77	90	4 (4	9	10	~	~	N
434	857 978	1010	1998	78	153	264	264	265	286
55.2 55.2	55.2 55.2	55.2 55.2	55.2	53.4	53.4	53.4	53.4	53.4	53.4
32 32	35 35 35	32	32	31	31	31	31	31	31
31 32	3 3 4	3 3 3 9	37	36	4.	45	43	44	45

## ALIGNMENTS

	RESULT 1	
	G70882	
	probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)	
	C; Species: Mycobacterium tuberculosis	
	C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 29-Sep-1999	
_	C; Accession: G70882	
_	R; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon	
_	; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,	
	Nature 393, 537-544, 1998	
_	A; Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua	
_	.; Taylor, K.; Whitehead, S.; Barrell, B.G.	
_	A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno	
	A; Reference number: A70500; MUID: 98295987	
_	A;Accession: G70882	
	A; Status: preliminary; nucleic acid sequence not shown; translation not shown	
	A; Molecule type: DNA	
	A; Residues: 1-309 <col/>	
	A:Cross-references: GB:AL008967: GB:AL123456: NID:g3261491: PIDN:CAA15591.1: PID:e129	

PID:e129

A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15591.1; PID:e129
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: Rv2776c
C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; fer
F;9-211,Donmain: cytochrome-b5 reductase homology <CBR>
F;240-297/Domain: ferredoxin [2Fe-25] homology <FER>

0; Gaps Score 40; DB 2; Length 309; Pred. No. 2; 1; Mismatches 0; Indels 69.0%; 88.9%; Query Match
Best Local Similarity 88.9
Matches 8; Conservative

ö

1 YRLAIRRIA 9 ||:|||||| 65 YRIAIRRIA 73 õ 셤

Na+/H+ antiporter cdu2 - Clostridium difficile
Na+/H+ antiporter cdu2 - Clostridium difficile
(5.95ecdes Clostridium difficile
(5.95ecdes Clostridium difficile
(5.05ecdes Clostridium difficile
(5.05ecdes Clostridium difficile
(5.05ecdes Clostridium difficile
(5.05ecdes Clostridium difficile
(6.05eccession: JC5342
R. Braun, V.: Hundsberger, T.; Leukel, P.; Sauerborn, M.; von Eichel-Streiber, C.
Gene 181, 29-38, 1996
A. Fitle: Definition of the single integration site of the pathogenicity locus in Clos
A. Reference number: JC5340; MUID:97128764
A. A. Residues: 1-313 CBRA>
A. Molecule type: DNA
A. Residues: 1-313 CBRA>
C. Comment: This protein contains 11 membrane spanning domain. It functionally links to C. Genetics:

The second

g

å

```
C;Species: Streptomyces griseus
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Mar-1998
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 20-Mar-1998
C;Accession: $17776
Mol. Gen. Genet. 228, 459-469, 1991
A;Title: Genetics of streptomycin production in Streptomyces griseus: nucleotide sequal A;Accession: $17775: MUID: 91375432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:Y00459; GB:S55493; NID:g1621271; PID:e275192; PID:g1621272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X54434
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
C;Species: Streptomyces glaudescens
C;Date: 13-4an-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S44230
R;Mayer, G.; Piepersberg, W.
Submitted to the EMBL Data Library, April 1994
A;Reference number: S44224
A;Reference number: S44224
A;Reference prelaminary
A;Molecule type: DNA
A;Residues: 1-281 <MAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein (insertion sequence ISH27-3) - Halobacterium halobium C;Species: Halobacterium halobium C;Species: Halobacterium halobium C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 30-Jun-1998
                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                 Length 281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 281;
                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                  A;Cross-references: EMBL:X78974; NID:g475235; PID:g581673
C;Genetics:
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
17;
                                                                                                                                                                                                                                                                                                                                    5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-281 <MAN>
                                                                                                                                                                                                                                                                                                                                 Score 35; DB 2
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35; DB;
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Mobile element: insertion sequence ISH27-3
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.3%;
70.0%;
                                                                                                                                                                                                                                                                                                                                    Query Match 60.3%;
Best Local Similarity 70.0%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:| ||:|||
234 RIAARRIALR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||| ||:|:|
234 RLAARRLAMR 243
                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-388 <PFE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                            2 RLAIRRIALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: strF
A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
Do, R.se. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-276 «KAN»
A; Residues: 1-276 «KAN»
A; Notes: references: EMBL:D90901; GB:AB001339; NID:g1651897; PID:d1017629; PID:g1651970
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C; Keywords: transport protein
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                          :Species: Macaca mulatta (rhesus macaque)
:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
:Accession: S29990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:221819; NID:938568; PIDN:CAA79885.1; PID:938569
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABC-type transport protein slr0977 - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein slr0977
                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: S74745
A;Status: nucleic acid sequence not shown; translation not shown
                           Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 276;
                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                       ore 36; DB 2;
ed. No. 12;
Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
14;
                                                                                                                                                                                                                                                                                                                                                      R:Bontrop, R.R.
submitted to the EMBL Data Library, February 1993
A:Reference number: $29990
A:Accession: $29990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB 2
Pred. No. 17;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Keywords: transmembrane protein
F;219-284/Domain: immunoglobulin homology <IMM>
                         Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S74322; MUID: 97061201
                                                                                                                                                                                                                                                                   histocompatibility antigen, HLA-F-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62.18;
54.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.3%;
                       62.1%;
ilarity 41.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 62.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 60.3
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                      Query Match
Best Local Similarity
-has 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |:|:|:: |||
98 RVALRKLLRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-348 <BON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S74745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues:
```

g

ð g

ò

```
Conserved hypothetical protein AF1684 - Archaeoglobus fulgidus
Conserved hypothetical protein AF1684 - Archaeoglobus fulgidus
C;Species: C6460
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weldman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Woose, C.R.; Venter, J.C.
A;Tile: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Accession: C69460
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-469 <a href="https://dx.doi.org/licenter-nucleosis-references: BB:AE0000987; GB:AE000782; NID:92689310; PIDN:AAB89565.1; PID:9264
C;Superfamily: hypothetical protein MJ0966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                     ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2; Length 573;
Pred. No. 53;
                                                                                                                                                                                                                                                                                                            Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.6%; Score 34; DB 2; Length 469; 58.3%; Pred. No. 44; ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                        A; Molecule type: DNA
A; Residues: 1-267 <MAY>
A; Residues: 1-267 <MAY>
Cross-references: EMBL:X78972; NID:g475227; PID:g581604
C; Genetics:
A; Start codon: GTG
                                                                                                                                                                                                                                                                                                         Score 34; DB 2;
Pred. No. 26;
2; Mismatches
submitted to the EMBL Data Library, April 1994 A; Reference number: S44224 A; Accession: S44225
                                                                                                                                                                                                                                                                                                         58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.6%;
66.7%;
                                                                                                                                                                                                                                                                                                         Query Match 58.6
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234 RVAARRIALR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          à
                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein APE2034 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Accession: D72507
C;Accession: D72507
C;Accession: D72507
C;Accession: D72507
C;Accession: D72507
A;Riwarabayasi, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kunahashi, T.; Tanaka, T.; Yamazaki, J.; Kunahashi, T.; Yamazaki, J.; Kunahashi, J.; Yamazaki, J.; Kunahashi, J.; Yamazaki, J.; Yamaz
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptomyces galbus
C;Date: 13-40n-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C;Accession: S44228
R;Mayer, G.; Piepersberg, W.
Submitted to the EMBL Data Library, April 1994
A;Reference number: S44224
A;Accession: S44228
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strf protein - Streptomyces bluensis (fragment)
C;Species: Streptomyces bluensis
C;Species: Streptomyces bluensis
C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 10-Sep-1997
C;Accession: S44225
R;Mayer, G.: Piepersberg, W.
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                        Score 35; DB 2; Length 388; Pred. No. 23; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-267 <MAY>
A;Cross-references: EMBL:X78973; NID:g475232; PID:g475234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 2;
Pred. No. 17;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2;
Pred. No. 26;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strf protein - Streptomyces galbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%;
63.6%;
                                                            60.3%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 58.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Experimental source: strain K1
C, Genetics:
A, Gene: APE2034
                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.6
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 RLAARRLAVR 243
                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLAIRRIALR 11
                                                                                                                                                                                                                       |||||:||:
154 YRLAVRRL 161
                                                                                                                                                                                 1 YRLAIRRI 8
                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                                                                                                                                                                    ò
                                                                                                                                                                                                                                          a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŏ
```

```
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 13-Aug-1999
C;Accession: H71504; I40747
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t
A;Reference number: A71570; MUID:99000809
                                                                                                                                                                                                                                                                        A; Residues: 26-115, 7R',117-141 <GUL>
A; Cross-references: GB:L33834; NID:g620026; PIDN:AAA74990.1; PID:g620030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 2; Length 141;
Pred. No. 22;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7, 2000, 18:04:42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: Escherichia coll ribosomal; Reywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: February
Job time: 22208 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||: |: :||
64 RLAVGRLMVRY 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                            R:Plamann, M.: Minke, P.F.; Tinsley, J.H.; Bruno, K.S.
J. Cell Biol. 127, 139-149, 1994
A;Title: Cytoplasmic dynein and actin-related protein Arpl are required for normal nucle
A;Reference number: A54802; MUID:95014704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
ö
                                                                                                                                                                                                                         dynein heavy chain, cytosolic - Neurospora crassa
N:Contains: dynein ATPase (EC 3.6.1.33)
C:Species: Neurospora crassa
C:Date: 10-Sep.1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein YDR360w - yeast (Saccharomyces cerevisiae) . C.Species: Saccharomyces cerevisiae C.Species: Saccharomyces cerevisiae C.Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 26-Aug-1999 C.Accession: S69745
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: The sequence of S. cerevisiae cosmid 9476.
A; Description: The sequence of S. cerevisiae cosmid 9476.
A; Reference number: S61146
A; Accession: S6945
A; Molecule type: DNA
A; Residues: 1-128 < DUZ>
A; Residues: 1-128 < DUZ>
Cosertics: RMBL: U28372; NID: 9849170; PID: 92194159; MIPS: YDR360w
C; Genetics: A; Map position: 4R
C; Superfamily: Saccharomyces hypothetical protein YDR360w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       microtubule binding; P-loop
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 4367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 33; DB 2; Length 128;
Pred. No. 20;
3; Mismatches 2; Indels
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: B54802
A; Molecule type: DNA
A; Residues: 1-4367 <PLA>
A; Cross-references: GB:L31504; NID:g473489; PID:g473490
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -100p)
  ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C. Superfamily: dynain heavy chain, cytosolic C. Superfamily: dynain heavy chain, cytosolic C. Keywords: APP; heterotetramer; hydrolase; microtubb F:1943-1950.Region: nucleotide-binding motif A (P-loc F:240-2247/Region: nucleotide-binding motif A (P-loc F:2947-2954.Region: nucleotide-binding motif A (P-loc F:2947-2954.Region: nucleotide-binding motif A (P-loc F:1949/Binding site: ATP (Lys) #status predicted F:2611/Binding site: ATP (Lys) #status predicted F:2611/Binding site: ATP (Lys) #status predicted F:2953/Binding site: ATP (Lys) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 1; I
Pred. No. 3.8e+02;
2; Mismatches 1;
  Mismatches
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 58.6%;
Best Local Similarity 66.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 56.9%;
Best Local Similarity 54.5%;
Matches 6; Conservative
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 104/1; 4205/3
C; Superfamily: dynein he
C; Keywords: ATP; heterot
F; 1943-1950/Region: nucl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1:1111: 1
2859 AVRRIAMEY 2867
                                                                                                320 AVREIAIRY 328
                                                 4 AIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 AIRRIALRY 12
                                                                                                                                                                                                                                                                                                                               Accession: B54802
.
9
  Matches
                                                 ô
                                                                                                යි
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
```

Gaps

; 0

g

1 YRLAIRRIALR 11

ö

Gaps

ö

protein L17

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

February 8, 2000, 01:26:02; Search time 68.63 Seconds (without alignments) 5.222 Million cell updates/sec

US-08-653-294-36 58 1 YRLAIRRIALRY 12 Title: Perfect score: Seguence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

Total number of hits satisfying chosen parameters:

82229

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Р33617 ша	P09397 streptomyce		_			P23865 escherichia					-					P05147 emericella							_	•••	_	Q57538 haemophilus		_	306	34		843	Q91437 squalus aca
SUMMARIES	ID	F	STRF_STRGR	DYHC_NEUCR	RL17_CHLTR	TSMT_MOUSE	BGL2_BACSU	PRC_ECOLI	YPHG_ECOLI	NH10_YEAST	HRMA_PSESY	SECY_BACSU	ACH6_CAEEL	PRXC_CURIN	YE7A_SCHPO	MDR3_CRIGR	RPOH_METJA	3DHQ_EMENI	YCD4_YEAST	DAPB_MYCTU	BIOB_MYCTU	DEGS_ECOLI	DNAJ_COXBU	ACH3_BOVIN	ACH3_CHICK	ACH3_RAT	ACH3_HUMAN	Y664_HAEIN	RUB2_BRANA	CRTI_CERNC	PRC_HAEIN	PRTP_VZVD	DNL4_HUMAN	RN12_YEAST	PYR1_SQUAC
	DB	1	-	~		٦	Н	-1		Н		Н	Н	Н	Н	-	-1	-	Н	Н	1	Н	Н	~1	Н	Н	~	Н	Н	Н		Н	-	Н	П
	Length	348	281	9	3	264	477	682	1124	203	375	431	487	609	723	1281	78	153	212	245	349	355	367	495	496	499	503	552	583	621	695	770	844	850	2242
d	Ouery Match	62	。	8	ġ.	٠,	56.9	ė.	ė.	S	ß	55.2	S	S	S	55.2	53.4	53.4	53.4	m	53.4	m	m	m	53.4	m	53.4	53.4	m	m	53.4	53.4	53.4	53.4	53.4
	Score	m	35	34	33	33	33	33	33	32	32	32	32	32	32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31	31
	Result No.		7	m	4	ហ	9	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	58	30	31	32	33	34

saccharopol emericella alcaligenes vaccinia vi variola vir inckettsia desulfovite mycoplasma enterococcu
Q03132 E P4544 P P45444 P P45444 P P03162 P P31083 P P33085 P P33085 P P33095 P P47248 M P472
ERY2_SACER DYHC_EMENI HEMN_ALCEU VJ05_VACCY VJ05_VACCC VJ05_VACC TASW BFDV TASW BFDV HMC5_DESYH DNJL_MYCGE VANT_ENTFA
наннаннанн
3567 4344 4344 124 1134 1133 110 126 310 310
53.4 53.4 52.6 51.7 51.7 51.7 51.7 51.7
30 30.5 30 30 30 30 30 30 30 30 30
00000000000000000000000000000000000000

## ALIGNMENTS

GN HIA-F OR HIAR.  MACAGOR MULLATA (Rhesus macaque).  CC Eutharia. Primates; Catarrhini; Cercopithecidae; Cercopithecinae;  CC Eutharia. Primates; Catarrhini; Cercopithecidae; Cercopithecidae;  RN BEDINES; 9324625.  RX MEDINES; DANTROP R.E.;  RX T. CHARCETIZATION Of the rhesus macaque (Macaca mulatta) equivalent  CC THIA-F. "INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO  THE INMUNES SYSTEM.  "INMUNES SYSTEM."  "INMUNES SYSTEM."  "INMUNES SYSTEM."  "INSS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  CC THIS SWISS-PROT entry is catement is not removed. Usage by and for commercial  CC THIS SWISS-PROT entry is tatement is not removed. Usage by and for commercial  CC THIS SWISS-PROT ENTRY IN THE PRODUCED IN THE SWISS-PROT ENTRY IN THE S
--

Length 348; DB 1;

Query Match

Score 36; 62.18;

```
PROSITE; PS01167; RIBOSOMAL_L17; 1.
PFAM; PF01196; Ribosomal_L17; 1.
                                                                                                                                                                                                                                                                                                              4367 AA;
                                                                                                                                                                                                                                                                                                                                                                                                      |:||||: |
2859 AVRRIAMEY 2867
                                                                                                                                                                                                                                                                                                                                                                                         4 AIRRIALRY 12
                                                                                                                                                                                                                                                                                2240
2605
2947
                                                                                                                                                                                                                                                           Heptad repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                        RL17_CHLTR
ID RL17_CHLTR
AC P47760;
                                                                                                                                                                                                                                                                                                     NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                    NP_BIND
NP_BIND
                                                                                                                                                                                                                                                                                           NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                               셤
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                               MEDLINE; 91375432.
MANSOORI K., PIEBERSBERG W.;
"Genetics of streptomycin production in Streptomyces griseus:
nucleotide sequence of five genes, strFGHIK, including a phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
            Gaps
                                                                                                                                                                                  Streptomyces griseus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                   -1- PATHWAY: STREPTOMYCIN BIOSYNTHESIS.
-1- SIMILARITY: LOW, TO THE AMINO-TERMINAL DOMAIN OF GLUCOSE-6-
           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                     Mol. Gen. Genet. 228:459-469(1991).
-!- FUNCTION: MAY BE INVOLVED IN THE FORMATION OF N-METHYL-L-GLUCOSAMINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 281;
6.5;
           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In blosynthesis.
281 AA; 31726 MW; 75CEB24C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC).
                                                                                                                               01-MAR-1989 (Rel. 10, Created)
01-MG-1992 (Rel. 23, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
STREPTOMYCIN BIOSYNTHESIS PROTEIN STRF.
                                                                                                         281 AA
 Pred. No. 5.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.3%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y00459; CAA68518.1; -. PIR; S17776; S17776.
 54.58;
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                          PHOSPHATE ISOMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                            |:|:|:: |||
RVALRKLLLRY 108
                               2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111 | 1:1:1
234 RLAARRLAMR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 REAIRRIALR 11
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=74-OR23-1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptomycin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (
01-NOV-1995 (
01-NOV-1997 (
                                                                               STRE_STRGR
ID STRE_STRGR
AC P09397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DYHC_NEUCR
P45443;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DYHC_NEUCR
                                                    86
                                                    셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           á
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                          K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
"Cytoplasmic dynein and actin-related protein Arpl are required for normal nuclear distribution in filamentous fungi.";

"Cytoplasmic dynein and actin-related protein Arpl are required for normal nuclear distribution in filamentous fungi.";

-i. ell biol. 127:139-149(1994).

-i. FUNCTION: DYNEIN HAS ATPASE ACTIVITY. CYTOPLASMIC DYNEIN ACTS AS MOTOR FOR THE INTRACELULAR RETROGRADE MOTILITY OF VESICLES AND ORGANELLES ALONG MICROTUBULES. REQUIRED TO MAINTAIN UNIFORM NUCLEAR DISTRIBUTION IN HYPHAE.

-i. SUBUNIT: CONSISTS OF AT LEAST TWO HEAVY CHAINS AND A NUMBER OF INTERMEDIATE AND LIGHT CHAINS.

-i. SUBCELLULAR LOCATION: CYTOPLASMIC.

-i. SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GU L.J., WENMAN W.M., REMACHA M., MEUSER R.U., COFFIN J.M., KAUL F
"Chlamydia trachomatis RNA polymerase alpha subunit: sequence and
structural analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 177:2594-2601(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 34; DB 1; Length 436
Pred. No. 2.1e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Microtubules; Dynein; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B81B5E92 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
50S RIBOSOMAL PROTEIN L17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP
ATP
ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequ
15-DEC-1998 (Rel. 37, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; L31504; AAA64908.1; -. Motor protein; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; L33834; AAA74990.1; -. PROSITE; PS01167; RIBOSOMAL_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%;
66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-434/BU / SEROVAR L2;
MEDLINE; 95247702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 58.6
Best Local Similarity 66.7
Matches 6; Conservative
```

SOW

<del>Q</del> ð

```
Bacteria; Firmicutes; Bacillus/Clostridium group;
                             Bacillus/Staphylococcus group; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M21672; -; NOT_ANNOTATED_CDS. 299105; CAB12135.1; -. P11546; 1PBG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D30762; BAA06429.1; -. EMBL; D50453; BAA08975.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 56.9
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBTILIST; BG11181; YCKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 RIGLRRITSRY 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    477 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLAIRRIALRY 12
                                                         SEQUENCE FROM N.A.
                                                                       STRAIN-168;
MEDLINE; 95219080.
                                                                                                                                                                           SEQUENCE FROM N.A.
 Sacillus subtilis.
                                                                                                                                                                                                            MEDLINE; 97124189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRC_ECOLI
ID PRC_ECOLI
AC P23865;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
 윰
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BEEFFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (1992), University of Louisville, U.S.A.
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIOMINE + DIMETHYL SULFIDE
S-ADENOSYL-L-HOMOCYSTEINE + TRIMETHYLSULFONIUM.
-!- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS EC 2.1.1.1,
EC 2.1.1.28 AND EC 2.1.1.96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROBABLE BETA-GLUCOSTDASE (EC 3.2.1.21) (GENTIOBIASE) (CELLOBIASE)
(BETA-D-GLUCOSIDE GLUCOHYDROLASE) (AMYGDALASE)
                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                      Score 33; DB 1; Length 122;
Pred. No. 6.5;
; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
WARNER D.R., HOFFMAN J.L.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
10-FEB-1995 (Rel. 31, Last sequence update)
01-ROV-1997 (Rel. 35, Last annotation update)
THIOETHER S-METHYLTRANSFERASE (EC 2.1.1.96) (TEMT).
Ribosomal protein.
SEQUENCE 122 AA; 13969 MW; B8C43F7D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 1;
Pred. No. 15;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29460 MW; 31B87F7A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   477 AA.
                                                                                                                                                                                                                         264 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS01100; NNWT PNWT_TEMT; 1.
PFAM; PF01234; NNWT_PNWT_TEMT; 1.
Transferase; Methyltransferase.
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M88694; AAA62365.1; -. MGD; MGI:102963; TEMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.9%;
                                                      Query Match 56.9%;
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                             musculus (Mouse).
                                                                                                                                   2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase: Methy SEQUENCE 264 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 YRAALRRLA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 YRLAIRRIA 9
                                                                                                                                                                                TSMT_MOUSE
ID TSMT_MOUSE
AC P40936;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BGLZ_BACSU
ID BGLZ_BACSU
AC P42403;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WARNER D.R.
                                                                                                                                                                                                                                                                                                                                Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
```

õ g CE DIT OF

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE: 8829868.

WEDLINE: 8829868.

VOSMAN B., KUIKEN G., KOOISTRA J., VENEMA G.;

VOSMAN B., KUIKEN G., KOOISTRA J., VENEMA G.;

VICHALLOGALION IN BACILLUS SUBTILIS: involvement of the
17-kilodalton DNA-entry nuclease and the competence-specific
18-kilodalton protein.";
J. Bacteriol. 170:3703-3710(1988).
-!- CATALYTIC ACTIVITY: HURROLYSIS OF TERMINAL, NON-REDUCING BETA-D-GLUCOSE RESIDUES WITH RELEASE OF BETA-D-GLUCOSE.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF GLYCOSYL HYDROLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00572; GIXCOSYL_HYDROL_F1_1; 1.
PROSITE; PS00653; GIXCOSYL_HYDROL_F1_2; 1.
PFAM; PF00232; Glyco_hydro_1; 1.
Hypothetical protein; Hydrolase; Glycosidase; Cellulose degradation.
FUJISHIMA Y., YAMANE K.;
"A 10 kb nuclectide sequence at the 5' flanking region (32 degrees)
of srfAA of the Bacillus subtilis chromosome.";
Microbiology 14:127-279(1995).
                                                                                                                                                                                                                                                                                             YAMANE K., KUMANO M., KURITA K.;
"The 25 degrees-36 degrees region of the Bacillus subtilis
chromosome: determination of the sequence of a 146 kb segment and
identification of 113 genes.";
Microbiology 142:3047-3056(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
12-DEC-1999 (Rel. 39, Last annotation update)
TAIL-SPECIFIC PROTEASE PRECURSOR (EC 3.4.21.-) (PROTEASE RE) (PRC
PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 477;
29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTON DONOR (POTENTIAL).
NUCLEOPHILE (BY SIMILARITY).
E92CD679 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           682 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.9%; Score 33; DB 54.5%; Pred. No. 29; tive 2; Mismatches
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
SEQUENCE FROM N.A.
STRAIN-12 / W3110;
MEDLINE; 91310589
HARA H., YAMAMOTO Y., HIGASHITANI A., SUZUKI H., NISHIMURA Y.;
"Cloning, mapping, and characterization of the Escherichia coli progene, which is involved in C-terminal processing of penicillin-binding protein 3.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 96161995.
KEILER K.C., SAUER R.T.;
"Sequence determinants of C-terminal substrate recognition by the Tsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protease.";
J. BALJ. Chem. 271:2589-2593(1996).
-i- FUNCTION: INVOLVED IN THE CLEAVAGE OF A C-TERMINAL PEPTIDE OF 11
-RESIDUES FROM THE PRECURSOR FORM OF PENICILLIN-BINDING PROTEIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 330-403 FROM N.A. MEDLINE; 93077473. SEOANE A., SABBAJ A., MCMURRY L.M., LEVY S.B.; SEOANE A., SABBAJ A., MCMURRY L.M., LEVY S.B.; Multiple antiblotic susceptibility associated with inactivation of the pro gene.; J. Bacteriol. 174:7844-7847(1992).
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDILINE; 97426617
BLATTNER; 97426617
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAXHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                             MEDLINE; 92108041.
SILBER K.R., KRILER K.C., SAUER R.T.;
SILBER K.R., KRILER K.C., SAUER R.T.;
Typ: a tail-specific protease that selectively degrades proteins with nonpolar C termin!";
Proc. Natl. Acad. Sci. U.S.A. 89:295-299(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 97251358.

ITOH T., AIBA H., BABA T., FUJITA K., HAYASHI K., INADA T., ISONO K., KASAI H., KIMARA S., KITAKAWA M., KITAGAWA M., MIKITA., MIZOBUCHI K., MORI H., MORI T., MOTOMURA K., MAKINO K., MIKITA., MAZOBUCHI K., MORI H., MORI T., MORI T., NAKAMURA Y., NASHIMOTO H., NISHIO Y., OSHIMA T., SAITO N., SAMPEI G., SEKI Y., SIVASUNDARAM S., TAGAMI H., TAKEDA J., TAKEMOTO K., WADA C., YAMAMOTO Y., HORIUCHI T.; A 460-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 40.1-50.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUNTE H.J., CRANE R.A., CULHAM D.E., RICHMOND D., WOOD J.M.; "Protein Prool influences osmotic activation of compatible solute transporter Prop in Escherichia coll K-12."; J. Bacteriol. 181:1537-1543(1999).
            Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE; 96081954.
KELLER K.C., SAUER R.T.;
Tidentification of active site residues of the Tsp protease.";
"laentification 270:28864-28868(1995).
                                                                                                                                                                                                                                                                                                                                                                       sequence of Escherichia coli K-12.";
                                                                                                                                                         Bacteriol. 173:4799-4813(1991).
                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequenc
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-33 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Res. 3:379-392(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBSTRATE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVE SITE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 99175453.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                   SEQUENCE FROM N.A.
                                   Escherichia.
OR TSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-K12
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baloinformatics and the FNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
(PBP3), PROTEASE THAT SELECTIVELY DEGRADES PROTEINS WITH NONPOLAR C-TERMINAL: MAY BE INVOLVED IN PROTECTION OF THE BACTERIUM FROM THERMAL AND OSMOTIC STRESSES.
                                                                                      LOCATION: ASSOCIATED WITH THE PERIPLASMIC SIDE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                   SUBCELLULAR LOCATION: ASSOCIATED WITH THE PERIPLASMIC SIDE OF CYTOPLASMIC MEMBRANE.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S41 (SERINE PROTEASE).
SIMILARITY: CONTAINS 1 PDZ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 9742617 6. III, BLOCH C.A., PERNA N.T., BURLAND V.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAXHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 127.3 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 1; Length 682; Pred. No. 44; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
TAIL-SPECIFIC PROTEASE.
PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   L -> Q (IN REF. 1)
3CF7B39A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 1124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D00674; BAA00578.1; ALT_INIT.
M75634; AAA24699.1; -
AE000277; AAC74900.1; -
D90826; CAB21562.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317 L
76663 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D90827; CAB21572.1; -. EMBL; S49803; AAB24313.1; -. EMBL; L48409; AAD41528.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D00674; BAA00577.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 56.9
Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Periplasmic; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A42475; A42475.
ECOGENE; EG10760; PRC.
PFAM; PF00595; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317
682 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 YKFAIRRLA 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLAIRRIA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPHG_ECOLI
P76585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACT_SITE
ACT_SITE
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
YPHG_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
```

```
Nucleic Acids Res. 18:1647-1647(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRLAIRRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacillus subtilis.
            HEMA PROTEIN.
                                                                                                                                                                                Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECY_BACSU
ID SECY_BACSU
AC P16336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region.";
                 SON SERVICE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A PAC 
modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NHP10 OR HWO2 OR YDL002C OR YD8119.05C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MURPHY L., RICHARDS C., GENTLES S., HARRIS D., BARRELL B.G.
RAJANDREAM M.A.;
Submitted (JAN.1995) to the EMBL/Genbank/DDBJ databases.
-: SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h 55.2%; Score 32; DB 1; Length 203; Similarity 45.5%; Pred. No. 18; 5; Conservative 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                0A06B4C6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 1;
Pred. No. 76;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMG BOX.
80A216B6 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 AA.
                                                                                                                                              EMBL, AE000341; AAC75602.1; -. ECOGENE: EG13468; yphG. Hypothetical protein. SEQUENCE 1124 AA; 127284 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 158 H
203 AA; 23857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP: P07155; 1HME.
SGD: L0002765; NHPIO.
PFAM: PF00505; HMG_box: 1.
Nuclear protein; DNA_binding.
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 56.9%;
Best Local Similarity 87.5%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z48008; CAA88059.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HRMA_PSESY

ID HRMA_PSESY STANDARD;

AC Q08370,

DT 01-NOV-1995 (Rel. 32, C;

DT 01-NOV-1995 (Rel. 32, L;

DT 01-NOV-1995 (Rel. 32, L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     412 YRLAIREI 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLAIRRI 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NHP10 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NH10_YEAST
Q03435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
NH10_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOUR REAL PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence and properties of the hrmA locus associated with the Pseudomonas syringae pv. syringae 61 hrp gene cluster."; Mol. Plant Microbe Interact. 6:553-564(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
MEDLINE; 90251170.
SUH J.-W., BOYLAN S.A., THOMAS S.M., DOLAN K.M., OLIVER D.B.,
SUH J.-W., BOYLAN S.A., THOMAS S.M., DOLAN K.M., OLIVER D.B.,
SUH J.-W., BOYLAN S.A., THOMAS S.M., DOLAN K.M., OLIVER D.B.,
ISOLATION Of a secY homologue from Bacillus subtilis: evidence for a common protein export pathway in eubacteria.";
Mol. Microbiol. 4:305-314(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                    STRAIN-PSS61;
HUANG H.C., HUTCHESON S.W., COLLMER A.;
HUARacterization of the hrp cluster from Pseudomonas syringae pv.
syringae 61 and TnphoA tagging of exported or membrane-spanning Hrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOSHIKAWA H., DOI R.H.; "Sequence of the Bacilius subtilis spectinomycin resistance gene
Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 32; DB 1; Length 375;
Pred. No. 36;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypersensitive response.
SEQUENCE 375 AA; 41458 MW; 733EEB06 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PREPROTEIN TRANSLOCASE SECY SUBUNIT.
                                                                                                                                                                                                                                                                                                                                            401. Plant Microbe Interact. 4:469-476(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L14926; AAA16545.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55.2%;
ilarity 58.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-PSS61;
MEDLINE; 94100578.
HEU S., HUTCHESON S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |||:|| | |
174 YRLSITRKTLSY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 90221911.
```

STANDARD;

```
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                    01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
ACETYLCHOLINE RECEPTOR, BETA-TYPE SUBUNIT ACR-3 PRECURSOR.
                                                                                                                                Caenorhabditis elegans.
                                             ACH6_CAEEL
093149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                셤
                                             ò
                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EmbL outstation the European Bioinformatics. Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                  -:- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH SECA AND SECE TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA MEMBRANE, BY FORMIC PART OF A CHANNEL.
-:- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THAT COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS.
-:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
-:- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                                  NAKAMURA K., NAKAMURA A., TAKAMATSU H., YOSHIKAWA H., YAMANE K.; "Cloning and characterization of a Bacillus subtills gene homologous to E. coli secy.";
J. Biochem. 107:603-607(1990).
                                                                                          SEQUENCE FROM N.A. MEDLINE; 96186897. SUH J.W., BOYLAN S.A., OH S.H., PRICE C.W.; "Genetic and transcriptional organization of the Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
1C8A4316 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                              EMBL; X51329; CAA35712.1; -.
EMBL; M31102; AAB59118.1; -.
EMBL; D00619; BAA00495.1; -I.
EMBL; L47971; AAB06819.1; -.
EMBL; 299104; CAB11912.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Translocation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47243 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00755; SECY_1; 1.
PROSITE; PS00756; SECY_2; 1.
PFAM; PF00344; SECY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SECY
                                                                                                                                              spc-alpha region.";
Gene 169:17-23(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S08629; BWBSSY
PIR; S12683; S12683
                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG10445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein transport;
           SEQUENCE FROM N.A. MEDLINE; 90292990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBTILIST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLCHOLINE RECEPTOR, BETA-TYPE SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRXC_CURIN STANDARD; PRT; 609 AA.
P49053;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VANADIUM CHLOROPEROXIDASE (EC 1.11.1.10) (VCPO) (VANADIUM CHLORIDE CPO.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE; 98269564.
MEDLINE; 98269564.

BAXLIS H.A., MATSODA K., SOUIRE M.D., FLEMING J.T., HARVEY R.J.,
BAXLISON M.G., BARNARD E.A., SATTELLE D.B.;
"ACR-3, a Caenorinabditis elegans nicotinic acetylcholine receptor
subunit. Molecular cloning and functional expression.";
Recept. Channels 5:149-158(1997).

Recept. Channels 5:149-158(1997).

-1 FOWCITION: POSSIBLE ACETYLCHOLINE RECEPTOR.

-1 SUBCELLULAR LOCATION: INTEGRAL MERRANE PROFEIN.

-1 SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; Y08637; CAA69927.1; -.
PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
PFAM; PF00065; neur_chan; 1.
Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
CYTOPLASMIC (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
102629B3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.2%; Score 32; 58.3%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56245 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 55.2
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314
439
460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219 YQIKIRRKALFY 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46
151
487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
PRXC_CURIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEERTAGE
```

ö

Gaps

ö

Indels

Pred. No. 42;

Query Match 55.2%; Score 32; Best Local Similarity 55.6%; Pred. No. 4 Matches 5; Conservative 4; Mismatch

|:|:||::| 237 AVRKIAIQY 245

යු *ද්* 

4 AIRRIALRY 12

á

DB 1; Length 431;

```
PGY3 OR PGP3
                                                                                                                                                                                                                                                                   MDR3_CRIGR
P23174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANNOT
                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRANSMEM
                                                                                                                                                                                                                                           RESULT 15
MDR3_CRIGR
                                                                                                                                                                              ö
윱
                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a alicense agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                            MESCRESCHAIDT A., WEYER R.;
MESSERSCHAIDT A., WEYER R.;
A. Tay Structure of a vanadum-containing enzyme: chloroperoxidase from the fungus Curvularia inaqualis.";
Proc. Natl. Acad. Sci. U.S.A. 93:392-396(1996).
-:- CATALYTIC ACTIVITY: 2 RH + 2 CHLORIDE + H(2)O(2) = 2 RCL + 2
           Eukaryota: Fungi; Ascomycota; Euascomycetes; Loculoascomycetes;
Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Curvularia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=972;
SKELTON J., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO YEAST YGL144C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                     MUIJSERS A.O., MESSERSCHMIDT A., WEVER R.; MUIJSERS A.O., MESSERSCHMIDT A., WEVER R.; Frinary structure and characterization of the vanadium chloroperoxidase from the fungus Curvularia inaequalis."; Eur. J. Blochem. 229:566-574(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.2%; Score 32; DB 1; Length 609; 50.0%; Pred. No. 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     454 454 P -> S (IN AA SEQUENCE).
609 AA; 67530 MW; 19112E80 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Oxidoreductase; Peroxidase; Vanadium; 3D-structure.
ACT SITE 404 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 80.1 KD PROTEIN C4A8.10 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   723 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
                                               SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                   -1- COFACTOR: VANADIUM.
-1- SUBCELLULAR LOCATION: SECRETED.
-1- PIM: THE N-TERMINUS IS BLOCKED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X85369; CAA59686.1; -. PDB; 1VNC; 08-NOV-96.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
 Curvularia inaequalis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 YNQIVRRIAVTY 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YE7A_SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPAC4A8.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
YE7A_SCHPO
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MISCELLANBOUS: PGP ISOFORMS DIFFER IN THEIR DRUG TRANSPORT CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92135896.
ENDICOTU J.A., SARANGI F., LING V.;
ENDICOTU J.A., SARANGI F., LING V.;
"Complete cDNA sequences encoding the Chinese hamster P-glycoprotein gene family.";
DNA Seq. 2:89-101(1991).
-!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DRUG ACCUMULATION IN MULTIDRUG-RESISTANT CELLS.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein; Transmembrane; Transport; Duplication;
                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                Score 32; DB 1; Length 723;
Pred. No. 74;
4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1991 (Rel. 20, Created)
U-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN 3 (P-GLYCOPROTEIN 3).
                                                                                                                                                                             al protein.
723 AA; 80090 MW; 159D795B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1281 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL. POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00211; ABC_TRANSPORTER; 1. PFAM; PF00005; ABC_tran; 2. PFAM; PF00664; ABC_membrane; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cricetulus griseus (Chinese hamster).
                                                                                                                                                                                                                                                                                                   55.2%;
                                                                                                                                              EMBL; 298762; CAB11480.1; -. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M60042; AAA68885.1; -.
                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 54.5
اتاتات 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        :||| |::|:|
647 HRLAWRKVAVR 657
                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLAIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Glyo
Multigene family
```

```
955 975 POTENTIAL.

978 958 POTENTIAL.

975 995 POTENTIAL.

996 1281 CYTOPLASMIC (POTENTIAL).

429 436 ATP (POTENTIAL).

1071 1078 ATP (POTENTIAL).

1281 AA; 140866 MW; 9FE9DF5C CRC32;
 TRANSMEM
TRANSMEM
DOMAIN
NP_BIND
NP_BIND
SEQUENCE
```

; 0 0; Gaps Ouery Match 55.2%; Score 32; DB 1; Length 1281; Best Local Similarity 70.0%; Pred. No. 1.4e+02; Matches 7; Conservative 1; Mismatches 2; Indels

Qy 2 RLAIRRIALR 11 |||||| :| |||||| 193 |||||| 193

Search completed: February 8, 2000, 01:26:02 Job time: 1562 sec

```
O86347 PRELIMINARY; PRT; 309 AA.
C86347.
01-NOV-1998 (Tremblrel. 08, Created)
01-NOV-1998 (Tremblrel. 08, Last sequence update)
01-NOV-1999 (Tremblrel. 12, Last annotation update)
HYPOTHERICAL 33.5 KD PROTEIN.
                                                                                                                                                                                                                                                                                                                     022063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
086347
1D 08
AC 08
DT 01
DT 01
DE HY
GN RV
                                                                                                                                                                                                                                                                                                 RESULT
Q22063
                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9zuj4 arabidopsis
O28589 archaeoglob
Q9ydg3 aeropyrum p
Q9xeg1 gossypium h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q22063 caenorhabdi
086347 mycobacteri
085853 sphingomona
09xb05 myxococcus
02694 trypanosoma
P7218 clostridium
026954 trypanosoma
P7288 synechocyst
054259 streptomyce
016382 caenorhabdi
09yaa5 aeropyrum p
053815 streptomyce
054257 streptomyce
054257 streptomyce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P87286 saccharomyc
084514 chlamydia t
                                                        8, 2000, 19:16:17; Search time 176.54 Seconds (without alignments) 4.713 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
                                                                                                                                                                                             225878
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                       225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                           summaries

    protein search, using sw model

                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q54259
Q9X876
Q9YAA5
Q53815
Q53815
Q54257
Q58203
Q5803
Q9YDG3
Q9YDG3
Q9YDG3
Q9XEG1
P87286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        085853
Q9XB05
Q97213
Q26954
P72880
                                                                                                                                                                                                                                                                                                                                                                                          sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
                                                                                                                                                                                                                                                                                                                    sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                           sp_organelle:*
sp_phage:*
                                                                                                  US-08-653-294-36
58
1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                       sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                 seq length: 0 seq length: 1000000
                                                                                                                                                                                                                                                                              SPTREMBL_12:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276
281
281
725
725
178
267
350
384
                                                                                                                                                                                                                                                                                                                                                   sp_mhc:*
                                                           February
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score
                                                                                                          Perfect score:
Sequence:
                                                                                                                                           Scoring table:
                                                                                                                                                                                                                Minimum DB :
Maximum DB :
                                        OM protein
                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                              Database
                                                            Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Result
No.
```

```
09yvn7 melanoplus
09yvn7 melanoplus
015455 homo sapien
09yn4 squash yell
09x789 chlamydla p
021162 caenorhabdl
060503 cricetulus
016763 caenorhabdl
09wzx9 thermotoga
029x28 arenoplus
023555 arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P95486 pseudomonas
007074 porphyromon
097211 leishmania
082630 arabidopsis
060313 homo saplen
                        Q924b6 escherichia
P91068 caenorhabdi
045795 caenorhabdi
Q9xil2 arabidopsis
Q59958 streptococc
Q49843 mycobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

WILD A.;

WILD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.7%; Score 41; DB 5; 58.3%; Pred. No. 7.6; ive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               795 AA
                                                                                                                                                                                                     099VNN7
098VNV
098HV4
098Z7S9
02215S2
02116Z
060503
016763
016763
099EXS9
029EXS9
02695Z
049569
067313
Q924B6
P91068
O45795
Q9XIL2
                                                                                                                                              Q59958
Q49843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q22063; Q93489;
01-NOV-1996 (TrEMBLE). 01, C;
01-MA-1999 (TrEMBLE). 10, L;
01-NOV-1999 (TrEMBLE). 12, L;
TOLC3.10 PROTEIN.
                                                                                     Query Match 70.7
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 YRTSLRRLATRY 17
122222222
12222222
1222222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
1222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
1222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
1222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
1222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
12222
1222
1222
1222
1222
12222
12222
1222
```

```
post-
xanthus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
cDU2, CDU1, TCDB, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4
GENES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                       "Genetic and functional analysis of genes required for the modification of the polyketide antibiotic TA of Myxococcus Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ132503; CB46503.1; - 4CC64E85 CRC32:
                                                                                                                                                                                                                                                             Myxococcus xanthus.
Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 2;
Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4F20347A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 AA.
                                                                                              325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37; DB
Pred. No. 18;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ER-15;
PAITAN Y., ORR E., RON E.Z., ROSENBERG E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03, Created)
03, Last sequ
                                                                                                                                             Created)
                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VON EICHEL-STREIBER C.;
Submitted (JAN-1997) to the EME
EMBL; X92982; CAA63559.1; -.
SEQUENCE 313 AA; 33380 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62.18;
41.78;
                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, MEMBRANE ASSOCIATED PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63.8%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01,
12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 63.8
Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. (TrEMBLrel. (TrEMBLrel. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. C
(TrEMBLrel. C
(TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||: ||:::|
259 YRVVARRLSIKY 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-VPI10463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1997
01-MAY-1997
01-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   026954
026954;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1999 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clostridium.
                                                                                           Q9XB05
Q9XB05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P97213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
Q26954
ID Q26
AC Q26
DT 01-
DT 01-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
P97213
                                               RESULT
09XB05
                                                                                                a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOREACCOSSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                 MEDLINE; 98295987.

COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., BEGLAEIER K., GAS S., BARRY III C.E., TERAIA F., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNESY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MIRPHY L., OLIVER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J., TAYLOR K., WHITEHEAD S., BARRELL B.G.; SQUARES R., SULSTON J.E., TAYLOR K., WHITEHEAD S., BARRELL B.G.; SOURES S., SOARES R., SULSTON J.E., SPECTON S., SQUARES S., SQARES R., SALLSON J.E., MOULE S., SALLSON J.E., SALLSON J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacterlaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ROMINE M.F., STILLWELL L.C., WONG K.-K., THURSTON S.J., SISK E.C., SENSEN C.W., GARSTERLAND T., SAFFER J.D., FREDRICKSON J.K.; "Complete sequence of a 184 kb catabolic plasmid from Sphingomonas surmaticivorans strain F199"; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF079317; AAD03868.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; alpha subdivision; Zymomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.8%; Score 37; DB 2; Length 243; 63.6%; Pred. No. 13; 2; Indels iive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 26.5 KD PROTEIN.
Sphingomonas aromaticivorans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00111; fer2; 1.
PFAM; PF00175; oxidored_fad; 1.
Hypothetical protein; Iron-sulfur.
SEQUENCE 309 AA; 33517 MW; B152B590 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein; Plasmid.
SEQUENCE 243 AA; 26455 MW; 40CDFBF4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 2
Pred. No. 4.5;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.0%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARKHILL J.;
Submitted (JUN-1998) to the
EMBL; ALO08967; CAA15591.1;
HSSP; P33164; 2PIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 63.8
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 RLAORRVTIRY 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-F199;
                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLAIRRIA 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmid pNL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sphingomonas
```

085853 085853; m

පු ò

RESULT 085853

ò 셤

ö

Gaps

.; o

ö

Gaps

```
BEYER S., DISTLER J., PIEPERSBERG W.;
"The str gene cluster for the biosynthesis of 5'-hydroxystreptomycin in Streptomyces glaucescens GLA.0 (ETH 22794): new operons and evidence for pathway-specific regulation by StrR.";
Mol. Gen. Genet. 250:775-78(1996).

EMBL; X78974; CAA55572.1;

EMBL; AJ006985; CAA07379.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE FROM N.A.
STAIN-MACC 19032 (GLA.O);
RETZLAFF L., MAYER G., BEYER S., AHLERT J., VERSECK S., DISTLER J.,
PIEPERSBEGG W.
                                                                                                                                                                           Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Streptomycin Production in Streptomycetes: a Progress Report."; (In) Baltz R.H., Hegeman G.D., Skatrud P.L. (eds.); Industrial microorganisms. Basic and applied molecular genetics, pp.183-194, ASM Press, Herndon (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.3%; Score 35; DB 2; Length 281; 70.0%; Pred. No. 38; 1; Indels Live 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                              MAYER G., PIEPERSBERG W.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
GLA O GENES STRB1, STRF, STRG, STRH, STRP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31427 MW; 30CD0C63 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-ATCC 13032 (GLA.0);
PIEPERSBERG W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-ATCC 13032 (GLA.0);
MEDLINE; 96204519.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                     Streptomyces glaucescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:| ||:|||
234 RIAARRIALR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        STRAIN-GLA 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09X876
09X876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
Q9X876
   DDD THE SERVICE OF SERVICE SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A REPAREMENT OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-PCC6803;
MEDLINES, 9706120.
KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIMA I., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
                                                                                          Sukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                           NETELINE; 98226175.

MEDLINE; 98226175.

TIBBETTS R.S., JENSEN J.L., OLSON C.L., WANG F., ENGMAN D.M.;

The DnaJ family of protein chaperones in Trypanosoma cruz1.";

MO1. Blochem. Parasitol. 91:319-326(1998).

ENEL: 146819; AAC18897.1; -..

HSSP; P08622; 1XBL.

PROSITE: PS00636; DNAJ_1; 1.

PFAM; PF00226; DnaJ_1; 1.

PFAM; PF00226; DnaJ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Length 441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JAN-1999 (TrEMBLrel. 09, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 2;
Pred. No. 37;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4DBF5330 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 5
Pred. No. 38;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain PCC 6803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Res. 3:109-136(1996).
EMBL. D90901; BAA16896-1; -.
PFAW: PF01061; ABC2_membrane; 1.
SEQUENCE 276 AA; 31542 MW; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 65.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 60.3
Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | | ||:||:|
23 RTAYRRLALKY 33
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                           'rypanosoma cruzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | || | ||:||
31 YTLAWRDIAVRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-PCC6803;
TABATA S.;
                                                                                                                                                                                 STRAIN-PBOL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P72880
P72880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q54259
Q54259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P72880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           054259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a y
```

Gaps

```
STRAIN-A3(2);
MURBHY L., HARRIS D.;
MURBHY L., HARRIS D.;
The S to fordered cosmids and a detailed genetic and physical map for the S Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                        Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=A3(2);
BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
                                                                                                                                                                                                                                                 Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                           01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN (FRAGMENT).
SCEIS.01.
436 AA.
PRT;
```

Last sequence update)
Last annotation update)

Created)

```
MEDLINE; 99310339.

KAWARABAYASI Y., HINO Y., HORIKAWA H., YAWAZAKI S., HAIKAWA Y.,
JINNO K., TAKAHASHI M., SEKINE M., BABA S., ANNAI A., KOSUGI H.,
HOSOYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,
TAKAMIYA M., MAGUDA S., FUNAHASHI T., TANNAKA T., KUDOH Y.,
YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
NOWURA N., SAKO Y., KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Complete genome sequence of an aerobic hyper-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19484 MW; FEA2CD00 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:83-101(1999).
EMBL; AP000063; BAA81044.1; -
SEQUENCE 178 AA; 19484 MW; FEA2CI
                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Crenarchaeota; Aeropyrum
                                                                                                                                                                                                                                                                                                                                       178AA LONG HYPOTHETICAL PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.6
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                        PRELIMINARY:
: ||||| | |
594 FSFAIRRIVLNY 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 RLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:| ||||: |
34 RMACRRIAIVY 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        Aeropyrum pernix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-K1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q53815
Q53815;
                                                                                                                                                                                                                         Q9YAA5;
                                                                                                                                                                                        O9YAA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
053815
053815
AC 053815
DT 01-NOV
DT 01-NOV
DF 18-55
OS STRE-
OC Bacter:
OC Bacter:
OC Actino
RN SEQUEN
RA MAYER (R
RL SUDMIT:
DR SEQUEN
RN SEQUEN
                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

C. STRAIN-BRISTOL. N2;
MEDILINE; 94150718.

A WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
A BONTIELD J., BURTON J., CONNELL M., COPERT J., COOPER J.,
COATAYON M., DEAR S., DU Z., DUTBIN R., FAVELLO A., FULTON L.,
CRAXTON M., DEAR S., DU Z., DUTBIN R., FAYELLO A., FULTON L.,
A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRELLE P.,
A JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATRELLE P.,
A PARSONS J., PERCY C., RIFKEN L., ROOPER A., SAUNDERS D., SHOWNKEEN R.,
A SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
A HIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
T. 2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                     genetic and physical map for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                     REDENBACH M., KIESER H.M., DENAPAITE D., EICHNER A., CULLUM J., KINASHI H., HOPWOOD D.A.;
"A set of ordered cosmids and a detailed genetic and physical mathe 8 Mb Streptomyces coeliscolor A3(2) chromosome.";
MOI. Microbiol. 21:77-96(1996).
EMBL: ALO49707; CAB41270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 725,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases. EMBL; AF016442; AAB65917.1; -. SEQUENCE 725 AA; 84926 MW; A4847D75 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEGUENCE FROM N.A.
STRAIN=BRISTOL N2;
JONES K., WOLDDWANN P.;
Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
99;
                                                                                                                                                                                                                                                                                                                                                                           436 436 436 4W; EDFD0658 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB (
59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB Pred. No. 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 725 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.3%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K12B6.2.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 368:32-38(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 RLAVRTLALR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                             FROM N.A.
                                                                                          STRAIN=A3(2);
MEDLINE; 97000351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K12B6.2 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    elegans.
                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             016382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              016382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                016382
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCOOR REPARED DO THE REPARED DO THE
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                         Straptomyces bluensis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Score 34; DB 1; Length 178;
Pred. No. 37;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-ISP 5564;
MAYER G., PIEPERBERG W.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; X78972; CAA55568.1;
                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 01, Last annotation update) cmp. 5564 GENES STRB AND STRF (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBC0D606 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58.6%; Score 34; DB 70.0%; Pred. No. 56; iive 2; Mismatches
                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267
29777: MW;
 58.6%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:| ||:|||
234 RVAARRLALR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

ö

Gaps

ö

4; Indels

Conservative

1 YRLAIRRIALRY 12

ò

```
Search completed: February
Job time: 21506 sec
  307 YRLAVRKI 314
                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
SEQUENCE
                                                                                                                       092UJ4
                                                                                                   092UJ
     셤
                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 94150718.

MEDLINE; 94150718.

MILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

LIGHTNING J., LLOYD C., MCHURRAY A., MORTINOKE B., O'CALLAGHAN M.,

PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditla; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                 Streptomyces galbus.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                    STRAIN-DSM 40480;
MAYER G., PIEPERSBERG W.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
EMBL; x78973; AAA55570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
LLOYD C., WILKINSON J.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                ©54257;
01-NOY-1996 (TIEMBLIEL: 01, Created)
01-NOY-1996 (TIEMBLIEL: 01, Last sequence update)
01-NOY-1996 (TIEMBLIEL: 01, Last annocation update)
DSM 40480 GENES STRB1 AND STRF (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 2;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 5;
Pred. No. 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                            82D9D7A4 CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40291 MW; A9117B4D CRC32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                            267 AA; 29909 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.6%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-38(1994).
EMBL: 282051; CABO4615.1; -.
PFAM: PF01461; 7tm_4; 1.
SEQUENCE 350 AA: 40291 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 h 58.6%;
Similarity 75.0%;
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAY-1999 (TrEMBLrel. 10, T23D5.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 70.v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     234 RLAARRLAVR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 RLAIRRIALR 11
                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      045803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            045803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
045803
                                                                                                                                                                             STRF
954257

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572

9572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         õ
```

8, 2000, 19:16:19

```
SEQUENCE FROM N.A.
VYSOTSKAIA V.S., SCHWARTZ J.R., YU G., TORIUMI M., LENZ C., LIU S.,
LI J., KREMENETSKAIA I., LUROS J., GONZALEZ A., ALTARI H., ARAUJO R.,
BUUTHLER E., CHAO Q., CONN L., CONWAY A.B., DUNN P., HANSEN N.,
HUIZAR L., KIM C., PALM C., ROWLEY D., SHINN P., WALKER M.,
DAVIS R.W., ECKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
"Arabidopsis thallana chromosome 1 BAC TZKIO sequence.";
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, euphyllophytes, Spermatophyta, Magnollophyta, eudicotyledons; core eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 10;
Pred. No. 81;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB0D711E CRC32;
384 AA
                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                     Created)
  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNAJ_1; 1.
                                                01-MAY-1999 (TEEMBLEEL 10, 01-MAY-1999 (TEEMBLEEL 12, 12, 12K10,3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||:||||
42 AYRRMALRY 50
```

THIS PAGE BLANK (USPTO)

us-08-653-294-36.rge

```
AF152405 Drosophila melanog
X99512 D.melanogaster PFTAI
AF152399 Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AC017966 8849 bp DNA HTG 09-DEC-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                     DMRNA3 1050 bp DNA INV 31-MAR-1992
Three Drosophila melanogaster genes for transfer RNAs (Glu specific).
V00238 J01146
V00238.1 GI:8458
transfer RNA; transfer RNA-Glu.
                                                                                                                                                                                                                                                fruit fly.

Drosophia melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;

Drosophilides; Drosophila.

I (Dases I to 1605)

Hosbach, H.A., Silberklang, M. and McCarthy, B.J.

Evolution of a D. melanogaster glutamate tRNA gene cluster

Gell 21 (1), 169-178 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 12
Gaps: 0
Percent Identity: 66.667

    1050
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
1. 1050

 3346
3526
3617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="FlyBase:FBgn0011851"
262. .333
/Gene="tRNA:E4:62Aa"
/note="tRNA Glu"
/hob_xref="FlyBase:FBgn0011851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref~"FlyBase:FBgn0011851"
190 c 213 g 323 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="trna:4:62Aa"
/note="transfer RNA:glu4:62Aa'
/allele=""
/db_xref="FlyBase:FBgn0011851"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
294.12
312.93
322.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         922 TACAGAAIGTCGAIGCAACGCATIGCTITACGITAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="tRNA:E4:62Aa"
/note="tRNA Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="tRNA:E4:62Aa"
/note="tRNA Glu"
                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
112.76
112.28
112.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC017966
AC017966.1 GI:6553224
HTG; HTG2_PHASE2.
fruit fly.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
 38.00
38.00
38.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 46.00.
Ratio: 3.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: DMRNA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-36 x DMRNA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_htg7:AC017966
                                                                                                               seq_documentation_block:
Locus DMRNA3
                                                                           seq_name: gb_in1:DMRNA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
 gb_in2:AF152405
gb_in1:DMPFTAIRE
gb_in2:AF152399
                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              trna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trna
                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1050 i V00238 Three Drosophila melanc 143914 i AC010564 Drosophila melanogast 143914 i AC010564 Drosophila melanogast 143914 i AC010564 Drosophila melanogast 268369 i AC010564 Drosophila melanogast 40245 i AC010564 Drosophila melanogast 1692 i AC0103710 Mycobacterium leprae close i AC01372 Homo sapiens clone 56237 i AC01372 Homo sapiens clone 56237 i AC01372 Drosophila melanogas 56414 i AL008967 Mycobacterium tubercul 15873 i AC013205 Drosophila melanogas 173970 i AC007352 Drosophila melanoga 183365 i AC007352 Drosophila melanoga 18326 i AC007352 Drosophila melanoga 173970 i AC002586 Drosophila melanoga 173970 i AC008289 Drosophila melanoga 17093 i AL033755 Homo sapiens chrome 226574 i AC033793 Caenorhabditis elegans 156243 i AC01145 Homo sapiens clone 226574 i AC033793 Caenorhabditis climan 1164 i AB009312 Escherichia coli 09 1164 i AB009313 Escherichia coli 09 1164 i AB009312 Escherichia coli 09 1164 i 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF15125 Linaria vulgaris cycl
AF152404 Drosophila melanogast
AF152404 Drosophila melanogast
AF152402 Drosophila melanogast
AF152405 Drosophila melanogast
AF152401 Drosophila melanogast
AF152401 Drosophila melanogast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E02902 DNA encoding octopus ri
                                                                                                                             Command line parameters:
-WODEL=frame+_p2n.model -DEV-x1p
-WODEL=frame+_p2n.model -DEV-x1p
-WODEL=frame+_p2n.model -DEV-x1p
-WODEL=frame+_p2n.model -DEV-x1p
-MODEL=frame+_p2n.model -DEV-x1p
-MODEL=frame+_p2n.model -DEV-x1p
-MODEL=frame+_p2n.model-10.00 -GAPEXT-4.000
-GAPEXT-4.000 -GAPET=0.000 -GAPEXT-0.000 -GAPEXT-4.000
-GAPEXT-7.000 -YGAPOP=10.000 -YGAPEXT-0.500 -BELOP-6.000
-DELEXT-7.000 -YGAPOP=10.000 -YGAPEXT-0.500 -BELOP-6.000
-DELEXT-7.000 -START-1 -MATRIX-blosum62 -TRANS-human40.cd1
-LIST-45 -DOCALIGN=200 -THR_SCORE-pct -ALIGN-15 -MODE-LOCAL
-OUTFMT-pfs -NORM-ext -MINLEN-0 -MAXLEN-1000000 -USER-US08653294
-NCPU-6 -ICPU-3 -NO_XLDXY -WAIT -THREADS-1
                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
   out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11164
11164
11164
11371
2428
2641
2755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EScore Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17.08
462.45
276.45
278.25
293.95
17.80
3.16+03
3.06+03
1.16+03
3.06+03
3.06+03
3.26+04
26+04
36+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.89
.3e+03
.1e+03
.2e+03
.5e+03
.1e+04
.1e+04
.4e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154.61
134.95
1009.23
1009.23
1103.19
1112.76
103.72
94.53
94.50
87.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.63
78.88
1113.74
1105.69
101.15
94.38
94.22
93.50
87.07
84.46
 OM of: US-08-653-294-36 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176.920000
                                       Date: Feb 8, 2000 10:25 PM
                                                                                                                                                                                                                                                                                                                                                                 Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strd
                                                                                                                                                                                                                                                                                                                                                                                   Query: US-08-653-294-36
Query length: 12
                                                                                                                                                                                                                                                                                                                                                                                                                         Database: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
9b_tn1:DMRNA3
9b_tn7:AC017966
9b_htq7:AC010564
9b_n12:AC005847
9b_a1:MLC82533
9b_ba1:U00017
9b_ba2:AF026541
9b_ba2:AF026545
9b_htq7:AC013772
9b_htq5:AC013772
9b_htq5:AC013772
9b_htq5:AC013205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_ba1:ECOPANBCD
gb_ba2:AE000122
gb_ba2:MSM238027
gb_htg4:AC012150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_bal:EC082K
gb_htg3:AC001349
gb_htg3:AC001145
gb_htg2:AC004555
gb_htg1:CEY49A3
gb_bal:AR003326
gb_bal:AR003326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_in2:AC005286
gb_htg2:AC007352
gb_htg2:HSDJ655C5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_bal:AB009320
gb_bal:AB009321
gb_bal:AB009322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_pl2:AF161252
gb_in2:AF152403
gb_in2:AF152404
gb_in2:AF152405
gb_in2:AF152405
gb_in2:AF152405
gb_in2:AF152401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_htg7:AC017383
gb_htg2:AC007417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_bal:MTCY427
gb_in1:CEC15H11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_ba1:AB009319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pat: E02902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            score_list:
```

```
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47499
49101
519372
519372
519372
51937
51937
51937
60133
60133
63495
64635
66835
66835
TITLE
JOURNAL
                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disapplication microbial arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Meptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 143914)

S Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Burkett, C., Burrows, J., Carter, M., Ding, Y., Domah-Rashid, N., Duyan-Rocha, S., Durbin, K. J., Ferraguto, D., Ding, Y., Domah-Rashid, N., Gorrell, J., Holloway, C., Haratz, P., Ganeah, R., Gorrell, J. H., Gorrell, J., Holloway, C., Haratz, F., Harnandez, J., Hodgson, A., Hogues, M., Holloway, C., Haratz, F., Harnandez, J., Hodgson, L., Jia, Y., Jones, M., Kelly, S., Kondejewski, N., Koyar, C., Leal, B., Liz, J., Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Lucter, R., Hartinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S., Nalson, A., Nguyen, S., Scharer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Scherer, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Scherer, S., Shah, E., Shen, H., Simon, M., Zhou, X., Nelson, D. and Gibbs, R., Weillignson, J., Weinstork, G., Weinstork, C., Wellson, D. and Gibbs, R., Milliamson, J., Wellson, J., Wellson, D. and Gibbs, R., Milliamson, J., Wellson, J., Menn, J., Mann, J., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AC010564 143914 bp DNA HTG 16-OCT-1999
DEFINITION Drosophila melanogaster chromosome 3L/62Al clone RPC198-2701, ***
SEQUENCING IN PROGRESS ***, 89 unordered pieces.
                                                                                                                                                 Addings, ....
Direct Submission
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10212817 by the submitter.
For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

Location/Qualifiers
   Sukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                  Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 1 (bases 1 to 8849)
Adams,M. and Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
1735 c 1884 g 2626 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 46.00 Length: 12
Ratio: 3.833 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 8849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC010564
AC010564.4 GI:5917942
HTG; HTGS_PHASE1.
fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 143914)
Worley, K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AC017966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-36 x AC017966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_htg4:AC010564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2604 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
```

```
Submitted (16-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Ruman Genetics, Baylor College of Medicine, One Baylor Plaza, Houstron, TX 77030, USA
60 Sep 22, 1999 this sequence version replaced gi:5916428
7 NOTE: This is a 'working draft' sequence. It currently
7 consists of 89 contigs. The true order of the pleces
7 is not known and their order in this sequence record is
8 arbitrary. Gaps between the contigs are represented as
8 runs of N, but the exact sizes of the gaps are unknown
8 This record will be updated with the finished sequence
8 as soon as it is available and the accession number will
8 be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                1220 bp in length
599 bp in length
613 bp in length
814 bp in length
819 bp in length
819 bp in length
819 bp in length
1056 bp in length
1185 bp in length
1185 bp in length
1185 bp in length
1185 bp in length
1186 bp in length
1111 bp in length
1111 bp in length
1111 bp in length
1112 bp in length
1122 bp in length
1122 bp in length
1133 bp in length
                                                                                                                                                                                      831 bp in length
874 bp in length
831 bp in length
831 bp in length
835 bp in length
1263 bp in length
844 bp in length
848 bp in length
840 bp in length
840 bp in length
875 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  848 bp in length
1450 bp in length
1036 bp in length
1572 bp in length
1572 bp in length
1271 bp in length
2074 bp in length
1977 bp in length
1977 bp in length
138 bp in length
1317 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 bp in 1
512 bp in 1
535 bp in 1
219 bp in 1
                                                                                                                                                                                                                                                                 contig
contig
contig
contig
                                                                                                                                                                                                                                                                                                                          contig
contig
contig
contig
                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
                                                                                                                                                                                                                                                                                                                                                                                                        conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                conti
                                                                                                                                                                                                                                                               5469:
6313:
7273:
8101:
8941:
10144:
11825:
13085:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21970:
                                                                                                                                                                                                                                                                                                                                                                                                                                     5972:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23026:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27681:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34092:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64634
65855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58815
                                                                                                                                                                                                                                                                                                                                                        10145
11020
11020
113086
13938
14753
15973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20392
21253
21971
23027
24542
25727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26571
27682
29231
30636
31758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34093
34929
35706
36892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41158
42006
43466
44891
45927
```

ო

Wed

```
Submitted (22-071-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley CA 94720, US Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.

Library locations: 11-34, 21-67, 44-36, 73-50, 92-76.
         Flanagan, J., Houston, K., Hummastl, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhano, R., Lead, L., and Rubin, G.M., Sequencing of Drosophila chromosome 3L, region 61F3-62A2

L. Unpublished (1997)

L. Opases 1 to 268369)

S. Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A.,
Blacej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Hummastl, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M. R., Woshrefi, M. W., Wan, R.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Shir, E., Twomey, B., Wan, K.H., Zhang, L.L., and Rubin, G.M., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ansp: ATP-dependent RNA helicase; ATP-phosphoribosyl transferase; ATPase; hisG 5-methyltetrahydrofolate-homocysteine methyl transferase; hisI L-asraragine permease; metH; mttB; phosphoribosyl-AMF cyclohydrolase; prcA; prcB; proteasome alpha subunit; proteasome beta subunit; protein translocation system;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 268369
                                                                                                                                                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/chromosome="3L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46162 TACAGAATGTCGATGCAACGCATTGCTTTACGTTAT 46127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: AC005847 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuAlaileArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS M.CB2533 40245 bp DNA
DEFINITION Mycobacterium leprae cosmid B2533.
VERSION AL035310 GI:4200258
                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="61F3-62A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-36 x AC005847/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_bal:MLCB2533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                TITLE
JOURNAL
                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Subclones in tet from Pl clones DS03179 (D226), DS06357 (D230), DS03404 (D231), DS06962 (D232), and DS07291 (D240)) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         557 others
                                       length
ength
                                                                length
length
length
                           ength.
                                                                                                                     ength
                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 66.667
                                       444444444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33523 c 32072 g 39042 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 143914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                        1981
2425
3011
2090
2807
                                                                                                                                                                                                                                                                          2799
                                                                                                                                                                                                                                                                                                                               contig of
                                                                                                                                                                                                                                                                                                                                                        contig of
                                                                                                                                                                                                                                                                                                                                                                    contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                    /chromosome="3L/62A1"
/clone="RPC198-2701"
                                                                                                                                                                                                                                                                                                     contig of
                                                                                                                                                                                                                                                                                                                   contig of
                                                                                                                                                                                                                                                                                                                                             contig of
                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref-"taxon:7227
contig
contig
contig
contig
contig
contig
contig
contig
contig
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                           contig
                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                  contig
                                                                                                                    contig
                                                                                                                                 contig
                                                                                                                                                                     contig
                                                                                                                                                                                  contig
                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                               contig
                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
                                    75834:
78389:
80840:
                                                                           82111:
84052:
86110:
87488:
89108:
                                                                                                                                                                                97095:
                                                                                                                                                                                                                                                                                                                                                                       43914:
                                                                                                                                                                      95337:
                                                                                                                                                                                                                                                                                                    21885:
                                                                                                                                                                                                                                                                           115204:
                                                                                                                                                                                                                         104497
                                                                                                                                                        9290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 3.833
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AC010564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-36 x AC010564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_in2:AC005847
                                                                                                               86111
81489
81489
81489
91488
91488
91488
91488
9111240
9111818
9111818
9111818
9111818
9111818
9111818
9111818
                       72324
73760
75835
78390
80841
82112
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ಹ
                                                                                                                                                                                                                                                                                                                                                                  137893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               38720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
```

27-AUG-1999

BCT

SOURCE

```
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.

Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. All CDS over 100 codons have been analysed. Gene prediction is based on positional base preference in codons especially where there is an increase in the observed/expected third position of + C GAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.

IMPORTANT This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence over lapping sections once, or longer, because we arrange for a
                                                                                                                                                                                                                                     Eiglmeier, K., Honore, N., Woods, S.A., Caudron, B. and Cole, S.T. Use of an ordered cosmid library to deduce the genomic organization of Mycobacterium leprae.

Mol. Microbiol. 7 (2), 197-206 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"MLCB2533.01c, ansP, probable L-asparagine permease, partial CDS, len: >366 aa; highly similar to many
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Details of M. leprae sequencing at the Sanger Centre are available on the World Wide Web.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The New York Community Trust.
Work in Paris is supported by the Heiser Trust, the Association
Francaise Raoul Follereau and the Groupement de Recherches et des
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the Sanger Centre is funded to complete the sequence of M. leprae
by the Heiser Program for Research in Leprosy and Tuberculosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (URL, http://www.sanger.ac.uk/Projects/)
CDS are numbered using the following system eg MLCB33.01c. ML (M.
leprae), CB33 (cosmid name), .01 (first CDS), c (complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note-"overlap with EMBL:ML017 cosmid B2126 from 1 to 31682. There are 16 conflicts between this sequence and ours. In each case our sequence has been checked and is thought to be correct" complement(<1. .1099)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (26-JAN-1998) Mycobacterium leprae sequencing project, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA E-mail: barrell@sanger.ac.uk Cosmids supplied by Dr. Stewart T. Cole, [3] Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France Requests for cosmids should be sent to Karin Eiglmeier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases I to 40245)
James, K. D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
                                                                                                        Sacteria; Firmicutes: Actinobacteria; Actinobacteridae;
                                                                                                                                        Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            small overlap between neighbouring submissions.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mycobacterium leprae"
pseudogene; RLEP; sec-independent.
Mycobacterium leprae.
Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="cosmid B2533"
complement(1. 1099)
/gene="ansp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:1769'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Etudes des Genomes (GIP-GREG)
                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 40245)
Hamlin, N. and Churcher, C.M.
                                                                                                                                                                                                            (bases 1 to 40245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .40245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kei@pasteur.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                     93188700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          strand).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                    ORGANISM
                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                          JOURNAL
MEDLINE
                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
```

COMMENT

```
Countereactions of the state of
                                     S.typhimurium AnsP. Lasparagine permease (L-asparagine transport protein) (497 aa), fasta scores; opt; 1508 2-score: 1696.8 E(): 0, 61.2% identity in 366 aa overlap. Equivalent to M.tuberculosis Rv2127, ansP (MYCZ561.26, M.tuberculosis permease Rv0346c, aroP2 (MYCZ1810.06c, 75.1% identity in 345 aa overlap). Also similar to Membrane protein, contains PS00218 Amino acid permeases signature. Pfam match to entry PF00324 aa_permeases aginature. Pfam match to entry PF00324 aa_permeases, amino acid permease. Annotated as ORF TR:049801, designated arop2 in M.leprae cosmid EMBL:000017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation-"MaTLAESPEPKSGASRAGVLGEEBGYHKGLKPRQLQMIGIGGAI
GTGLFLGAGGRLARAGPGLFLVYAVCGVFVFLLILRALGELVLHFPSSGSFVSYAREFF
GRAAYVGWLYFLDWAATAIVDTTAIATYTHRWTIFTALPQWTLALLALAVULWML
ISVEWFGELEFWAALIVOXALMAFLVVGTIFFLGGRYPVDGHNTGLSLWTSHGGLFPTG
VAPLIVVSSGVWFAYAAVELVGTAAGFTVEPKKIMPRAINSVIARIAIFYVGSVILLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISVEWFGELEFWAALIKVCALMAFLVVGTIFLGGRYPVDGHNTGLSLWTSHGGLFPTG
VAQLIVVSSGVWFAYAAVELVGTAAGETVEPKKIMPRAINSVIARIAIFYVGSVILLA
LLLPYSAFKASESPFVTFFSKVGFYGAGDLMNIVVLTAALSSLNAGLYATGRVWHSIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLLPYSAFKASESPFVTFFSKVGFYGAGDLMNIVVLTAALSSLNAGLYATGRVMHSIA
INGSGPKFTARMSKNGVPYGGILLAAVICLCGVALNAFNPGQAFEIVLSVAALGIIAG
WGTIVLCQLRLHKMAKAGIMRRPRFRMPLAPYSGYLTLAFLFAVLVVMAFDKPIGTWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGLFLGAGGRLAKAGPGLFLVYAVCGVFVFLILRALGELVLHRPSSGSFVSYAREFF
GEKAAYVVGWLYFLDWAMTAIVDTTAIATYLHRWTIFTALPQWTLALLALAVVLVMNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MATLAESPEPKSGASRAGVLGEEAGYHKGLKPRQLQMIGIGGAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VASLIVIVPALIAGWYSIRKRVMTIARERMGYTGPFPAIANPPVQPSERSHSQNP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Pfam match to entry PF00324 aa_permeases, Amino acid permease, score 245.80, E-value 6e-70"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1354. .2691)
/gene="ansP2"
/note="Ffam match to entry PF00324 aa_permeases, Amino
acid permease, score 501.80, E-value 5.1e-147"
amino-acid permeases e.g. ANSP_SALTY (EMBL:U04851)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="PS00218 Amino acid permeases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="putative L-asparagine permease"
/protein_id="CAA22915.1"
/db_xref="GI:4200259"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="putative L-asparagine permease"
/protein_id="CAA22916.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="1168 bp perfect direct repeat"
complement(2. .991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="conflict: T is TG EMBL:ML017"
complement(1249. .2766)
/gene="ansP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INGSGPKFTARMSKNGVPYGGILLAAVICLCG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="ambiguous base T /G" complement(833. .925)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1249. .2766)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:4200260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="ansP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="ansP'
```

Wed Feb

```
/protein_id="AAA17190.1"

Abaxef="-61:467005"

/translation="MOSISSPHWVLVVVVVVLLFGAKKLPDAARSLGKSMRIFKSELR
EMQTENQAQASALETPMQNPTVVQSQRVVPPWSTEQDHTEARPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAPFDOFMLRIKVGNAAGIVLASPVNFYQLARFITPGLYTKERFTVAFVVPAAVLFA
GGTVLAYLVLSKALGFLLIVGSGVOVTALSGDRYFGFLNLLVVFGVSFEFPLLIVML
NIAGLLTYQRLKSWRRGLIFAMFVFAAVFTPGSDPFSMTALGAALTVLLELAIQLVRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MATSKVERLVNLVIALLSTRGYMTAEKIRSSVAGYSDSPTVEAF
SRMFERDKNELRDLGIPLEVGKVSALDPSEGYRINRDAYALPPVELTPDEAAAVAVAT
QLWESQELITATQGALLKLRAAGVDIDPLDTPVVIASSSGVSSLRGSEDFLSILLSAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="mngcravvracdllkrikQhyrrsrtnpdatmslidhltElrtr
LLISLAAIVVTTIFGFIWYSHSIFGLESLGEWLRRPYCSLPQSARADISPDGQCRLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MSWIFEYYPMRQAHELPDGSFQAVMTYASDAWMTRLVLGFGSAV
QVQAPEALAYRVRNAAVAALESYQVTAQA"
complement(1701. .2444)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /traislation="MYOLSTRLVRLLNMVPYFOANPRITRAEAAADLGVSAKQLDQDF
NQLWVCGLPGYGPGDLIDFEFSGDTIEVTFSAGIDRPLQLTSPEAIGLLVALRALANI
PGVVDPEAVRSAIAKIEAAAVVMGNEAFGSVASVDTRFFSESHAVAAVRAAVRIKQAL
VIDYYSASHPTLTSRIVDPIRVLLVGDHSYLEAWSREAEGVRLFRFDRIVVARELDEP
AAAPEYVRRCQTHRSSMTTRCCRRRRCG"
complement(2441. .3436)
                                                                                                                                                        Submitted (01-NOV-1993) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
3 (bases 1 to 42157)
                                                                                                                                                                                                                                                                                        Submitted (01-MAR-1994) Department of Genetics, Harvard Medical School, 200 Longwood Avenue, Boston MA 02115
On Mar 31, 1994 this sequence version replaced gi:414223.
This sequence data was produced by the Genome Sequencing Center located at Collaborative Research Incorporated (1365 Main St., Waltham MA, 02159).

(Smith@cr.cric.com). The annotation should be considered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preliminary and incomplete.

Location/Qualifiers
1. 42157
Corganism="Mycobacterium leprae"
/db_xref="taxon:1769"
complement(133. 1086)
/note="match to yigu and yigv E.coli; B2126_C1_183"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"match to yigT E.coli; B2126_C1_182"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HDKRRVKHEALIADDEASVIEPPSSIPERSYTATRSHDDVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"B2126_C1_181"
/protein_id-"AAA17189.1"
/db_xref-"G1:467004"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"B2126_C2_220"
/protein_id-"AAA17199.1"
/db_xref-"G1:467014"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA17191.1"
/db_xref="G1:467006"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="B2126_C3_266"
/protein_id="AAA17208.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1471. .1692)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(1132. .1398)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"u2126a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/transl_table=11
/product="u2126b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                     2 (bases 1 to 42157)
Robison, K.
  1 to 42157)
                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                     Direct Submission
                                                       Unpublished
     1 (Dases
Smith, D.R.
                                                                                                                                                                                                                                         Robison, K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                 complement(2903..3856)
/gene="MLCB2533.03c", hypothetical protein, len: 317 aa;
/gene="MLCB2533.03c", hypothetical protein, len: 317 aa;
/note="MLCB2533.03c, hypothetical protein Rv2125
similar to M.tuberculosis hypothetical protein Rv2125
(MTCV261.21) (EMBL:207559) (292 aa), fasta scores; opt:
1648 2-score: 2382.2 E(): 0, 84.1% identity in 290 aa
overlap. Also some similarity to M.leprae hypothetical
protein TR:Q49847 (29.7% identity in 279 aa overlap).
Annotated as OMF TR:Q4977, hypothetical protein in
M.leprae cosmid EMBL:U00017"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="STREMBL:049797"
Atanslation="MPPHRAYTRHASSALKPYADSVTLRDGGPDRGALPELHNTVVV
AAFEGWNDASDAASGALEHLANVWEADPIVEIDDEAYYDYGVNRPVIRQUGGFRELY
WPAMRISYCRPPGSDRNVVLMHGVEPNWRWRTFCTELLIIADRLNVDTVVILGALLAD
HTRRVPVSGAAYSPESARRRGLEERTREGFGIAGVFGDACVAARIPAVWFRAAVP
HYSHPPNPKATVALLRRVEDVLDVBYPLADLPTQAEDWEGAITEIAAEDDELAGEYVH
SLEGRGDAEVDVDALGKIDGDALAAEFERYLRRRRPGFGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MLCB533.04, metH, probable 5-methyltetrahydrofolate-homocysteine methyltransferase, 5-methyltetrahydrofolate-homocysteine methyltransferase, 1en: 1183 aa; similar to many members of vitamin-Bl2 dependent methionine synthase family e.g. METH_BCOLI (EMBL:X16584) E.coli metH (1226 aa), fasta scores; opt: 1617 z-score: 1000.7 E(): 0, 31.6% identity in 1228 aa overlap. Equivalent to M. tuberculosis Rv2124c (MTCY261:20c, 88.7% identity in 1183 aa overlap). Annotated as METH_MYCLE, designated metHZ in M.leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium leprae.
Mycobacterium leprae
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium.
                                                                                                                                                                                 /note-"PS00218 Amino acid permeases signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product="hypothetical protein MLCB2533.03c"
/protein_id="CAA22917.1"
/db_xref="G1:4200261"
                                                                                                      /note="conflict: C is CT in EMBL:ML017" complement(2500. .2592)
1668. .2835
/note="1168 bp perfect direct repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17534 TATCGATTGGCAAGTCGCAGAATATCTGCACGGTAT 17569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuAlaileArgArglleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 40245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U00017 42157 bp DNA
Mycobacterium leprae cosmid B2126.
U00017
                                                                                                                                                                                                                complement(2903. .3856)
/gene="MLCB2533.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                             'gene="ansP2'
                                                                                                                                                           /gene="ansP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4004. .7555
/gene="metH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4004. .7555
/gene-"metH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U00017.1 GI:466994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.00
4.400
83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: MLCB2533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-36 x MLCB2533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS U00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_ba1:U00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                    misc_feature
                                                                                                                                  misc_feature
  repeat_unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
ORGANISM
                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
```

CDS

```
/translation="miksepdrlptnlafpgisvingssfydllrrqapellpvyslgg
GQSGGGQQLSHGTTIVVLKYPGGVVIAGDRRSTQGNMIAGRDVRKVYITDDYTATGIA
GIAAVAVEFARLYAVELEHYEKLEGYPLTFAGKVNRLAIMYRSNLTAAMQGLLALPLL
AGYDIAHDPDQSAGRIVSFDAAGGWNIEEEGYQSVGSGSIFAKSSIKKLYSQVSDDS
ALRVAIEALYDAADDDSATGGPDLVRGIYPTAVTIGAEGAAEVTESRIAELAREIIES
RSRAYTLGSFGGSEK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="B2126_c2_217"
/protein_id="AAA17197.1"
/brotein_id="1467012"
/bc.xref="61:467012"
/translation="MSFKKVFNDVIRDSVLGRFEPHRFTACITDLALSAVNLDWALPI
AAEFEDEELVRRLSGFGHERRSFLSHRLAPHRLPARIITIHENRRRERAAVFR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MSFPYFISPEQAMREQRELARKGIARGRSVVALAYAGGVLFVAE
MPSHSLQKYSELYDRYGFAAAGKFWEFDNLERGGIOFADTRGYXDDRFDVYGRQLAN
YAQTLGTIFTEQAKPYEVELCVAEVAHYGETKPPELYRITYDGSINDEPHFWWGGTT
ESIANALKESYAENASLTDALGIAVAALRAGSADAAGSDQFTLGYASLEVAVLDANRP
RRAFRRIIGSGLEALLREKDSKGSKGAQNPKGARDSKNSKSYGESTD"
                            VAPIGPAGAVTVPDGVDLRRIVSDAVAEVSTGATARVWVVDGRATALRHAGRFAGVRR
LGGRDGQVIELDIGSIDRLARDIAGHGADAVVLEPDALRDDVLIRLRAHAGTGPS"
complement(3443. .3841)
                                                                                                                                                                                                                                                                                                            /translation="MDTEIDWVIKRKLFQRYODRDNMELTDFKIAQLDLAYHDIKRGR
CYDDLOKRGILARNYTDEDIADAVNHEPQTFRARLRGEFISAAQAAGRDFTVDWVHL
KLNDQAQRTVLCKDFRAVDERVKRLIASM"
complement(3861. .4871)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDVLLPFLVTRQLICGAGKVLQTPKAATFCLSQRAEHIWEGVSSATTRSRPIINTRDE
PHADAEKYRRLHVIVGDSNMCETTMLKVGTAALMLEMVETGVPFRDFSLDNPIRAIR
EVSHDITGRRPVRLAGGRQASALDIQREYYTRAFEHLQTREPNVQFEQVVDLWGPSAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MKIADANVLLYSGNTSSEHTGHPCAGSTVRLSCADRIGFGWVPL
LVFVRPATKMGLVLRTMSSEDAIGQVADWLTGPSAVLMCLTVRHAAFLVKILV"
complement(6822. .7115)
GSRQAVQFPYRPSRAEPYTMRNVEPWGVITENSCWYLVGHDCDRNATRTFRLSRIGSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRLSPDEVARYLFRRVVSWGRSSNVFLRNGARLYLDVQSHPEYATAECDNLVQLVTHD
RAGEWVLEDLLVDAEQRLADEG1GGD1YLFKNNTDSAGNSYGCHENYL1VRAGEFSR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation-"MORIIGTEVEYGISSPSDPTANPILTSTQAVLAYAAAAGIQRVK
RTRWDYEVESPLRDARGFDLSRSAGPPPVVDADEVGAANMILTNGARLYVDHAHPEYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MVGWYPWAWLAHRDAQTTSTLKDVQRRIMGIETEFGVTCTFHGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="proteasome, beta subunit; B2126_C1_173"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
/product="B2126_C3_261"
/protein_id="AAA17266.1"
/db_xref="G1:467021"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="B2126_C2_219"
/protein_id="AAA17198.1"
/db_xref="G1:467013"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product-"B2126_C3_260"
/protein_id-"AAA17205.1"
/db_xref-"G1:467020"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"B2126_C1_172"
/protein_id-"AAA17187.1"
/db_xref-"G1:467002"
                                                                                                                                                                                                   /product-"B2126_C3_265"
/protein_id-"AAA17207.1"
/db_xref-"G1:467022"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAA17188.1"
/db_xref="GI:467003"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(9142. .10686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(6569. .6862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(7253. .8050)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(8047. .8922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /transl_table=11
                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
```

CDS

```
/product="12126_C1_169"
/product="12126_C1_169"
/protein_id="AAA17186.1"
/db_xxef="01:467001"
/tb_xxef="01:467001"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"B2126_C3_259"
/protein_id-"AAA17204.1"
/bc.xref-"G1:467019.
/translation-"AAVGDDDRHSAGLLSSIDRHDWGWLQPQSSPAASTVQPLPASR
IPKTSFKPYHVPMLGSRGKASSSLTLAALVQAALDPVKQNCTRSRVLFGT"
                                MSRQTPFSAIIAGLTPFLVSRQVVTGSGRVGIGPAGDEPGFQLSQRSDVIEVEVGLET
TLKRGIINTRDEPHADADRYRRLHVIVGDANLAETSTYLKLGTTALVLDLIEEGPVHG
IDLTDLTLARPVHAVHAISRDASLRATVTLVDGRELTGLALQRIYLDRVAKLVDSRDP
DPRAADVVKTWVHVLDQLERDPMDCAELLDWPAKLRLLEGFRQRENLMWSAPRLHLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MVAVTTATIYICISCEVAITKTTLRRSALVSAALGEASSIAATG
SVRGPAFRSSYGSSTVDFIVGLTRFDGGGEDTGAFAVPVRKIIASHSAP"
14353. .14763
apectdpldaviwdkagervmeaarhvasvpgaaklolyknnvdgkgasygahenyl
                                                                                                                                                                                                                LQYSDVRLDKGLYNRLVARGSMKRLVNEHQVLRAVNNPPTDTRAYFRGECLRRFSADI
                                                                                                                                                                                                                                                                  aaaswdsvifdlggdslvriptleplrgskahvgalldsvdsaaelveqlttrpvdpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MVIVKSERVADLLSSVLVVARNTDLGYQRFGIRAGMGDAHDTVT
PSDSRCPGGPNPPVVLLTTLVVFNTYVWIVATTLIREHYGWR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-OCT-1998
complete cds; and CeoC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteriae;
Actinomycetales; Corynebacterinee; Mycobacteriacee;
Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis CeoB (ceoB) gene, (ceoC) gene, partial cds.
AF026541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 42157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuAlalleArgArglleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: U00017 from: 1
                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="RLEP"
complement(11986. .12465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/product="B2126_F1_17"
/proteln_id="AAA17209.1"
/db_xref="GI:467024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(13640. .13921)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="B2126_C3_258"
/protein_id="AAA17203.1"
/db_xref="G1:467018"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13405. .13665
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF026541.1 GI:2582553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44.00
4.400
83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-36 x U00017/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_ba2:AF026541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF026541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
```

AUTHORS TITLE

REFERENCE

MEDLINE REFERENCE

JOURNAL

AUTHORS JOURNAL

TITLE

source

FEATURES

gene

CDS

```
Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.

CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gt, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="hypothetical protein Rv2680"
/protein_id="cAB09496.1"
/db_xref="di:3261796.1"
/db_xref="di:32617917"
/db_xref="sPrEMBL:086317"
/translation="MTSAGDDAERSDEEERRITSAEFALFREAVAANNAVTVRPEIEL
VARYQADLDSSEANDPLIPPENASHIVDALTRRIDOWRALGGTVTATTSVRYGDISGP
PRAHQLELRASWITATTPDLGAHVQAFCDVLEHAAGLPPAGVTDLGSRSRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
tuberculosis sequencing and mapping teams. Sanger Centre, Wellcome
Trust Genome Campus, Hinxton, Cambridge CB10 15A Unite de Genetique
Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux,
75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
On Jun 27, 1998 this sequence version replaced gi:2181970.
                                                                                                                                                            Cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Harris, D., Gordon, S.V., Eiglmeier, R., Gas, S., Barry III, C.E.,
Fekale, F., Badocock, K., Basham, D., Erown, D., Chillingworth, T.,
Connor, R., Davies, R., Feltwell, T., Gentles, S.,
Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Barrell, B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="Rv2680"
102. .734
/gene="Rv2680"
/note="Rv2680, (MTV010.04), len: 210. Unknown but very
similar to M. leprae protein U1764v. FASTA scores;
sptr|Q50005|Q50005 U1764v (213 aa) opt: 1136 z-score:
12311 E(): 0;83.9% identity in 193 aa overlap. TBparse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="fragment designated v010. Does not represent a
                                                                                                                                                                                                                                                                                                                                                                                                                               Deciphering the biology of Mycobacterium tuberculosis from the
                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Erratum:[[published erratum appears in Nature 1998 Nov 12:396(6707):190]]
2 (bases 1 to 38631)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .38631 /organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome sequence
Nature 393 (6685), 537-544 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref-"taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
     Mycobacterium tuberculosis. Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physical clone"
102. .734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="H37Rv"
                                                                                                                                       (bases 1 to 38631)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       initiation codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Notes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
  SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
                                                                                                                                             REFERENCE
                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAC69359.1"
/db_xref="G1:2582554"
/translation="MRVVVMGCGRVGASVADGLSRIGHEVAIIDRDSAAFNRLSPQFA
GERVLGQGERDVLLRAGIQGAFAAVSSGDNSNIISARLARETFGVPRVVARIYDA
KRAEVYERLGIPTITYPWTTORLLNALMQDTETAKWRDPTGYVANAEVVLHEDWYGH
RATDLEQATGARIAFLIRFGTGVLPEPKTVLQAGDKVYIAAISGRAAEAAAIAALPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC69360.1"
Ab_xref="-G1:288255"
/translation="kvVVAVAGAQAVGRSVTRELVENGHDITLIERNPDHLDAAAIPEA
HWRLGDACELSLLESIHLEEFDVVVAATGDDKVNVVLSLLAKTEFAVPRVVARVNDPR
                                                                                                                                                                                                                                              Submitted (23-55P-1997) Molecular Microbiology and Immunology,
Johns Hopkins University, 615 N. Wolfe Street, Baltimore, MD 21205,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS MTCYO5A6 38631 bp DNA BCT 17-JUN-1998
DEFINITION Mycobacterium tuberculosis H37Rv complete genome; segment 120/162.
ACCESSION 296072.1 GI:3261793
1 (bases 1 to 1692)
Chen, P. and Bishai, W.R.
Novel selection for isoniazid (INH) resistance genes supports a role for NAD+-binding proteins in mycobacterial INH resistance Infect. Immun. 66 (11), 5099-5106 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="TrkA homolog; complements the INH-sensitive phenotype of oxyR deletion mutant of E. col1" /codon_start=1 /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="TrkA homolog; complements the INH-sensitive phenotype of oxyR deletion mutant of E. coli"

    1692
/organism-"Mycobacterium tuberculosis"
/strain-"H37Rv"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'product~"CeoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="CeoC"
                                                                                                                                                                 2 (bases 1 to 1692)
Chen, P. and Bishai, W.R.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 681. .1364
/gene="ceob"
681. .1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1361. .>1692
/gene="ceoC"
1361. .>1692
/gene="ceoC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="ceoB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               544 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDFESGARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NEWLFNDA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: AF026541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-36 x AF026541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_bal:MTCY05A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
```

gene

CDS

BASE COUNT

sed\_name:

σ

Wed Feb

source

gene

CDS

```
4611. 5900

/gene="arsA"
/gene="arsA"
/gene="arsA"
/gene="arsA"
/note="Rv2684, (MTCY05A6.05), len: 429. Function: arsA,
corresponds to antigen 45 of M. leprae, a transmenbrane
protein related to arsenical pumps. FASTA best: Ad45_MYCLE
P46838 46 kd membrane protein (429 aa) opt: 2060; E(): 0;
MTCY05A6.06, (428 aa) E(): 0; 76.6% identity in 427 aa
overlap. TBparse score is 0.891"
                       /translation-*mkvnidptaptfatyrrdmraegmaedypvysidsdaldaarmi
AEHRLPGLLVTAGAGKQYAVLPASGVVRFIVPRYVQDDPLLAGVLNESTADRCAERLS
GKKVRDVLPDHLVEVPPANADDTIIEVAAVMARLRSPLLAVVKDGSLLGVVTASRLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jobber RAZ685, (MTCYO5A6.06), len: 428. arsB, Function: windrown membrane procein very similar to M. leprae antigen 45(P468B) MTCYO5A6.05; related to arsenical pumps. FASTA best: AG45_MYCLE P46838 46 kd membrane protein (429 and opt: 2041; E(): 0; 74,08 identity in 427 as overlap. Highlysimilar to MTCYO5A6.05; E(): 0; 76.6% identity in 427 as overlap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AC013772 142796 bp DNA HTG 09-DEC-1999
DEFINITION Homo sapiens clone RP11-7024, WORKING DRAFT SEQUENCE, 6 unordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5968. .5973
/note="possible RBS, GGAGGA, for Rv2685"
5980. .7266
/qene="arsB"
5980. .7266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SAPISFWEFTRKGAVVTAVSIALAAIYLWLRYFVLLH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 12
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 38631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="CAB09495.1"
/db_xref="G1:2181975"
/db_xref="SPTREMBL:007186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB09476.1"
/db_xref="G1:2181976"
/db_xref="SPTREMBL:007187"
_xref-"SPTREMBL:007185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC013772
AC013772.2 GI:6553994
HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/product="arsA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="arsB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5980. .7266
/gene="arsB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: MTCY05A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-36 x MTCY05A6
                                                                                                             AALKT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_htg7:AC013772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jobes TRY2682c, (MTCY05A6.03c), len: 638. dxs, PROBABLE 1-DEOXYXXLULOSE-5-PHOSPHATE SYNTHASE (DXP SYNTHASE) unknown but highly similar to M. Leprae (669189 TRTB, similar to transketolases (EC 2.21.1). FASTA best: 6699189 TRTB. opt: 3635; E(): 0; 86.4% identity in 632 aa overlap. Now known as Spl007184/DAS_MYCTU PROBABLE 1-DEOXXXXLUCOSE-5-PHOSPHA (638aa) opt: 4214 z-score: 4949.7 E(): 0; 100.0% identity in 638 aa overlap. Similar (ARV3779CMTV004.37c). TBparse score is 0.888"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="Sprendl:007183"
//translation="MCPEPSHAGAAESEGTESEPTPLLRPAGGIPDLCVTVGEIAAAA
//translation="MCPEPSHAGAAESEGTESEPTPLLRPAGGIPDLCVTVGEIAAAA
LLDRGRGFRYDAERASGFRYSGRAYLIOIRRAAGTVLDPVSHGGDPLTVTLAPVA
EVLSTNEWILHSADQDLPCLAEVGMRPPALVDTELAGRLAGFDRVNLAAMVERLLGLG
LTKGHGAADWSKRPDESAWLNYAALDVELLIELRAALSRVLARQGKTDWAADFEEHLR
SFESRPPPAAARQDRWRRTSGIHKVHDRRGLAAVRWAALAARESPDPPEIAFPRILPD
SAIIDAALDADKSVDDLVALPVFGGRRQRRSAVWAALAAARESPDPPEIAFBRNGP
PPPGRWVRRRPAAAARLDAARAALTEVSGRRQRRSPRVPTENLVSPDLVRRLCWEWEDISGSS
PDPIAAVEAYLRTGGARAQUELVVPLITAALTGAPDAGAQGDDGS"
complement (2049. . 3965)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="cab09493.1"
/db_xref="G1:2181973"
/db_xref="SWISS-PROT:007184"
/translation="MLQIRGFADLOHLSOAOLRELAAEIREFLIHKVAATGGHLGPN
LGVVELTLALHRVFDSPHDPIIFDTGHQAXVHKMLTGRSODFATLRKKGGLSGYPSRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESEHDWVESSHASAALSTADGLAKAFELTGHRNRHVVAVVGDGALTGGMCWEALNNIA
ASRREVIIVVNDNGRSYAPTIGGVADHLATLKLQPAYEQALETGRDLVRAVELVGGLW
FRFLHSVKAGIKDSLSPQLFTDLGLKYVGPVDGHDERAVEVALRSARRFGAPVIVHV
VTRKGMGYPPARADDADARGMUSTVPIDPATGQATKVAGPGWTATFSDALIGYAGKRRDI
VAITAAMPGPTGLTAFGQRFPDRLFDVGIAEQHAMTSAAGLAMGGLHPVVAIYSTFLN
                                                                                                                                                                                                                                                /note-"Rv2681, (MTCY05A6.02), len: 438. Function: unknown but very similar to hypothetical M. leprae protein U17640. EASTA best: G699161 U17640 (429 aa) pot: 2146; E(): 0; 77.4% identity in 416 aa overlap. TBparse score is 0.915"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAFDQIMMDVALHKLPVĪMVLDRAGITGSDGASHNGMMDLSMLGIVPGIRVAAPRDAT
RLREELGEALDVDDGPTALRFPKGDVGEDISALERRGGVDVLAAPADGLNHDVLLVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAFAPMALAVAKRLHNOGIGVTVIDPRNVLPVSDGVRETAVOHKLLVTLEDNGVNGGA
GSAVSAALRRAEIDVPCRDVGLPQEFYEHASRSEVLADLGLTDQDVARRITGWVAALG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4109. .4606
/gene="Rv2683, (MTCY05A6.04), len: 165. Function: unknown
hout highly similar to M. leprae protein U1764Q. FASTA
best:G699165 U1764Q (184 aa) opt: 750; E(): 0, 73.8%
identityin 164 aa overlap. TBparse score is 0.926"
                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical protein Rv2681"
/protein_id-"CAB09492.1"
/db_xref-"GI:2181972"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"hypothetical protein Rv2683"
/protein_id-"CAB09494.1"
/db_xref-"GI:2181974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4099. .4102
/note="possible RBS, GGAG, for Rv2683"
4109. .4606
                          'organism="Mycobacterium tuberculosis"
'strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(2049. .3965)
                                                                                /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  table=11
                                                                                                                                                                                              736. .2052
/gene="Rv2681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="Rv2683"
4109. .4606
                                                                                                       'clone="Y05A6"
                                                                                                                                  736. .2052
/gene="Rv2681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"dxs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGVCASDAIPEHLD"
                                                                                                                                                                                                                                                                                                                                                                 /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="dxs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="dxs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trans]
```

gene

CDS

gene

RBS

us-08-653-294-36.rge

```
AC013205 56237 bp DNA HTG 03-NOV-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCUS MTV002 56414 bp DNA BCT 17-JUN-1998.
DEFINITION Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was identified as CDM:10214117 by the submitter. For further information on this sequence you may e-mail to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fruit fly.

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 56237)

Adams, M. and Venter, J.C.

Direct Submission

Submitted (03-NOV-1999) Celera Genomics, 45 West Gude Drive,

Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NoTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
                                   /clone_lib="RPCI-11 Human Male BAC"
47989 a 24580 c 24540 g 45686 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 142796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
| 12291 c 11944 g 15645 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 11
Gaps: 0
Percent Identity: 72.727
                                                                                                                                                                                                                                        Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: AC013772 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrargleualaileargargilealaleuargTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AC013205 from: 1 to: 56237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ArgleuAlaileArgArgileAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
       /clone="RP11-7024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pieces.
AC013205
AC013205.1 GI:6223127
HTG: HTGS_PHASE2.
fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS MTV002 56414 bp
                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-36 x AC013772/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56237 bp
                                                                                                                                                                                                                                                                            4.200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-36 x AC013205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fly@celera.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_htg5:AC013205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AC013205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_bal:MTV002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16357 a
                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                          UpDublished

Saldwin, J., Barna, N., Backerly, R., Boguslawkiky, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslawkiky, L., Boukhgalter, B.,

Baldwin, J., Barna, N., Beckerly, R., Boguslawkiky, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., Fitzhqy, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Heaford, A.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKeran, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Fersfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Nyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Submitted (15-NOV-1999) Whitehead Institute/MIT Center for Genome Submitssion

Submitted (15-NOV-1999) Whitehead Institute and St. (16425750.

All repeats were identified using RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Center Genome Center.

Center: Whitehead Institute/ MIT Center for Genome Research

Center: Whitehead Institute/ MIT Center for Genome Center
                                   Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142796)
Birren, B. Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-7024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
Web Site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project name: L2959
Center clone name: 7_0_24
Center clone name: 7_0_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2142: contig of 2142 bp in length gap of unknown length 4834: contig of 2692 bp in length gap of unknown length 9211: contig of 4377 bp in length gap of unknown length 25157: contig of 15946 bp in length gap of unknown length gap of unknown length 66208: contig of 41051 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers 16588 bp in length.

    142796
    rorganism="Homo sapiens"
/db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66208:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                   ORGANISM
                                                                                                                                    REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
SOURCE
```

```
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed(expected third position G + C. CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gt, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon. If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge EBID 15A Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                       Cole,S.T., Brosch,R.,
Harris,D., Gordon,S.V., Eiglmeler,K., Gas,S., Barry III,C.E.,
Harris,D., Gordon,S.V., Eiglmeler,K., Gas,S., Barry III,C.E.,
Harris,D., Gordon,S.V., Basham,D., Ehrliningworth,T.,
Connor,R., Davies,R., Devlin,K., Feltwell,T., Gentles,S.,
Hamlin,N., Holroyd,S., Hornsby,T., Jagels,K., Krogh,A., McLean,J.,
Moule,S., Murphy,L., Oliver,S., Osborne,J., Quail,M.A.,
Rajandraem,M.A., Rogers,J., Rutter,S., Seeger,R., Skelton,S.,
Squares,S., Sqares,R., Sulston,J.E., Taylor,K., Whitehead,S. and
Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Rv2736c, (MTV002.01c), len: 174 aa. recx, similar to eg. RECX_PSEAE P37860 regulatory protein recx from Pseudomonas aeruginosa (153 aa), fasta scores; opt: 161 z-score: 257.2 E(): 3.6e-07, 30.7% identity in 137 aa overlap. Overlaps and extends CDS from ovelapping cosmid MTCX154.16c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <1. .>56414
/note="fragment designated v002. Does not represent a
physical clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jun 27, 1998 this sequence version replaced g1:2624256.
Notes:
                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterlaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Erratum: [[published erratum appears in Nature 1998 Nov 12:396(6707):190]] (bases 1 to 56414)

    . 56414
/organism-"Mycobacterium tuberculosis"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:1773"
/clone="Y154"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(3. .527)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(3. .527)
                                                                                             Mycobacterium tuberculosis.
                                                                                                                          Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
AL008967 AL123456
AL008967.1 GI:3261491
                                                                                                                                                                                                                                          Cole, S.T., Brosch, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="recX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             initiation codon.
                                                                                                                                                                                                                    Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                      KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
REMARK
   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
```

```
/gene="reck"
/note="Rv2737c, (MTV002.02c), len: 790 aa. reck,
/note="Rv2737c, (MTV002.02c), len: 790 aa. reck,
denticallor RECA_MYCTU P26345 reca protein (790 aa).
dontains self-splicing protein element (intein) from 2294
to 969 (c), similar to intein II from TR:E332317
to 969 (c), similar to intein II from TR:E332317
Thermococcuus sp. (1829 aa), fasta socres; opt: 81 z-score:
235.2 E(): 6e-06, 24.6%identity in 183 aa overlap.
Contains PSO0017 ATP/GTP-blindingsite motif A (P-loop),
PSO0321 reck Asynature, and PSO0088IProtein splicing
signature. See Davis et al. (1992) cell71(2):201-210*
                                                                                                                                                                           /translation="wivscpppstsereeqaralclrlitarsrtraelagolakrgy
pedignryldrlaavglyddtdfaeqwvqsrranaakskralaaelhakgvdddvitt
vlggidagaergraeklyrarlrrevliddgtdearvsrrlvamlarrgygqtlacev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /traislation-"MTQTPDREEXALELAVAQIEKSYGKGSVMRLGDEARQPISVIPTG
SIALDVALGIGGLPRGRVIETYGPESSGKTTVALHAVANAQAGGVAAFIDABBALDP
DARKKLGVDTDSLLVSQPDTGEQALETADMLIRSGALDIVVDSVAALVPRAELEGEM
GDSHVGLQARLMSQALKMTGALNNGSTTAFINOLADKIGVMFGSPETTTGGRALKF
VASVRADVRRVETLKDGTNAVGNRTRVKVVKNKCLAEGTRIFDPVTGTTHRIEDVVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RKPIHVVAAAKDGTLHARPVVSWFDQGTRDVIGLRIAGGAIVWATPDHKVLTEYGWRA
AGELRKGDRVAQPRRFDGFGDSAPIPADHARLLGYLIGDGRDGWVGGKTPINKINVQR
ALIDDVTRIAATLGCAAHPQGRISLAIAHRPGERNGYADLCQQAGIYCKLAWBKRTPN
WFFEPDIAADIVGNLLFGLFESDGWYSRGYGALRVGYTTSEQLAHQIHWLLRFGV
GSTYRDYDPPORREYSTYNGRRIQSRROYFEVRISGMDNYTAFRESVPRWGPRGAALIQ
AIPEATQGRRRGSQATYLAAEWTDAVLNYLDERGVTAQEAAMIGVASGDPRGGMRQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGASRILREDRYQALADALDDRFLHDM.AEELRYSVIREYLPTRRARTFOLEVEEHTL
VAEGVYVHNCSPPFKQAEFDILYGKGISREGSLIDMGVDQGLIRKSGAMFTYEGEQLG
QGKENARNFLVENADVADEIEKKIKEKLGIGAVVTDDPSNDGVLPAPVDF"
complement(790. .2112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3247. .3453)
/gene="Rv2738c"
/note="Rv2738c" (MTV002.03c), len: 68 aa. Unknown,
/note="Rv2738c" (MTV002.03c), len: 68 aa. Unknown,
/note=minus is highly similar to the N-terminus of the
upstream ORFMTV002.07c (78.4% identity in 37 aa overlap);
also similarto ALOSOS8 (SC4182.5 Streptomyces coelicolor
cosmid 4H8 (64aa) opt: 185 z-score: 283.5 E(): 2.9e-08;
39.7% identityin 63 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="recA"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="PS00881 Protein splicing signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(2873. .2877)
/note="possible RBS upstream of Rv2737c"
complement(3247. .3453)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein Rv2738c"
/protein_id="caa15534.1"
/db_xref="G1:2624260"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"PS00321 recA signature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"recA"
/protefl_id-"CAA1553.1"
/db_xref-"G1:2624258"
/db_xref-"SWISS-PROT:P26345"
                                                                                                                                            /db_xref="SPTREMBL:033280"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:033281"
                                                                    /protein_id="CAA15532.1"
/db_xref="GI:2624257"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(2197. .2223)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2644. .2667)
                                                                                                                                                                                                                                                                                                                           complement(493. .2865)
/gene="recA"
                                                                                                                                                                                                                                                                                                                                                                                                        complement(493. .2865)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(790. .807)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note-"recA intein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /qene="recA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="recA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="recA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
```

```
40.00
4.444
75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1. fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: AC017383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-36 x AC017383
                                       HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_htg2:AC007417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31582 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LRQRAAAVRVEIGLPARDPGPLRRLIATLPALEVPRPDWPAEAVVVGPLHFEPTDRVLA
PAGTGPVVVVAPSTRALTGTAGLTEFAEETVPSGSRLVVSRLGSADLFVPPW
AVAGLGSOAELLTRADLVICGGGHGWVAKTLLAGVPWVVVPGGGGDOWELANRVVRQGS
AVLIRPLTADALVAAVNEVLSSPRFREAARRAAASVAGAADPVRVCHDALALAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
/product = hypothetical protein Rv2740"
/protein_id="Cas15536.1"
/db_xref="GI:2634262"
/db_xref="SPTREMBL:033283"
/db_xref="SPTREMBL:033283"
/translation="MAELTETSPETPETTEAIRAVEAFLNALQNEDFDTVDAALGDDL
/YENVGFSR.RGGRATATLLERMOGNVGFEVKIHRIGADGAAVLTESTDALIGFLRV
OFWVCGVFEVDDGRITLWRDYFDVYDMFKGLLRGLVALVVPSLKATL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AC017383 115873 bp DNA HTG 09-DEC-1999
DEFINITION Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MLAGVRLTEFHERVALHFGAAYGSSVLLDHVLTGFDGRSAAQAI
EDGVEPRDVWRALCADFDVPHDRW"
                                                                                                                     /note="Rv2739c, (MTV002.04c), len: 388 aa. Probable transferase, similar to eg. TR:051560 (EMBL:L28170) Pseudomonas aeruginosa rhamnosyl transferase (426 aa), fasta scores: opt: 178 z-score: 226.3 E(): 1.9e-05, 25.9% identity in 425 aaoverlap. Equivalent to Mycobacterium leprae protein MLCB33.02c (392 aa); fasta scores gpl294723|MLCB33_2 Mycobacteriumleprae cosmid B33 opt: 2112 z-score: 2364.5 E(): 0; 80.9%identity in 388 aa overlap."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4674. .5123
/gene="Rv2740, (MTV002.05), len: 149 aa. unknown, similar.
to M. leprae hypothetical protein TR:049850 (EMBL:294723)
MLCB33.03 (B2235_F3_140) (178 aa), fasta scores; opt: 498
z-score: 538.9 E(): 7.3e-23, 51.6% identity in 161 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Rv2741, (MTV002.06), len: 525 aa; Member of tuberculosis PE_ PGRS subfamily, similar to many eg
                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
/product="hypothetical protein Rv2739c"
/protein_id="CAA15535.1"
/db_xref="GI:2624261"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 56414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                         complement(3464. .4630)
                                                                                complement(3464. .4630)
/gene="Rv2739c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuAlaIleArgArgIleAla 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: MTV002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5355. .6932
/gene="PE_PGRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5355. .6932
/qene="PE_PGRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4674. .5123
/gene="Rv2740"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-36 x MTV002/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.444
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_htg7:AC017383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores
                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
```

```
NECRONS AND CONTROL OF THE CONTROL OF THE CONTROL OF SETTINGS AND CONTROL OF S
```

us-08-653-294-36.rge

COMMENT

```
unknown length
of 1609 bp in length
unknown length
of 1436 bp in length
unknown length
of 1417 bp in length
                                                                                                                                                                                                                                                        of 866 bp in length unknown length of 1187 bp in length of 1767 bp in length unknown length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown length
of 2824 bp in length
unknown length
of 3316 bp in length
unknown length
of 2997 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
of 14853 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
of 1007 bp in length
                                                                                         unknown length
of 1542 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
bp in length
                                                                           in length
                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                  length
                                                                                                                                                                     in length
                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             863 bp in length
                                               948 bp in length
                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                998 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 80,
unknown leny
of 2101 bp in ler
                                                                                                                                                                                unknown length
of 1706 bp in le
unknown length
of 1497 bp in le
unknown length
                                                                                                                                                                                                                                                                                                                                    know...
2 930 bp in ...
n length
 unknown length
of 1065 bp in le
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                             unknown length
of 1015 bp in l
                                                                                                                         unknown length
of 984 bp in le
                                                                                                                                                    unknown length
of 1378 bp in l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
of 1991 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ļp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T
L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
of 1337 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown 1
of 1468 t
unknown 1
of 3388 t
unknown 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown of 1619 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown of 2765 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 1405 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 2856 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown of 1253 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
 gap of ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of
 24124:
25189:
25269:
26217:
26297:
27312:
27392:
                                                                                                         28934:
                                                                                                                                                        0078
                                                                                                                                                                                                                                                                                         7032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81455
224045
224125
225190
225270
226218
227313
227393
30079
                                                                                                                                                                                                                                                                                                    33377
33377
33377
3338888
3388880
3388880
3388880
338880
338880
338880
338880
338880
338880
338880
338880
338880
338880
338880
338880
338880
338880
338880
                                                                                                                                                                                 31457
33243
333243
34820
34820
35766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49851
51952
53653
53655
53735
53735
56771
56851
58824
60372
63360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66477
66557
69322
69402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  70807
70887
73743
                                                           Direct Submission

Submitted (28-APR-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, MS 64-121, Berkeley, CA 94720, USA

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Aug 2, 1999 this sequence version replaced gi:5629944.

For further information about this sequence, including its location
and relationship to other sequences, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email
to bdgggefruitfly.berkeley.edu. All contigs in this submission meet
the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently
* consists of 94 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                 f unknown length
g of 1029 bp in length
f unknown length
g of 1091 bp in length
f unknown length
f of 1218 bp in length
g of 1218 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 581 bp in length
t unknown length
g of 1011 bp in length
t unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
of 1310 bp in length
...known length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown length
of 1037 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 1072 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 1150 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in length
                                                                                                                                                                                                                                                                                                                                  969 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 754 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 594 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown length
of 733 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 724 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 658 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 654 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
of 963 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 646 bp in length
unknown length
of 701 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 546 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown length
of 799 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length
of 622 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 604 bp in length
unknown length
of 1093 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 635 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 850 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                  contig
gap of
contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
gap of
contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5048:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6897:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10645
11656
11736
12460
12540
13198
13278
14315
14395
15049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15129
16092
16172
16818
16898
17599
17599
17679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20256
20336
20938
21038
22188
22268
22872
22872
                                                                           TITLE
JOURNAL
```

```
Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Moshrefi, M., Mixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Shir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.E.

L. Submitted (15-Jur.1999) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@mhgc.lbl.gov.
Library locations: 75-21, 43-37, 68-85.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AC007352 183365 bp DNA HTG 02-AUG-1999
DEFINITION Drosophila melanogaster chromosome 2 clone BACR19116 (D626) RPCI-98
19.116 map 47A-47B strain y; cn bw sp, *** SEQUENCING IN PROGRESS
ACCESSION AC007352
VERSION AC007352.5 GI:5670591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DS03499 (P217) is a bridge, sequence extending from 83,000 to bp 111,462, and DS08132 (D174) extends from bp 102,799 to bp 173,970.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eutergota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 183365)

Eutenheff.C., Champe.M., Arcaina.T.T.; Baxter,E., Blazej,R.G.,

Butenhoff.C., Champe.M., Chaver,C., Chew,M., Ciesiolka.L.,

Doyle,C.M., Parfan,D.E., Galle,R., George,R.A., Harris,N.L.,

Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,

Kim,E., Lee,B., Lewis,C., Li,P., Lomotan,M.A., Mazda,P.,

Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,

Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Fis DS01995 (D179), DS03499 (D217), and DS08132 (D174)" /note="DS01995 (d179) extends from bp 1 to bp 83,422,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .173970
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 11
Gaps: 0
Percent Identity: 72.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37569 g 47761 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88820 CGACTGGCACTGCGACGTACTACGCTCCGATAC 88852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ArgLeuAlaIleArgArgIleAlaLeuArgTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="56F7-56F9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="2R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37725 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.00
4.000
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AC005286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-36 x AC005286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_htg2:AC007352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50915 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Dases 1 to 173970)

Svirskas, R. R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flandqan, J., Houston, R.A., Hummasti, S. R., Karra, K., Kearney, L., Kim, S. H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S., Moshrefi, A.R., Noshrefi, M., Nixon, R., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R., Yee, A., Zhang, R., Zieran, L.L. and Kimmel, B.

Sequencing of Drosophila chromosome 2R, region 56F7-56F9 Unpublished (1997)

E. (Dases I to 173970)

E. (Calniker, S. E., George, R. A., Galle, R. F., Hoskins, R. A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS
AC005286 173970 bp DNA IS-NO1995 (D179), D803499
DEFINITION Drosophila melanogaster DNA sequence (PIS D801995 (D179), D803499
AC05286 AC004294 AC003448 AC003449 AC003456 AC003451 AC003451
AC003459 AC003453 AC003454 AC003456 AC003456 AC003457
AC003469 AC003822 AC003460 AC003456 AC003457
AC003401 AC003402 AC003460 AC003404 AC003406 AC003407
AC003401 AC003409 AC003401 AC003411 AC003412 AC003407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Subclones in sac from P1 clones DS01995 (D179), DS03499 (D217), and DS08132 (D174)) DNA.
Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: AC007417 from: 1 to: 125448
                                           unknown length
of 604 bp in length
                                                                                                                                             of 220 bp in length
unknown length
                                                                                                                                                                                                                  of 575 bp in length
unknown length
                                                                                                                                                                                                                                                                                       of 723 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                         of 501 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                              of 710 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 711 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 607 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 684 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 627 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 757 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 66.667
                                                                                                                unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
       contig
gap of contig
contig
gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of contig contig contig capp of contig capp of contig capp of capp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AC003415
AC005286.1 GI:3320125
                                                                                                                                          104112:
104192:
104767:
104847:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110807:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-653-294-36 x AC007417/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110040:
                                                                            .03812:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10120:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_in2:AC005286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
```

```
172452 TATTIGCIAGCIGCGCGCGCGTGGCTIGICGTIAC 172487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrargLeualaileargargilealaLeuargTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AC007352 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-36 x AC007352
                                                                          178638
179251
                                                                                                                                                                                                                                                                                       182673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores;
                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                               Direct Submission

Submitted (22-ARP-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Aug 2, 1999 this sequence version replaced 91:5629943.

For further information about this sequence, including its location and relationship to other sequence, including its location and relationship to other sequence, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a "working draft' sequence record is consists of 30 contigs. The true order of the pieces a shotner and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                       Celniker S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G. Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Bottenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Hoskins, R.A., Harris, N.L., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, E., Lee, B., Lewis, S., Li, P., Lomotan, M.A., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Petifer, B., Poon, L., Sequeira, A., Sethi, H., Snir, E., Syliskas, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zleran, L.L. and
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and Rubin,G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 13336 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 43847 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 1347 bp in length
unknown length
of 1469 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 8936 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1174 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1340 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 5580 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 935 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 509 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nown length
747 bp in length
nown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         678 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         985 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 593 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
                                        Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3084:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17391
                                                        Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9085
9165
9758
9838
11178
11258
12993
13073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76881
.20728
120808
177031
                                                                                                                                                                                                                                    Rubin, G.M.
                                        TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                    TITLE
JOURNAL
```

to: 183365

```
/clone="BACR19J16 (D626) RPCI-98 19.J.16"
/clone_llb="RPCI-98 (Roswell Park Cancer Institute
Drosophila melanogaster BAC llbrary, partial EcoRI in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2321 others
                                                             gap of unknown length
contig of 613 bp in length
gap of unknown length
gap of unknown length
contig of 718 bp in length
contig of 718 bp in length
gap of unknown length
gap of unknown length
contig of 707 bp in length
gap of unknown length
contig of 525 bp in length
                                                                                                                                                                                                                                                                                        gap of unknown length contig of 714 bp in length gap of unknown length
                     unknown length
of 634 bp in length
                                                                                                                                                                                                                                                                                                                                                            contig of 693 bp in length
733 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                           1. .183365
/organism="Drosophila melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37925 c 39574 g 51982 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="47A-47B
                                                                                                                                                                                                                                                                                                                                       182672:
183365:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.00
```

COMMENT

```
Human p16p27 fusion protein
Human p16p27 fusion protein
CDK inhibitory fusion prote
Human p16(GS)p27 fusion pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 1639-1641; 2084pp; English.
A computer readable medium has been developed which has recorded on it
A computer readable medium has been developed which has recorded on it
982 nucleotide sequences isolated from the Enterococcus faecalis genome.
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences, also known as contigs. The computer-based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
diagnosing Enterococcal infection in an animal and monitoring
progression of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
another related organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus faecalis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
                                                                                                                                                                                                                                                                                             Entercoccus faecalis; contig; detection; Entercoccus faecalis; contig; detection; Entercoccus faecalis; contig; detection; Entercoccus faecalis; contig; detection; Entercoccus faecalis; computer readable medium; ds.

Entercoccus faecalis.

WO9850555-A2.

D 12-NOV-1998.

WO9850555-A2.

O4-MAY-1998; U08985.

A -NOY-1997; US-066009.

R 14-NOY-1997; US-066009.

R 16-MAY-1997; US-066009.

B 16-MAY-1997; US-066009.

A (HUMA-) HUMAN GENOME SCI INC.

B Barash SC, Dillon PJ, Kunsch CA;

WPI; 99-045171/04.

T New isolated Entercoccus faecalis polynucleotides and polypeptides

T used to develop products for the detection of Entercocccus and for use in vaccines for prevention or attenuation of Entercocccus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 11
Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ຜີ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= membrane protein
322. .327
  207.14
211.99
216.63
216.63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1110 AGAATTGCCTTACGACGATTAGCTAGTCGCTAT 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-SEP-1991 (first entry)
Octopus rhodopsin membrane protein.
Octopus; rhodopsin; membrane; helix; Key
Location/Qualifiers
cds
  107.91
107.73
107.56
107.56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: X13357 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1334 A;
                                                                                                                                                                                             seq_documentation_block:
ID X13357 standard; DNA; 4114 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  012225 standard; DNA; 1371 BP 012225;
                                                                                                                                                                                                                                                                            19-MAR-1999 (first entry)
     35.00
35.00
35.00
                                                                                                                                          seq_name: N_Geneseq_36:X13357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.00
3.900
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:Q12225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-36 x X13357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
     N_Geneseq_36:X26224
N_Geneseq_36:X26235
N_Geneseq_36:T74052
N_Geneseq_36:X26223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                            FIFEWER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            414 | Enterococcus faccalis genome c

414 | Enterococcus faccalis genome c

861 | Bacterial antibiotic resitance

1371 | Octopus rhodopsin membrane pro

862 | Bacterial antibiotic resitance

1400 | Sequence encoding Serratia pho

1402 | Bacterial antibiotic resitance

1402 | Bacterial antibiotic resitance

1402 | Brain Weated Brain genomic sequency

1402 | Brain human breast and ovariance

1402 | Brain human breast and ovariance

1402 | Brain human breast and ovariance

1402 | Mutated Brain genomic sequency

1403 | Mutated Brain genomic sequency

1403 | Mutated Brain genomic sequency

1404 | Mutated Brain genomic sequency

1405 | Mutated Brain genomic sequency

1507 | KSHV long unique coding reginal mutated by 17 protein encoding the

1507 | CKI/KIP protein inhibitin

1507 | CKI/KIP protein inhibitin

1508 | Truncated p27/pl6 fusion protein

1008 | Truncated p27/pl6 fusion protein
                                                                                                                                                                                  Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-MCPCII_1/USPTO_spool/US08653294/runat_04022000_160701_15807/app_query.fasta.2
-DF=N_Geneseq_36 -QFMT=fastap -SUFFT=rng -GAPOP=12.000
-GAPDEXT=4.000 -MIRMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GAPDP=4.500 -GAPEXT=0.050 -XAAPOP=10.000 -YGAPDEXT=0.500
-GAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-ALIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN-0
-MAIGN=15 -MODE-LOCAL -OUTFMT=pfs -NORM=ext -MINLEN-0
-MAXLEN-1000000 -USER-US08653294 -NCPU=6 -ICPU=3 -NO_XLPXY -WAIT
                                                                                                              About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144.91

667.21

667.21

1008.74

40.34

40.34

41.100.35

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.36

41.100.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.2e+03
2.8e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49.24
102.01
104.75
104.95
104.95
104.95
192.46
201.88
  OM of: US-08-653-294-36 to: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25,000e
110,000e
1110,000e
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111,000
111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search information block.
Query: US-08-653-294-36
Query length: 12
                                                        Date: Feb 8, 2000 7:32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
N_Geneseq_36:X13357
N_Geneseq_36:Q12225
N_Geneseq_36:T28565
N_Geneseq_36:T28565
N_Geneseq_36:WG0877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N. Geneseq 36:117516
N. Geneseq 36:117516
N. Geneseq 36:117518
N. Geneseq 36:117519
N. Geneseq 36:117521
N. Geneseq 36:117521
N. Geneseq 36:117523
N. Geneseq 36:117524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Geneseq_36:T17529
N_Geneseq_36:T17530
N_Geneseq_36:T17520
N_Geneseq_36:T17520
N_Geneseq_36:T17525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:099804
N_Geneseq_36:044280
N_Geneseq_36:17455
N_Geneseq_36:1717515
N_Geneseq_36:1718325
N_Geneseq_36:1717513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:V19941
N_Geneseq_36:Q60295
N_Geneseq_36:X26229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:V73802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N_Geneseq_36:T16336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36:V16719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:X17752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:X26232
N_Geneseq_36:T74053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Geneseq_36:V47517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:X21817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_36:X2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              score_list:
```

```
actam antib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO8606743-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serratia sp
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N60877:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Key
 P.PSBS R12562.

Genetic engineering of membrane protein - by division of protein into cartridge genes corresp. to helix structure polypeptide(s) Disclosure: Fig 1: 17pp; Japanese.

A gene cassette is prepd. by division of the OR membrane protein encoding helix structure polypeptides. Restriction sites are indicated. A base sequence contg. such a sequence downstream to the tryptophan regulating gene derived from the E. coli tryptophan operon, the trpi, or the trpe polypeptide translation regulating base sequence, and the N-terminal Met of the trpi. (or trpE) or trpE polypeptide, respectively, is introduced in an expression vector for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacterial antibiotic resitance gene, aacC2, probe.
Detection: probe: amplification primer: bacterial pathogen; pneumonia;
Becherichia coll: Klebsiella pneumoniae; Pseudomonsa seruginosa;
Proteus mirabilis: Streptococus pneumoniae; Staphylococcus aureus;
Staphylococcus epidermidis: Enterococcus faecalis; respiratory tract;
Staphylococcus saprophyticus; Streptococcus pyogenes; urinary tract;
Haemophilus influenzae; Moraxella catarinalis; septicaemia; meningitis;
infection; intra-abdominal infection; skin infection;
bacterial resistance; beta-lactam antibiotic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                     Ë
                                                                                                                                                                                                                                                                                                                                                                                                                     354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: Q12225 from: 1 to: 1371
                                                                                                                                                                                                                                                                                                                                                                                                                     351 G;
/*tag= a
/label- Sphl
/note= "restriction enzyme site"
592. .597
                                                                                                                                                           note= "restriction enzyme site"
                                            /*tag= b
/label= MluI
/note= "restriction enzyme site"
884. .889
                                                                                                              'note* "restriction enzyme site"
                                                                                                                                                                                                      /note= "restriction enzyme site"
                                                                                                                                                                                                                                                                                                                                                                                                                     .368 C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= e
/label= BamHI
                                                                                                                                                                                                                                                                                                                                                                                                      transformation of host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID T28565 standard; DNA; 861 BP.
                                                                                                                                     '*tag= d
'label= NheI
                                                                                          /*tag= c
/label= NdeI
                                                                                                                          1069. .1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1997 (first entry)
                                 . 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-36 x Q12225/rev
                                                                                                                                                                                                                          27-MAY-1991.
06-OCT-1989; 260261.
06-OCT-1989; JP-260261.
(HTA ) HITACHI KK.
WPI; 91-197925/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:T28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAK-1995.
12-SEP-1995; CA0528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9608582-A2.
                                  misc_feature
                                                                             misc_feature
                                                                                                                          misc_feature
                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAR-1996
```

```
Margin 96-179953/18.

Bergeron MG, Ouellette M, Roy PH;
WHI; 96-179953/18.

WII; 96-179953/18.

WHI; 96-179953/18.

WHI; 96-179953/18.

We method for the detection and quantification of antibiotic callows detection and quantification of antibiotic resistant bacteria in patients, the environment and food primers - allows detection and quantification of antibiotic resistance genes which were used as probes in the restrict of the invention for the detection of bacterial species in a particular swild antibiotic resistance genes which were used as probes in the method of the invention comprises using probes and/or amplification primers which are specific, ubiquitous and sensitive for determining the presence and/or amount of nucleic acid comprises a selected target region hybridisable with the probes or primers. The method comprises contacting the sample with the probes or primers and detecting the presence and/or amount of the bacterial species. This method may be used to primers or amplification products as and indication of the presence and/or amount of the bacterial species. This method may be used to detect commonly encountered bacterial pathogens, e.g. Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, Proteus mirabilis, Streptococcus progenes, Haemophilus influenzae and Moraxalla catarrhalis. Streptococcus pyogenes, Haemophilus influenzae and Moraxalla catarrhalis. These bacterial species are associated with approx. 90% of urinary tract infections and with a high percentage of other severe infections. The analy and the membranes in the self-under severe infections. The analy and the percentage of other severe infections. The analy and other severe respiratory tract infections. The analy and the percentage and exterial resistance to beta-langer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-OCT-1991 (first entry)
Sequence encoding Serratia phospholipase and promoter.
Phospholipids; fatty acids; pNU121; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 37.00 Length: 12
Ratio: 3.700 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TyrargleualaileargarglealaleuargTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag- a
216. .1175
/*tag- b
/note- "Claim 23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T28565 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID N60877 standard; DNA; 1400 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 A;
                                                                        (ROYP/) ROY P H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: N_Geneseq_36:N60877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .215
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DK-002100.
DK-005000.
DK-006060.
WO-DK0051.
DK-000097.
12-SEP-1994; US-304732.
(BERG/) BERGERON M G.
(OUEL/) OUELLETTE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-36 x T28565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1985; DK-00606
09-MAY-1986; WO-DK005
09-JAN-1987; DK-00005
(BENA ) BENZON A AS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-1986.
09-MAY-1986; I
10-MAY-1985; I
```

```
A single-stranded DNA (or its complementary strand or the corresp. double-stranded DNA) which comprises one of the 7837 "GS" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of cDNA was initiated from the 3'-end of mRNA by using polyT) as the sole primer. Since the 3'-untranslated sequence is unique to a particular mRNA species, almost all the 3'-oriented cDNAs hybridise with specific mRNAs. Beach library is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived.
                                                                                                          Disclosure; Fig 9; 66pp; English.

The gene product may be expressed by an E.coli host transformed with a plasmid encoding the phospholipase gene esp. under control of a Serratia regulatory sequence. The phospholipase product may be used to hydrolyse fatty acids from phospholipids and lipids. Sequence 1400 BP; 283 A; 420 C; 453 G; 244 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsubara K, Okubo K;
WPI: 95-206931/27.
Identifying gene signatures in 3'-directed human cDNA library - e.g.
for diagnosis of abnormal cell function, by preparing cDNA that
reflects relative abundance of corresp. mRNA in specific human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-0CT-1996 (first entry)
Human gene signature HUMGSO8571.
Human gene signature; messenger RNA; mRNA; relative abundance; frequency;
human; cloning; mapping; non-biased library; diagnosis; detection;
cell typing; abnormal cell function; ss.
w0951472-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of disquosing abnormal cell function or for recognising different cell types.

Sequence 382 BP; 118 A; 72 C; 85 G; 102 T;
                                                            Producing bacterial enzyme esp. nuclease - using hybrid plasmid which contains DNA from Serratia spp. encoding extracellular
                                                                                                                                                                                                                                                             Length: 11
Gaps: 0
Percent Identity: 54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 2058-2059; 2245pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                to: N60877 from: 1 to: 1400
                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuAlalleArgArglleAlaLeuArg 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T26331 standard; cDNA to mRNA; 382 BP
(MOLI/) MOLIN S.
Molin S, Givskov M, Riise E;
WPI; 86-318851/48.
                                                                                                                                                                                                                                                                              Ratio: 3.364
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
(OKUB/) OKUBO K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:T26331
                                                                                                                                                                                                                                                             37.00
                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-36 x N60877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                             Quality:
                                                P-PSDB; P61318
                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissues
```

Length:

36.00

Quality:

alignment\_scores:

```
Prepage Naily Maily Mail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PR-1 like gene PR-1mz.
SAR; tobacco; protein-synthesis independent gene; cyclohexamide;
systemic acquired reistance response; anti-pathogen; plant protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 9
Gaps: 0
Percent Identity: 77.778
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ryals JA, Uknes SJ, Ward ER;
                                                                                                                                                                                                                                                                                                                                                             36 TACAGGGGTGAACTACCGGGGCTGGCCCTCAGATAT 71
                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: Q99804 from: 1
                                                                                                                                                                                                                                         to: 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 CIGGCGCIGCGCGCGTAGCTCTGCGC 205
                                                                                                                                                                                                                                         Align seg 1/1 to: T26331 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LeuAlaIleArgArgIleAlaLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID Q44280 standard; DNA; 1092
AC Q44280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID 099804 standard; cDNA; 731
AC 099804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-36 x Q99804/rev
4.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seg_name: N_Geneseg_36:Q44280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:099804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JAN-1995; IB0002.
13-JAN-1994; US-181271.
(CIBA ) CIBA GEIGY AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag=
                                                                                                                        alignment_block:
US-08-653-294-36 x T26331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alexander DC, Ryal
WPI; 95-263872/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
    Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maize; PR-1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9519443-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
```

```
*tag= f'
note= "indefinite interval within intron 2"
141
                                                                                                                                                                                                                                                                                                                                                                                      1261. .2677

**tag- 1

**tag- 1

1569. .2581

**tag- 1

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4391. 4392
/*tag- y
/note- "known polymorphic site"
4602. 4614
/*tag- z
/*ote- "indefinite interval within intron 7"
6538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79598. .3610
/*tag- q
hote- "indefinite interval within intron 5"
653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= u
note= "site of 1 nucleotide deletion"
076. .4088
*tag= v
note= "indefinite interval within intron
225. .4364
  "*tag= c
note= "known polymorphic site"
[513. .1611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= .1
note= "known polymorphic site"
789. .3328
                                                                                                                                                                                                                                                                           g
"known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag= r
note= "known polymorphic site"
814. .3902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2789. .3328
/*tag= m
/note= "intron 4"
3063. .3075
                                                                                                                                   *tag= e
note= "intron 2"
925. 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= p
note= "intron 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag= t
note= "intron 6"
223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= w
/note= "exon 7"
4365. .6571
/*tag= x
/note= "intron 7"
                                                                     /*tag= d
/note= "exon 2"
1612. .2206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= 0
/note= "exon 5"
3407. .3813
                                                                                                                                                                                                                                                                                                                                              *tag= h
note= "exon 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    '*tag= k
'note= "exon 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *tag= s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4364
                                                                                                                                                                                                                                                                                                                      . 2260
                                                                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                  intron
                                                                                                                                                                                                                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-0CT-1996 (first entry)
Mutated BRCAl genomic sequence from sample set MSKCC family 19921.
Cancer therapy, breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCAl; ds.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3401. The genes were designated lipb (Q44280) and limD (Q44281) and they code for a lipse and a lipses modulator protein, respectively. Due to the extreme GC content of the DNA, the sequence was difficult to determine (hence the "others" in the sequence). The limD start codon is positioned 3 bp downstream of the lipD stop codon. Lipp and LimD were found to be homologous to Liph and LimA, respectively. In denaturation/renaturation experiments, LimA chaperone protein was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prepn. of active lipase in high quantities - by subjecting to denaturation and restructuring in presence of chaperone molecule Example 10; Page 43; 78pp; Bng1ish.
Two genes were cloned and sequenced from Pseudomonas cepacia DSM
09-DEC-1993 (first entry)
Pseudomonas cepacia DSM 3401 lipD gene.
Lipase, LipD; lipase modulator; limD; chaperone molecule;
lipolysis; detergent; ss.
Pseudomonas cepacia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joergensen ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: Q44280 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                 18-DEC-1992; DK0391.
20-DEC-1991; WO-DK0402.
AUVOVO ) NOVO-NORDISK AS.
BUCKLBY CM, DIGETICHSEN BK, HODSON A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       353 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LeuAlalleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
256. .355
/*tag= a
/*tag= a
356. .1512
/*tag= b
/*tag= b
1295
                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID T17455 standard; cDNA; 24025 BP.
AC T17455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    able to produce active LipD. Sequence 1092 BP; 188 A;
                                                                                                                                                             /*tag= a
480
                                                                                                                                                                                                                                                   /*tag= c
712. .714
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-36 x Q44280/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.00
4.000
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:T17455
                                                                                                                                                                                                        /*tag=
481
                                                                                                                                                                                                                                                                                                                                              /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McConnell DJ;
WPI; 93-227318/28.
P-PSDB; R39396.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                 WO9313200-A
                                                                                                                                                                                                                                                                                                                                                                                             )8-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                          unsure
                                                                                                                                                                                   unsure
                                                                                                                                                                                                                                unsure
                                                                                                                                                                                                                                                                             unsure
                                                                                                                                                                                                                                                                                                                           unsure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 intron
```

•

FT misc_featurerTT	FT misc_featur	FT misc_featur FT	FT misc_featur FT	FT FT intron FT	FT FT misc_feature pr	FT FT exon	FT FT intron		FT MISC_IECULE	FT exon	FT FT misc_feature FT	FT FT intron FT	FT misc_featur	FT aliqnment_scores	Qual.	Feicent Similar	alignment_block: US-08-653-294-3	Align seg 1/1	Z Argreum.         1313 AGATTGG	sed_name: N_Gene	seq_documentati	AC T17515; DT 04-0CT-1996	DE Mutated BRC2 KW Cancer there	KW gene therap:		FT FT intron FT	FT misc_feature
					<del></del>				-					v													
"known polymorphic site" .6677 .a.	ab " " " " " " " " " " " " " " " " " " "	acintron 8"	=	= O1	af . "exon 9"	. ag "known polymorphic site"	.10530 .10530 .1ntron 9"		. Known polymorphic site. 1.10607			. al "indefinite interval within intron 10" .15023		an "known polymorphic site"	80 1		. ap . "known polymorphic site"	. aq . "known polymorphic site"	ar "known polymorphic site"		E	ar "known polymorphic site"	. au . "known polymorphic site"	av "known polymorphic site"	aw "known nolvmorphic	ax "known polymorphic	av av
/note= 6572.	/" tag= /note= 6678	/*tag= /note= 6823	/*tag= /note= 9106	/*tag= /note= 9164	/*tag= /note= 9207	/*tag= /note=	9210. /*tag= /note=	9376 /*tag=	/note= 10531. /*tag=	/note- 10608.	/*tag= /note= 11384.	/*tag- /note- 11598.	/*tag= /note=	11908 /*tag= /note=	11994 /*tag=	12952	/*tag= /note= 13004	/*tag= /note=	13009 /*tag= /note=	13048 /*tag=	/note= 13238	/"tag= /note= 13448	/*tag= /note=	/*tag= /note=	13951 /*tag= /note=	14041 /*tag= /note=	14046
exon	intron	misc_feature	misc_feature	exon	mico fosturo	irsc_reacute	ıntron	misc_feature	exon	intron	misc_feature	exon	•	misc_reature	misc_feature	misc_feature	misc_feature		misc_reature	misc_feature	misc_feature	misc feature		misc_reature	misc_feature	misc_feature	misc_feature

```
36 (first entry)

RCA1 genomic sequence from PM15.

PARA1 genomic sequence from PM15.

PARA1, breast and ovarian cancer predisposing gene; immunogen; production; germline alteration; probe; lesion neoplasia; human; py; protein replacement therapy; protein mimetic; BRCA1; ds. ens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
/*note= "known polymorphic site"
/*note= "known polymorphic site"
/*tag= bf
/*t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 24025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 11
Gaps: 0
Percent Identity: 63.636
14475
/*tag= az
/note= "known polymorphic site"
/4434
/*tag= ba
/note= "known polymorphic site"
/*tag= bb
/note= "known polymorphic site"
/4566
/*tag= bc
/note= "known polymorphic site"
/*tag= bc
/note= "known polymorphic site"
/*tag= bc
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bc
"known polymorphic site"
.15424
bd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= bj
fnote= "known polymorphic site"
[6127. .16565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AlaileArgArgileAlaLeuArgTyr 12
||||||||||||
|GCCATCAGAAACTGGTTCTGATGTAC 11281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to reverse of: T17455 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
256. .355
.4tag a
.mote= "exon 1"
356. .1512
/*tag b
.mote= "intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= bk
/note= "intron 13"
16243
/*tag= bl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "intron 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on_block:
indard; cDNA; 24025 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :
36 x T17455/rev ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             es:
ality: 36.00
Ratio: 3.600
arity: 90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eseq_36:T17515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag=
/note=
15284
                                                                                                                                                                                         ė,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i.e
                            19
                                                                                                                                                                                                                                                                                                                                                           Ü
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 i.e
```

```
misc_feature
                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                             nutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intron
                                                                                                                                                                                                                                                                                                                                        intron
          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                         /*tag-
//tag-
//
/note= "known polymorphic site"
1513. .1611
/*tag=
//ote= "exon 2"
1612. .2206
//tag= e
//ote= "intron 2"
1925. .1937
//tag= f
//ote= "indefinite interval within intron 2"
2141
                                                                                                                                                                                                            misc_feature
                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ntron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Intron
                                                                                     Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                             exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
```

```
/note= "n at 1925-1937 represent an indefinite interval within the intron" 2207. 2260 f. 2261 f. 2677 f. 2261. 2677 f. 2261. 2677 f. 2261. 2678 f. 2261 f. 2678 f. 2261 f. 2678 f. 22788 f. 22788 f. 22788 f. 22788 f. 22788 f. 22789 f. 2278
                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= k
/note= "n at 3598-3610 represent an indefinite
interval within the intron"
3814. .3902
/*tag= 1
3903. .27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*teg= t
10608. .11597
/*etag= u
//note= n at 11383-11396 represent an indefinite
interval within the intron"
11598. .15023
/*etag= v
15024. .15424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *ttag= Y foot= n at 15647-15659 represent an indefinite interval within the intron" 15953. .16126 ** tage = z foot= x 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         notes "n at 16370-16382 represent an indefinite interval within the intron" .6566. .16692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ^*tag= ac
hote= "n at 17290-17302 represent an indefinite
interal within the intron"
[7536..17726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ae
"n at 18299-18312 represent an indefinite
                                                                                                                                                                                                                                                                                                                                                   /*tag= 1 to 3063-3075 represent an indefinite incrval within the intron" 3329. .3406 /*tag= 1 /*tag= 1 /*tag= 1 /*tag= k /*tag= k
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag o /*tag 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3903. .4224
/*tag= m
/*tag= m
/*tag= m
/*tag= m
/*tag= m
/*tag= m
/*tag= n
/*tag= n
/*tag= n
/*tag= n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -04. .9207
/*tag-
9208. .10530
/*tag-
10531. ]/
*tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .15511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .17535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .15952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p , , e . . 9163 /*tag=  q 9164.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag-
15425.
/*tag-
15512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tag-
                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                         Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
               seq_documentation_block:

ID T18325 standard; DNA; 24026 BP.

AC T18325;
DT 05-JUN-1996 (first entry)
DF BRCA1; human breast and ovarian cancer predisposing gene.

KW BRCA1; breast cancer; ovary cancer; predisposing gene;

KW susceptibility gene; diagnosis; prognosis; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 24025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.00 Length: 11
3.600 Gaps: 0
90.909 Percent Identity: 63.636
      14873
Artag= az
Artag= "Known polymorphic site"
14890
Artag= ba
Anotes "Known polymorphic site"
14965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= bi
/note= "known polymorphic site"
/fols6. 16564
/*tag= bj
/note= "intron 13"
                                                                                                                                                                                                                         **tag= bb
note= "known polymorphic site"
5023. .15423
                                                                                                                                                                                                                                                                                                                                                                                                                                            "known polymorphic site"
.15510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= bk
/note= "known polymorphic site"
16369. 16381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: T17515 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 ArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. 55
7.tag= a
56. .155
/*tag= b
/*tag= c
1533 .1611
/*tag= 2d
/*tag= e
/*tag= e
                                                                                                                                                                                                                                                                                                                      bc
"intron 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= bh
/note= "exon 13"
16076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-36 x T17515/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T18325
                                                                                                                                                                                                                                                                                                               /*tag=
/note=
/*tag=
/note=
/note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
            misc_feature
                                                                                                      misc_feature
                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intron
                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
```

misc\_feature alignment\_scores intron '\*tag= ag /note= "n at 18952-18964 represent an indefinite interval within the intron" 19299. 19386 \*tag= ai note= n at 19887-19899 represent an indefinite nterval within the intron" 10191. 20267 \*\*tag= aj \*\*tag= ak notes "n at 20767-20779 represent an indefinite nterval within the intron" 1095. 21135 ttag= am note= "n at 21341-21353 represent an indefinite note=val within the intron" 1584. .21667 \*tag= ao
note= n at 21921-21933 represent an indefinite
terval within the intron"
2234. .22288 \*tag= aq note= "n at 22567-22579 represent an indefinite nterval within the intron" 2833. .22906 \*tag- as note- "n at 23050-23062 represent an indefinite niterval within the intron" \*tag- at \*tag- at 3349. .23598 \*tag= au note= "n at 23580-23592 represent an indefinite nterval within the intron"

\*tag= bd note= "polymorphic site" 1908 \*tag= be note= "polymorphic site" 1994 bi "polymorphic site" \*tag= bl note= "polymorphic site" /\*tag= bo /note= "polymorphic site" 14046 bh "polymorphic site" bj "polymorphic site" \*tag= bk note= "polymorphic site" \*tag= bm note= "polymorphic site" bn "polymorphic site" bf "polymorphic site" bg "polymorphic site" /\*tag-

Length: 11 Gaps: 0 Percent Identity: 63.636 36.00 3.600 90.909 Quality: Ratio: Percent Similarity:

alignment\_block: US-08-653-294-36 x T18325/rev

to: 24026 Align seg 1/1 to reverse of: T18325 from: 1

seg\_name: N\_Geneseg\_36:T17512

seq\_documentation\_block:
ID T17512 standard; cDNA; 24026 BP.
AC T17512;

04-077-1996 (first entry)
Mutated BRCA1 genomic sequence from PM04.
Cancer therapy: breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.

Location/Qualifiers 256. .355 /\*tag= a

/note- "intron 1" / rag= a /note= "exon 1" 356, 1512 tag=

/\*tag= c /note= "known polymorphic site" 1513. .1611

			ag "known polymorphic ar "known polymorphic as "known polymorphic au "known polymorphic av "known polymorphic av "known polymorphic av "known polymorphic ax
misc_feature misc_feature exon misc_feature	intron misc_feature exon intron misc_feature	exon misc_feature misc_feature misc_feature	misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature
/*tag- d /note="axon 2" 16122206 /*tag= e /note="intron 2" 19251937 /*tag= f /note="indefinite interval within intron 2" 2141 /*tag= g /note="known polymorphic site"	/*toy2260 /*toy2261 22612677 /*toy- i /*toy- i /*toy- j /*toy- j	27893328 /*teg= m	/ / / / / / / / / / / / / / / / / / /
on _feature _feature	exon intron misc_feature exon misc_feature	intron misc_feature exon intron misc_feature misc_feature	exon intron misc_feature exon intron misc_feature misc_feature misc_feature misc_fiature intron

us-08-653-294-36.rng

```
/*tag- r
/note- "known polymorphic site"
3814- 3902
/*tag- s
/note- "exon 6"
3903. 4224
/*tag- t
/note- "intron 6"
4076. 4088
/*tag- u
/rote- "indefinite interval within intron 6"
                                                                                                                                                                                                                   *tag= 1
note= "indefinite interval within intron 3"
678. 2788
*tag= k
note= "exon 4"
                                                                 *tag= f
note= "indefinite interval within intron 2"
                                                                                                                                                                                                                                                                                                                                                                        "tag- n
note- "indefinite interval within intron 4"
329. .3406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= q
note= "indefinite interval within intron 5"
653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= y
note= "indefinite interval within intron 7"
538
                                                                                                                                                                                                                                                                                              /*tag- 1
//note= "known polymorphic site"
2789. 3328
//tag- m
/note= "intron 4"
3063. 3075
                                                                                                      - g
- "known polymorphic site"
.2260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag= x
note= "known polymorphic site"
602. .4614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        z
"known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4365. .6571
/*tag- w
/note- "intron 7"
1391. .430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6572. .6677
/*tag= aa
/note= "exon 8"
(6678. .9163
/*tag= ab
/note= "intron 8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= p
/note= "intron 5"
3598. .3610
                                                                                                                                                                               *tag= 1
note= "intron 3"
569. .2581
                             *tag= e
note= "intron 2"
- "exon 2" .2206
                                                                                                                                                       - "exon 3" .2677
                                                                                                                                                                                                                                                                                                                                                                                                                  e o
e exon 5"
3813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "exon 7"
                                                                                                      *tag=
note= 1
207. .:
                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
note= '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= 'note= '572..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
note=
365. .
                                                     misc_feature
                                                                                          misc_feature
                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                     intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intron
              intron
                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                        intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       intron
                                                                                                                               exon
                                                                                                                                                                                                                                                 exon
                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-001-1996 (first entry)
Mutated BRCA1 genomic sequence from PM05.
Cancer therapy, breast and ovarian cancer predisposing gene; immunogen, antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.
Homo saplens.
                                                                                                                                             "C to A mutation at known polymorphic site"
                                                                                                                                                                                                                                                 bg
"indefinite interval within intron 12"
.16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 24026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps: 0
Percent Identity: 63.636
                                                  bb
"known polymorphic site"
.15424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                            "known polymorphic site".16382
bl
                                                                                                                                                                                                                                                                                                                                     "known polymorphic site"
.16565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11314 AGATTGGCCATCAGAAACTGGTTCTGATGTAC 11282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: T17512 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 ArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
256. .355
/*tag= a
/note= "exon 1"
356. .1512
/*tag= b
/note= "intron 1"
                                                                                                     "intron 11"
                                                                                                                                                                                                                                                                                                                                                                          "intron 13"
                                                                                                                                                                                                                     "intron 12"
.15659
                                                                                                                                                                                  "exon 12"
                                                                                                                                                                                                                                                                                                 "exon 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID T17513 standard; cDNA; 24026 BP.
AC T17513;
                                                                                                                                                                                             .15952
                                                                                                                                                         .15511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36.00
3.600
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-36 x T17512/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: N_Geneseq_36:T17513
                                                                                                                                                                                              $512.
*tag=
note=
5647.
                                                     *tag=
                                                                                          tag=
                                                                                                                               *tag=
                                                                                                                                             note=
5425.
                                                                                                                                                                                                                                              *tag=
note=
5953.
                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
/note=
16370.
/*tag=
                                                                                                                                                                                                                                                                                                                                                               tag-
                                                                                                                                                                                                                                                                                                                           tag-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
   Quality:
   Ratio:
   Percent Similarity:
  misc_feature
                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                  nutation
                                                                                                                                                                                                                                                                                                                                                  intron
                                                                             intron
                                                                                                                                                                                             intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                         exon
                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
```

The same of

```
Mutated BRCA1 genomic sequence from PM11.

Cancer therapy: breast and ovarian cancer predisposing gene; immunogen; antibody production; germline alteration; probe; lesion neoplasia; human; gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.

Homo saplens.
                                                                                                                                                                                                                         bg
"indefinite interval within intron 12"
.16126
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 11
Gaps: 0
Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag- c
fnote- "known polymorphic site"
1513. .1611
/*tag- d
/note- "exon 2"
                                   bb
"known polymorphic site"
.15424
                                                                                                                                                                                                                                                                                                             "known polymorphic site"
.16565
                                                                                                                                                                                                                                                                                                                                                                       /*tag- bk
//note- "known polymorphic site"
//41870. 16382
/*tag- bl
 ba
"known polymorphic site"
                                                                                                                        "known polymorphic site".
.15511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to reverse of: T17513 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
256. .355
.4tag= a
.note= exon 1"
356. .1512
/*tag= b
.7tag= b
1295
                                                                                                                                                            /note= "exon 12"
15512. .15952
/*tag= bf
/note= "intron 12"
15647. .15659
                                                                                    "intron 11"
                                                                                                                                                                                                                                                                                                                                              notě- "intron 13"
6243
                                                                                                                                                           "exon 12"
.15952
bf
                                                                                                                                                                                                                                                                       "exon 13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seg_documentation_block:
ID T17514 standard; cDNA; 24026 BP.
AC T17514;
                                                                                                                                                                                                                                                                                                                                                                                                                                              36.00
3.600
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-36 x I17513/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T17514
                                                                         '*tag=
'note= "
5284
                                                                                                             *tag=
note=
5425.
*tag=
                                                                                                                                                                                                                          *tag=
                                                                                                                                                                                                                                                                                                                                      tag-
                                                                                                                                                                                                                                                               *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
Percent Similarity:
                         misc_feature
                                                                                                misc_feature
                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                             intron
                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intron
                                                                                                                                                                                                                                                    exon
                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                        "indefinite interval within intron 10". 15023
                                               /*tag= ad
/note= "known polymorphic site"
/144. 9209
/*tag= ae
/note= "exon 9"
6823
A'tag= ac
//orte= "known polymorphic site"
9106
                                                                                                                      *tag= af
note= "known polymorphic site"
210. .10530
                                                                                                                                                                                                             "known polymorphic site". 10607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ap
"known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aq
"known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ar
"known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= az
/note= "known polymorphic site"
|4891
                                                                                                                                                                                                                                                                                                                                                                                                "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "known polymorphic site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "known polymorphic site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= ay
note= "known polymorphic site"
4874
                                                                                                                                                                                                                                                                                                                                                                                                                                     "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "known polymorphic site
                                                                                                                                                                                                                                /*teg= ai
/note= "exon 10"
/10608. 11597
/*tog= ai
/note= "intron 10"
11384. 11396
/fog= ak
/fog= ak
/note= "indefinite
                                                                                                                                                            *tag= ag
note= "intron 9"
376
                                                                                                                                                                                                                                                                                                                                                             "exon 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= "
4041
*tag= "
note= '
4046
*tag=
note= '
                                                                                                                                                                                                *tag=
note=
0531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             tag=
100te=
1004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
note=
3539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     *tag=
note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
note=
                                                                                                              misc_feature
                                                                                                                                                                                   misc_feature
misc_feature
                                     misc_feature
                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                  intron
                                                                                                                                                                                                                                                              intron
                                                                          exon
                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                       exon
```

to: 24026

/*tag= /note= 9106 /*tag= /note=	91649209 /*tag= ae /note= "exon 9" 9207	at known p 10530 ag	/note= "intron 9" 9376 /*tag= ah /note= "known polymorphic site" /nota= nota		/note- 11384. /*tag- /note- 11598.	/*tag= /note= 11908 /*tag=	/note= known polymorphic site:  /tige an /hote= "known polymorphic site"   12952	/*tag= ao /note="known polymorphic 13004 /*tag= ap	/note= 13009 /*tag= /note=		/note- 13448 /*tag- /note- 13539	/*tag= au /note= "known polymorphic site" e 13951 /*tag= av /note= "known polymorphic site"	14041 /*tag= aw /note= "known polymorphic 14046 /*tag= ax	/note= " 14475 /*tag= " 14874 /*tag- /note= "	14891 /*tag= ba
FT FT misc_feature FT	FT exon FT FT misc_feature	FT FT intron	FT misc_feature FT FT FT FT		FT misc_feature FT FT FT FT FT EXON	FT FT misc_feature FT	FT misc_feature FT misc_feature FT misc_feature			FT misc_feature FT FT misc_feature FT	FT misc_feature FT misc_feature FT misc_feature	FT FT misc_feature FT	FT misc_feature FT misc_feature FT misc_feature	FT misc_feature FT FT F	FT misc_feature
													·		
	/note= "indefinite interval within intron 2" 2141 /*tag- g /note= "known polymorphic site"	22072260 /*tab /note= "exon 3" 22612677	/*tag= "1 1 3" //note= "1.11ron 3" 25692581 /*tag= "1.11ron 3" //note= "1.11ron 3"	2788 k "exon 4"	/*tag= 1 /note= "known polymorphic site" 27893328 /*tag= m /note= "intron 4"	33293406	/*tag= o /note= "exon 5" 3407 .3813 /*tag= p /note= "intron 5"	35983610 /*tag= q /note= "indefinite interval within intron 5" 3653	r "known 3902 s	/note= "exon 6" 39034224 /*tag= t /note= "intron 6" 40764088		4365. 6571 /*tag= w /note= "intron 7" 4391. 4392 /*tag= x	. 4 .	/*tag= 2 /note= "known polymorphic site" 65726677 /*tag= aa /note= "excn 8" 66789163	/note= "intron 8" 6823
intron misc_feature	misc_feature	exon intron	misc_feature	exon misc_feature	intron	misc_reature exon	intron	misc_feature misc_feature		intron misc_feature		intron misc_feature	misc_feature misc_feature	exon	misc_feature

us-08-653-294-36.rng

```
*tag- p
note- "intron 5"
508. 3610
frag- "indefinite interval within intron 5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag= y
note= "Indefinite interval within intron 7"
                                                                                                                                                                                  *tag= j
note= "indefinite interval within intron 3"
678. .2788
                                                                                                                                                                                                                                                                                                                                  *tag- n
note- "indefinite interval within intron 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= t
note= "intron 6"
.4088 (*tag= u
note= "indefinite interval within intron 6"
                                        *tag= f
note= "indefinite interval within intron 2"
                                                                                                                                                                                                                                                        /*tag= 1
/note= "known polymorphic site"
/note= "3328
/*tag= m
/note= "intron 4"
                                                                      /*tag= g
/note= "known polymorphic site"
2207. .2260
/*tag= h
/note= "exon 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= r
/note= "known polymorphic site"
3814. .3902
3814. .302
/note= "exon 6"
3903. .4224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag= x
note= "known polymorphic site"
602. ,4614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= z
note* "known polymorphic site"
572. .6677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag- ab
/note- "intron 8"
6823
/*tag- ac
     = e
= "intron 2"
.1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= w
/note= "intron 7"
{391. .4392
                                                                                                                                                *tag= 1
note= "intron 3"
569. .2581
                                                                                                                                                                                                                                                                                                                                                                    /*tag= o
/note= "exon 5"
3407. .3813
                                                                                                                                                                                                                      *tag= k
note= "exon 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "exon 7"
365. .6571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= aa
/note= "exon 8
5678. .9163
                                                                                                                                                                                                                                                                                                                                                         .3406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4364
                           misc_feature
                                                               misc_feature
                                                                                                                                                                        nisc_feature
                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nisc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                             Intron
                                                                                                                                     Intron
                                                                                                                                                                                                                                                                                  Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Intron
                                                                                                   exon
                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     noxe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                noxe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq_documentation_block:

ID 117516 standard; cDNA; 24026 BP.

AC 117516;

DT 04-OCT-1996 (first entry)

E Mutated BRCAl genomic sequence from PM16.

KW Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;

KW qene therapy; protein replacement therapy; protein mimetic; BRCAl; ds.

CS PMOS Sapiens.

CS PMOS Sapiens.
                                                                                                                                                                                                                     noté- "indefinite interval within intron 12"
5953. .16126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 24026
                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
Quality: 36.00 Length: 11
Ratio: 3.600 Gaps: 0
Percent Similarity: 90.909 Percent Identity: 63.636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/note= "known polymorphic site"
| 1513. .1611
| /*tag= d
/note= "exon 2"
| 1612. .2206
                                                                                                                                                                                                                                                                                *tag- bi
note= "known polymorphic site"
6127. 16565
                                                                                                                                                                                                                                                                                                                                                          **tag= bk
foote= "known polymorphic site"
16370. .16382
/*tag= bl
/note= "known polymorphic site"
14966
                                     "known polymorphic site"
.15424
                                                                                                           "known polymorphic site".
15511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: T17514 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
256. 355
/*tag= a
/*tote= "exon 1"
356. .1512
/*tag= b
/*tag= b
1295
                                     /note= "known polymc
15024. 15424
/*tag= bc
/note= "intron 11"
15284
                                                                                                                                  bj
. "intron 13"
                                                                                                                                                                                                                                             /*tag= bh
/note= "exon 13"
16077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-36 x T17514/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:T17516
                                                                                                                                                                                                                                                                                                                    /*tag=
/note=
16243
                                                                                                   *tag=
note=
5425.
                                                                                                                                                                                                           *tag=
                                                                                    misc_feature
                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                misc_feature
                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                            intron
                                                                                                                                                                                                                                                                                                          intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
                                                                                                                          exon
                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
```

```
misc_feature
                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                    'tag- ak
note- "indefinite interval within intron 10"
1598. .15023
/note= "known polymorphic site"
9106
                                 "known polymorphic site"
                                                                                                "known polymorphic site".10530
                                                                                                                                                                "known polymorphic site".
.10607
                                                                                                                                                                                                                                                                                                                                                   an
"known polymorphic site'
                                                                                                                                                                                                                                                                                                                                                                                                                 ap
"known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag= as
note= "known polymorphic site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               au
"known polymorphic site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4046
*tag= ax
note= "known polymorphic site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               *tag= ay
note= "known polymorphic site"
4874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag= az
note= "known polymorphic site"
4891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= ba
/note= "known polymorphic site"
                                                                                                                                                                                                                                                                                                                              "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                           "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                  aq
"known polymorphic site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag= at
note= "known polymorphic site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "known polymorphic site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "known polymorphic site
                                                                                                                                                                                                                               "intron 10"
                                                                                                                                                                                                                                                                                      al
"exon 11"
                                                                                                                               "intron 9"
                                                                                                                                                                                               "exon 10"
.11597
                      /*tag= ad
/note= "known po]
9164. .9209
7.tag= ae
/note= "exon 9"
                                                                                                                                                                                                                                          .11396
                                                                                     /*tag= "note= ")210. .1
                                                                                                                                                      *tag=
note=
0531.
                                                                                                                                                                                    *tag=
note=
0608.
*tag=
note=
1384.
                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
note=
3238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
note=
                                                                                                                                                                                                                                                                                                                                                     *tag=
note=
2952
                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
note=
3009
                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
note=
3048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
note=
4041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                *tag=
note=
3951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3448
                                                                                                                                           misc_feature
             misc_feature
                                                                          misc_feature
                                                                                                                                                                                                                                           misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                            intron
                                                                                                                                                                                                           intron
```

```
*tag= bg
note= "indefinite interval within intron 12"
5953. .16126
                                                                                                                                                                                                                                                                             Length: 11
Gaps: 0
Percent Identity: 63.636
*tag= bb
note= "known polymorphic site"
5024. .15424
                                                bd
"known polymorphic site"
.15511
                                                                                                                                                                                                                           '*tag- bk
/note- "known polymorphic site"
16370, 16382
/*tag- bl
                                                                                                                                                                          *tag- bi
note- "known polymorphic site"
6127, 16565
                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: T17516 from: 1
                        bc
"intron 11"
                                                                                                       note- "intron 12"
5647. .15659
                                                                                                                                                                                                            "intron 13"
                                                                                                                                                    note- "exon 13"
6077
                                                                                 "exon 12"
.15952
                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-36 x T17516/rev
                                                                                                                                                                                                                                                                            36.00
3.600
90.909
                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:T17517
                                                                          *tag=
                                                                                                   *tag=
                                                 *tag=
                                                                                                                                                                                                     *tag=
                                                                                                                                                                                                                                                                    alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                  misc_feature
                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                            misc_feature
                                         misc_feature
                                                                                                                                                                                                                    misc_feature
                 intron
                                                                                           intron
                                                                                                                                                                                             intron
```

FT misc_feature FT	FT exon	FT FT misc_feature FT	FT intron	FT misc_feature	FT exon	FT intron	FT FT misc_feature FT	FT exon	FT FT misc_feature FT	FT FT misc_feature FT	FT FT misc_feature FT	FT misc_feature FT	FT FT misc_feature FT	FT FT misc_feature FT	FT FT misc_feature FT	FT FT misc_feature FT	FT FT misc_feature FT	FT misc_feature	FT misc_feature FT	FT misc_feature FT	FT FT misc_feature FT	FT FT misc_feature FT	FT FT misc_feature FT	FT misc_feature
	·			<del></del>														<del></del>	-		. 1902	<u></u>		· 
,												•												
note= "intron 2" 99251937		= 13	/*tag= h //note= "exon 3" 2261. 2677	"tage" "intron 3" 'note= "intron 3" '5692581	"tag- ; note= "indefinite interval within intron 3" 66782788	.cay note exon 4" 725	= m	* w.	*tag- n note= "indefinite interval within intron 4" 3293406	*tag= o note= "exon 5" 407. 3813		<pre>**tag= q 'note= "indefinite interval within intron 5" 1653</pre>	*tag= r note= "known polymorphic site" 8143902		/*tag= t note= "intron 6" 10764088	<pre>/*tag= u /note= "indefinite interval within intron 6" 1254364</pre>	= vo	*Lag* "	"tag= "x note= "known polymorphic site" 6024614	.*tag=_ y 'note=_"indefinite interval within intron 7" 5338	/*tag= z /note= "known polymorphic site" 6572. 6677	/*tag= aa /note= "exon 8" 678. 9163	/*tag= ab //note= "intron 8"	oozo /*tag= ac /note= "known polymorphic site"
~~		/*te	/*ta /nod 226:	///	/noi 2671	//0	/*t		/*ta /nod 3329	340.1	<b>\</b> \(\mathrea{\pi}\)	(11)	· \ \(\)	/*ta /not 3900	//4	/*te	/*të /nod 436	//4,	//4		/*te /not 657:	/*ta /not 6678		
misc_feature	misc_feature	exon	intron	misc_feature	exon	misc_feature	intron	misc_feature	exon	intron	misc feature	misc feature	exon	intron	misc_feature	exon	intron	misc_feature	misc_feature	misc_feature	exon	intron	misc feature	שרמכן דעם בכלי שרמכן דעם בכלי

misc\_feature 9106

misc\_feature

```
*tag= bf
note= "intron 12"
5647, 15659
*tag= bg
*tag= bndefinite interval within intron 12"
5953. 16126
                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:

Quality: 36.00 Length: 11
Ratio: 3.600 Gaps: 0
Percent Similarity: 90.909 Percent Identity: 63.636
                                                                                                                                                                                                                                                                            /*tag= bi
/note= "known polymorphic site"
/note= "loss bi
/note= "intron 13"
/*tag= bk
/note= "known polymorphic site"
/*tag= bk
/*tag= bl
/*tag= bb
/note= "known polymorphic site"
                                                                              *tag= bd
note= "known polymorphic site"
5425. .15511
                                        *tag= bc
note= "intron 11"
5284
                                                                                                                                                                                                                                        /*tag= bh
/note= "exon 13"
16077
                                                                                                                                 "exon 12"
                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                 misc_feature
                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                           intron
                           intron
                                                                                                                                                intron
                                                                                                         exon
                                                                                                                                                                                                                                exon
```

Align seg 1/1 to reverse of: T17517 from: 1 to: 24026

alignment\_block: US-08-653-294-36 x T17517/rev

```
AQ057253 CIT-HSP-2343E21.TF
AQ114390 CIT-HSP-2377N1.TF C
AQ870816 nbeb0041C06f CUGI R
                                                                                                                         seq_documentation_block: 724 bp DNA GSS 18-OCT-1999
LOCUS AQ851612
DEFINITION CPG1352B CPIOWAGDNA1 Cryptosporidium parvum genomic similar to SKB1
homologue (negative regulator of mitosis) (regulator of 5hkl, a
p21(cdc42/Rac)-activated kinase (PAK)), genomic survey sequence.
ACCESSION AQ851612.1 G1:6063307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 415 206 8846
Tel: 415 206 8846
Exa: 415 206 8845
Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db.ref="tona" / /db.ref="tona" /db.ref="ton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (http://sequence-www.stanford.edu/group/techdev/shear.htm). The randomly whw.stanford.edu/group/techdev/shear.htm). The randomly sheared gDNA was chromatographed on Sephacryl S-400 to remove any small fragments and DNA aluting in the void volume was subcloned into an EcoR V-digested, alkaline phosphatase-treated pBlueScript II (SS-) vector and transformed into E. coll strain XL2 Blue MRF'. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7
                                                                                                                                                                                                                                                                                                   Cryptosporidium parvum.
Cryptosporidium parvum
Cryptosporidium parvum
Cryptosporidium parvum
Cryptosporidiude: Alveolata; Aplocomplexa; Coccidia; Elmeriida;
Cryptosporidiidae; Cryptosporidium.

I (bases 1 to 724)
Strong, W. B. and Nelson, R. G.
Cryptosporidium parvum GSS Project
Unpublished (1997)
On Sep 10, 1998 this sequence version replaced gi:3553959.
Contact: Nelson, R. G.
Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  San
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
0
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .724
/organism="Cryptosporidium parvum"
/strain="IOWA"
  455
456
462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps:
Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
278.00
278.72
283.03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: AQ851612
126.54
126.52
126.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-36 x AQ851612/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primers."
37.00
37.00
37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.00
                                                                                     seq_name: gb_gss6:AQ851612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               264
  gb_gss8:AQ057253
gb_gss9:AQ114390
gb_gss6:AQ870816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV13299 AV13299 Mus musculus
N76762 yv45c0l.rl Soares fetal
330048 HHEA2OC Arrium cDNA libr
AQ908311 GSTC05069 Trypanosome
AQ075626 CIT-HSP-2354C2.TR CIT-
AQ044478 CIT-HSP-2354C2.TR CIT-
AN110273 BSBMMFS244D195K Brugia
AN110273 BSBMMFS244D195K Brugia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIT-HSP-2329021.TF CIT
LMAJFV1_lm23c02.x1 Le1
CIT-HSP-2383B10.TF CIT
CIT-HSP-2329013.TF CIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG000734 Homo sapiens genomic d
AQ840156 nbxb0052C09f CUGI Rice
AQ327491 nbxb0041M03r CUGI Rice
                                                                                                                                            Command line parameters:
-MODEL-framet-pln.model -DEV=xlp
-Q-/cgnl_1/USFTO_spool/US08633294/runat_04022000_160700_15770/app_query.fasta.2
-Q-/cgnl_1/USFTO_spool/US08633294/runat_04022000_160700_15770/app_query.fasta.2
-DB=SST -OFMT=fastap -SUFFIX=ref -GAPOP=12.000 -GAPDFT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GAPOP=6.000
-GAPEXT=7.000 -XGAPOP=10.000 -XGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=A.5 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE-LOCAL
-OUTFNT=pfs -NORM=axt -MINLEN-0 -MAXLEN-1000000 -USER-US08653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ111833
AQ040090
                                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EScore 1
27.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20

727.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.40
27.40
26.90
126.78
1125.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZSCOTE
144.66
1136.79
1136.04
1137.07
1134.53
1131.90
1131.90
1131.26
1131.26
1131.26
1131.26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128.35
128.16
128.16
128.16
128.12
128.12
128.12
127.69
127.69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128.33
128.81
127.01
127.01
126.89
126.74
126.74
126.70
126.62
EST:*
                                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
Ouery: US-08-653-294-36
Query length: 12
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 7600.090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orig
OM of: US-08-653-294-36 to:
                                             Ā
                                          6:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est20:D25244
gb_gss8.AQ075747
gb_est27.A1943775
gb_gss3:B74688
gb_gss9:A0122064
gb_est19:AA802286
gb_est27:A165570
                                          Date: Feb 8, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_est5:H72837
gb_est37:A1949481
gb_est1:L33574
gb_est12:AA983105
gb_gss9:AQ137850
gb_est44:AV396088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est25:A1297201
gb_est26:A1380173
gb_est28:A1517485
gb_est25:A1258274
gb_est25:A1258370
gb_est25:A1258370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_gssl:AG000734
gb_gss6:AQ840156
gb_gssll:AQ327491
gb_est34:AV132998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est27:AI402928
gb_est28:AI513785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_gss5:AQ815582
gb_est23:AI107515
gb_est23:AI135307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss8:AQ044478
gb_est23:AI110273
gb_gss6:AQ869567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_gss10:AQ193772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3b_gss6:AQ851612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_gss9:AQ111833
gb_gss8:AQ040090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_gss7:AQ908311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3b_gss8:A0075626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQ846844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss8:AQ043928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est6:N76762
gb_est1:230048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gssb_db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gssb-db
```

REFERENCE AUTHORS

```
Tumor Gene Index
Inpublished (1997)
On Jun 22, 1998 this sequence version replaced gi:3247088.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-11550
Email: Robert_Strausbergenh.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert_Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Mashington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                      A1949481 547 bp mRNA EST 06-SEP-1999 wq10g04.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470902 3',
                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 547) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="lwGE:2470902"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
                            289 TACCCACTAGCCCTGAAAAGGGTAAAACTTCGATAT 254
1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: -40UP from Gibco
High quality sequence stop: 454.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host-"DH10B"
                                                                                                                                                                                                                                                   AI949481.1 GI:5741713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AI949481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-653-294-36 x AI949481
                                                                                     seq_name: gb_est37:A1949481
                                                                                                                                                                                                        mRNA sequence.
A1949481
                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134
                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Source
                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              H72837 504 bp mRNA EST 27-0CT-1995 ys06c01.s1 Soares fetal liver spleen lNFLS Homo sapiens cDNA clone IMAGE:213984 3', mRNA sequence.
                                                                                                                                                                                                                                              Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 504)
Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,
Mardis,E., Moorte,B., Morris,M., Parsons,J., Prange,C., Rifkin,L.,
Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,
Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996) 97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
Insert Size: 528
High quality sequence stops: 380
Source: IMAGE Consortium, LLNL
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 528
Std Error: 0.00
Seq primer: promega -21ml.3
High quality sequence stop: 380.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On May 8, 1995 this sequence version replaced gi:799648. Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:213984"
/clone_lib="Soares fetal liver spleen lNFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:3779288"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
                                                                                                                                                                           H72837.1 GI:1044653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-36 x H72837/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.00
                                                                seq_documentation_block:
LOCUS H72837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and Marra, M.
                     seq_name: gb_est5:H72837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                           DEFINITION
                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
```

FEATURES

```
**Note="Organ: Kidney; Vector: pT713D-Pac (Pharmacia) with a modified polylinker: Site_1: Not I: Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Pollowing HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clone1Ds 1333912-1325831, 1471368-1472903 and Patima Bonaldo. "Subtraction by Bento Soares and M. Patima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 12
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrargLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 547
                                                                                                                                                                                                                                                                                                          109 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
```

to: 504

to reverse of: H72837 from: 1

Align seg 1/1

ORIGIN

```
T 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into RNA browided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AQ137850 461 bp DNA GSS 24-SEP-1998
LOCUS AQ137850 AFF CIT Approved Human Genomic Sperm Library D Homo saptens: genomic clone plate=3058 Col-18 Row=F, genomic survey
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fat: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:697495
Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 352.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, Reller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                     1. 429
/organism="Mus musculus"
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="ImAcE:1348703"
/sex="male"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||||||::|||||||::
185 CTCGCGGTGCGTAGGGTCAGGCTGAGGTAT 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence.
AQ137850
AQ137850.1 GI:3528503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo."
116 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AA983105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-36 x AA983105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_gss9:AQ137850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . ummu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                          seq_documentation_block:
LOCUS L33574 325 bp mRNA EST 08-OCT-1996
DEFINITION BNAESTF350 Mustard flower buds Brassica rapa cDNA clone F0350, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AA983105 429 bp mRNA EST 27-MAY-1998
DEFINITION UA35512.rl Scares mouse mammary gland NDMMG Mus musculus cDNA clone
IMAGE:1348703 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 429)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 325)
Lim.C.O., Kim.H.Y., Kim.M.G., Lee,S.I., Chung,W.S., Park,S.H., Hwang,I. and Cho,M.J.
Expressed sequence tags of Chinese cabbage flower bud CDNA Plant Physiol. 111 (2), 577-588 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Waterston, R.

The Washu-HHMI Mouse EST Project
Unpublished (1996)
On Apr 13, 1998 this sequence version replaced g1:2958638.
Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 11
Gaps: 0
Percent Identity: 63,636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="pekinensis"
/db_xref="taxon:3711"
/clone="10350"
/note="lb="Mustard flower buds"
/note="Devel_stage = flower bud
115 c 58 g 82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Lim,C.O., Hwang,I. and Cho,M.J.
Email: pmbbrc@nongae.gsnu.ac.kr.
Location/Qualifiers
1. .325
/organism="Brassica rapa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to reverse of: L33574 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA983105
AA983105.1 GI:3160383
                                                                                                                   sequence.
L33574
L33574.1 GI:508041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-36 x L33574/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 3.545
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est21:AA983105
                                                                                                                                                                                                             Brassica rapa.
                                                                                                                                                                                                                                    Brassica rapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
       seq_name: gb_est1:L33574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                           Brassica
                                                                                                                                                                                                                                                                                                                                                                                                                                                      96255495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
```

BASE COUNT ORIGIN

REFERENCE AUTHORS

ACCESSION

JOURNAL

COMMENT

TITLE

FEATURES

Holzman, T., Adams, M.D. and

ORGANISM

ACCESSION KEYWORDS SOURCE

/ERSION

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

and

us-08-653-294-36.rst

Length: 10 Gaps: 0 Percent Identity: 70.000

from: 1

```
D25244 572 bp mRNA EST 12-MAR-1998 HUMRES417B Clontech catalog #CLHL1076b Homo sapiens cDNA clone RES4-17, mRNA sequence.
                                                                                                                                                                                                                                                                                                  2 ArgleuAlalleArgArglleAlaLeuArg 11
                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: Av396088
                                                                                                                                                                      alignment_block:
US-08-653-294-36 x AV396088/rev
                                                                                 Quality: 39.00
Ratio: 3.900
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_gss8:AQ075747
                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_est20:D25244
                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            namn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakame@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonadaceae; Chlamydomonas.
1 (bases 1 to 529)
Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
A Large Scale Structurai Analysis of cDNAs in a Unicellular Green Alga, Chlamydomonas reinhardtii. I. Generation of 3451
non-redundant Expressed Sequence Tags
DNA Res. (1999) In press
On May 18, 1998 this sequence version replaced gi:3137395.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="CL56h04_r"
/clone_lb="Chlamydomonas reinhardti1 C9"
/dev_stage="photoautotrophic growth"
/note="vector: pBluescriptII SK-: Site_1: EcoRI; Site_2:

    1. .461
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone="Plate=3058 Col=18 Row=F"
    /clone=1lb="CIT Approved Human Genomic Sperm Library D"
    /sex="male"

                                                                                                                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B" 125 c 102 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AV396088 529 bp mRNA EST 09-DEC-1999
DEFINITION AV396088 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii cDNA clone CL56h04_r, mRNA sequence.
High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallacedu.washington.edu
Sequence Tagged Connector
Plate: 3058 row: F column: 18
Class: BAC end8
High quality sequence stop: 461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .529
/organism="Chlamydomonas reinhardtii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 CATCGACTCACTATAAGGCGAATTCTGGCCAGGTAC 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TyrArgLeuAlaIleArgArgIleAlaLeuArgTyr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref-"taxon:3055"
                                                                                                                                                                                                                                                                                                                                                                                                102 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AQ137850 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AV396088.1 GI:6550304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.00
3.900
83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-36 x AQ137850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est44:AV396088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106
                                                                                                                                                                                                                                                                                                                                                                                                  132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
```

```
Ikeda,J.
Isolation and characterization of 21 novel expressed DNA sequences
Isolation and characterization of thuman chromosome 4p
Genomics 22 (2), 302-312 (1994)
95104839
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 572)
Ishida;Y., Hadano,S., Nagayama,T., Tomiyasu,H., Wakasa,K. and
                                                                                                                                                                                                                                                                                                                                            on May 9, 1995 this sequence version replaced gi:804176.
Contact: Yoshikazu Ishlda
Ikeda GenosHERE project/ERATO/JRDC
Tokal University School of Medicine
Bohseidai, Isehara, Kanagawa 259-1193, Japan
Emall: shinjienga.med.u-tokai.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="RES4-17"
/clone_llb="Clontech catalog #CLHL1076b"
/tlssue_type="caudate"
/dev_stage="20-year-old adult" 18 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 3.900 Gaps: 0 Percent Similarity: 83.333 Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to reverse of: D25244 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="4p15-4p16.1"
D25244
D25244.1 GI:434739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-36 x D25244/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.00
```

```
University
University
Unpublished (1999)
On Dec 20, 1995 this sequence version replaced gi:1135666.
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 227
FAX: 650 728 821
Email: walbot@stanford.edu
Plate: 618045 row: E column: 09.
 Walbot, V.
Maize ESTs from various cDNA libraries sequenced at Stanford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 ceegracccreceaaeegraeccrecec 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B74688.1 GI:2770375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AI943775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-36 x AI943775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_gss3:B74688
                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSS.
                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                   JOURNAL
COMMENT
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                Venically J.C.

Venically J.C.

Venically J.C.

Venically J.C.

Venically J.C.

Map Building

Unpublished (1998)

Other_GSSs: CIT-HSP-2354G2.TF

Contact: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page:

http://www.tigr.cog/tdb/humgen/bac_end_search/bac_end_search.html.

Seg primer: Mi3 Reverse

Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
ephyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
Poaceae; Zea.
1 (bases 1 to 408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI943775 408 bp mRNA EST 09-AUG-1999 618045E09.x1 618 - Inbred Tassel CDNA Library Zea mays CDNA, mRNA
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 360)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K. Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
AQ075747 360 bp DNA GSS 20-AUG-1998
CIT-HSP-2354G2.TR CIT-HSP Homo sapiens genomic clone 2354G2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 11
Gaps: 0
Percent Identity: 72.727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AQ075747 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .360
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2354G2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        б
                                    genomic survey sequence.
                                                   AQ075747
AQ075747.1 GI:3437403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AI943775.1 GI:5713783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-36 x AQ075747/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38.00
3.800
90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est37:A1943775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AI943775
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
AI943775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays.
Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                           ORGANISM
                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                COMMENT
```

```
Human:

Butherials

Butherials
/organism="Zea mays"
/cultivar="Ohio43"
/Cultivar="Ohio43"
/db_xref="taxon:4578"
/clone_lib="618 - Inbred Tassel cDNA Library"
/tissue_type="tassel"
/tasue_type="tassel"
/lab_host="XLOLR"
/lab_host="XLOLR"
/note="Organ: tassel; Vector: pAD-GAL4-2.1 (Hybrizap);
Inbred tassel library from Schmidt lab"
120 c 136 g 72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seg_documentation_block: 440 bp DNA GSS 24-OCT-1998
LOCUS B74688 CIT-HSP Homo sapiens genomic clone 2034Ell,
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 70.000
```

us-08-653-294-36.rst

```
. Align seg 1/1 to reverse of: AA802286 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-36 x AA802286/rev
   Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fruit fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
Ratio:
Percent Similarity:
 159
                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                   Align seg 1/1
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 455)
Mahahas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A0122064 455 bp DNA GSS 22-SEP-1998 HS_3077_B2_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3077 Col-20 Row=F, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=3077 Col=20 Row=F"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                1. .440
/organism="Homo saplens"
/db_xref="taxon:9606"
/clone="2034511"
/clone="2034511"
/sax="Male"
/cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
VGI Oueen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                           38.00 Length: 12
4.222 Gaps: 0
75.000 Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138
                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence Tagged Connector
Plate: 3077 row: F column: 20
Class: BAC ends
High quality sequence stop: 455.
Location/Qualifiers
                                     Location/Qualifiers
                                                                                                                                                                                                                                      ρ
                                                                                                                                                                                                                                    78
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: B74688 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ122064
AQ122064.1 GI:3499230
                                                                                                                                                                                                                                    88
C
 Seq primer: M13-21
Class: BAC ends.
                                                                                                                                                                                                                   "IIIDUII"
                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-653-294-36 x B74688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_gss9:AQ122064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AQ122064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
MEDLINE
COMMENT
                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
```

```
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="GM04141"
/clone="ILb="GM Drosophila melanogaster ovary BlueScript"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AA802286 561 bp mRNA EST 25-NOV-1998
DEFINITION GM04141.5prime GM Drosophila melanogaster ovary BlueScript
Drosophila melanogaster cDNA clone GM04141 5prime, mRNA sequence.
ACCESSION AA802286
VERSION AA802286.1 GI:2871405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Preryota; Neoptera; Endopteryota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 561)
S Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,
Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
Unpublished (1997)
On Sep 12, 1996 this sequence version replaced gi:1402170.
Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="newly eclosed females: germarium-stage 6"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: http://www.fruitfly.org/EST, estefruitfly.berkeley.edu
plate: 41 row: D column: 5
High quality sequence stop: 411.
Location/Qualifiers
    1 others
                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 58.333
ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
  122
                                                                                                                                                                                                                                                                                      ;
t
                                                                                                                                                                                                                                                                                                                                                               17 CGACTIGCTATACGTCGAATCACTATACGG 46
                                                                                                                                                                                                                                                                                                                                  2 ArgleuAlalleArgArglleAlaLeuArg 11
       9
                                                                                                                                                                                                                                                                                      from: 1
    8
       ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.455
91.667
                                                                                                                     Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
    81
                                                                                                                                                                                                                                                                                 to: AQ122064
                                                                                                                                                                                                                  alignment_block:
US-08-653-294-36 x AQ122064
                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est19:AA802286
```

to: 561

us-08-653-294-36.rst

```
alignment_scores:
        ORGANISM
                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // organism="Drosophila melanogaster"
// db_xeref="taxon:727"
// clone="GH25611"
// clone="GH25611"
// clone="GH25611"
// clone="GH25611"
// sex="male and female"
// dev_stage="adult"
// lab_host="DH5" - alpha"
// note="Organ: head; Vector: pOT2; Site_1: EcoR1; Site_2:
// note="Organ: head; Vector: poT2; Site_1: gite_2:
// note="Organ: head; Vector: poT2; Site_1: coR1; Site_2:
// lab_host="DH5"
// lab_hos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exit. fiy.

Exaryora: Mecanogaster

Endaryora: Mecanogaster

Endaryora: Mecanogaster

Pterygota: Meoptera; Endopterygota: Diptera; Brachycera;

Muscomorpha: Ephydroidea; Drosophila.

I (bases 1 to 572)

S Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C.,

Brockstein, P., Lewis, S. and Rubin, G. M.

BDGP/HHMI Drosophila EST Project

L Upublished (1997)

On May 7, 1998 this sequence version replaced gi:3118953.

Contact: Harvey, D.

G. M. Rubin-Molecular and Cell Biology
University of California Berkeley

539 LSA, Berkeley, CA 94720-3200, USA

Fax: 510 643 9947.
                                                                                                                                                                                                                                   seq_documentation_block: 572 bp mRNA EST 08-FEB-1999 DEFINITION GH25611. Sprime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH25611 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block: 13 bp mRNA EST 08-FEB-1999 LOCUS A1402928 573 bp mRNA EST 08-FEB-1999 DEFINITION GH22268.5prime GH Drosophila melanogaster cDNA clone GH22268 5prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC005707; hit genomic sequence AC006089
Plate: 256 row: A column: 11
High quality sequence stop: 450.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 58.333
                                        504 CACCGTCTGCAGATACGGCGAGTTGGGCTGCGGCAC 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuAlaileArgArgileAlaLeuArgTyr 12 :::|||||| |||||||||||:::::||||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AI405570 from: 1
                                                                                                                                                                                                                                                                                                                                                                                         AI405570
AI405570.1 GI:4248657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI402928.1 GI:4246015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-36 x AI405570/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.00
3.455
91.667
                                                                                                                                                      seq_name: gb_est27:A1405570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est27:AI402928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fruit fly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
```

```
/.organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/db_xref="taxon:7227"
/clone_lib="GH Drosophila melanogaster head pOT2"
/sex="male and female"
/sex="male and female"
/sex="male and female"
/lab_host="bh="clonale"
/note="organ: head; Vector: pOT2; Site_1: EcoRI; Site_2:
/note="organ: head; Vector: pOT2; Site_1: EcoRI; Site_2: EcoRI; EcoRI; EcoRI; Site_2: EcoRI; EcoRI; EcoRI; EcoRI; EcoRI;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Petryqota; Neoptera; Endopteryqota; Diedrycera; Brachycera; Muscomorpha; Ephydroidea; Drosophila.

E 1 (bases 1 to 573)
S Harvey, D., Hong, L., Evans-Holm, M., Pendleton, J., Su, C., Brokstein, P., Lewis, S. and Rubin, G.M.
BDGP/HHMI Drosophila EST Project
U npublished (1997)
On Apr Z.1, 1998 this sequence version replaced gi:3071085.
Contact: Harvey, D.
G. M. Rubin-Molecular and Cell Biology
University of California Berkeley
539 LSA, Berkeley, CA 94720-3200, USA
Fax: 510 643 9947
Email: http://www.fruitfily.org/EST, est@fruitfly.berkeley.edu
htt genomic sequence Ac005707; hit genomic sequence Ac006089
plate: 222 row: F column: 8
High quality sequence stop: 506.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 12
Gaps: 0
Percent Identity: 58.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TyrArgLeuAlaileArgArgileAlaLeuArgTyr 12 :::|||||| ||||||||||:::::|||||||::: 527 CACCGTCTGCAGATACGCCGAGTTGGGCTGCGGCAC 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: AI402928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-08-653-294-36 x AI402928/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 38.00
Ratio: 3.455
Percent Similarity: 91.667
```

THIS PAGE BLANK (USPTO)

.

## GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

sw model OM protein - protein search, using

8, 2000, 04:05:45 February Run on:

Search time 133.56 Seconds (without alignments)
1.773 Million cell updates/sec

US-08-653-294-37 Title: Perfect score:

51 1 RVDLRTLRGY 10 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45

summaries

A\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Consensus sequence	T-cell modulating	Human HLA-A2-(62-8	Human MHC 1 and HL	٦.	1 61	e)		HLA-A2.1.60-84. Co	Chimeric HLA-A2.1/	HLA epitope. HIV G	Peptide fragment o	HLA-Bw46 CTL modul	-09	HLA-alpha-1. Use o	ф С	HLA-C exon Cb-2. H	Breast cancer asso	Peptide fragment o	T-cell modulating	Alpha-1 domain of	9	MHC class I-derive	Peptide fragment o	T-cell modulating	Human MHC 1 alpha		m	Human MHC 1 alpha	modu	Glucose transport	MHC 1	MHC 1 al	Human MHC 1 alpha
SUMMARIES		Δī	P80911	51	R71439	44	R84876	R84875	R41222	R83074	R95420	W68385	R44112	R41206	R83072	R95418	R71629	R12465	R12466	x07033	R41211	W07521	P90513	R08111	R69618	R41210	W07516	R71431	W52846	R84869	R71430	W07524	2	44	а.	142
		DB	П	٦	٦	٦	٦	Н	-	н	Н	Н	Н	Ч	Н	Н	Н	-	Н	-	-	-	Н	н	-	-	-	-	-	Н	Н	ч	-	П	Η,	Н
		Length	27	10	17	17	24	24	25	25	25	412	22	25	25	25	45	9	366	9	10	10	25	25	25	10	10	-	5069	σ	17	10	13	17	17	17
	Ϋ́	'		m				•		•	•	m	4.				7.			7.	'n	'n	5	'n	'n									9.		
•	8 Ouerv	Mat	88	86	86	86	8	89	8	86	86	8	78	78	78	78	78	78	78	78	76	76	76	16	76	7	74	74	74	72	72	70	2	70	2	70
		Score	45			44	44	44	44	44	44	44	40	40	40	40	40	40	40	40	39	39	39	39	39	38	38	38	38	37	37	36	36	36	36	36
	Result	SO.	щ	7	m	4	ស	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34

ö

Gaps ö

Length 274; 1; Indels

Score 45; DB 1; Pred. No. 0.1; 0; Mismatches 1

88.2%; 90.0%;

Query Match Best Local Similarity 90.0. 1 RVDLRTLRGY 10 

g

à

04-AUG-1997 (first entry)
T-cell modulating peptide #6.
T-cell modulating perforing perforing perforing mamman #6.
Theumatoid athritis; psoriasis; pemphigus vulgaris; Sjogren's disease; thyroid disease; Hashimoto's thyroidditis; myasthenia gravis; granzyme; autoblogous target cell; cytokine release; T cell activation; therapy.

W07517 standard; peptide; 10 AA. W07517;

Human MHC 1 alpha MHC peptide repeat 581 MHC peptide repeat MHC peptide repeat 682 MHC Deptide repeat 610 MHC 1 alpha Human MHC 1 alpha Human MHC 1 alpha MHC 1 peptide Dk-( Human MHC 1 alpha MHC 1 peptide Dk-( Human MHC 1 alpha MHC peptide having	n constitute the alpha-1, alpha-2 and ecules alpha-1, alpha-2 and alpha-3n"	UGS-008846.  US-008846.  US-008846.  US-008846.  US-10
R71433 W32583 W32581 W29422 W42422 R71427 R71427 R71427 R71420 W32582	cotein; 274 AA.  entry) of peptides which cons a class I HLA molecule tracellular domains al ation/Qualifiers 90 ce="alpha-1 region" 180 180 ct="alpha-2 region" 180 180 180 180 180 180 180 180 180 180	Jer C; histoco T-lymph Seases hi. ved fro Lved fro Lved ex The The Seases
	ttry) ttry) peptides peptides peptides cellular con/Quali alpha-1 80 "alpha-2 272	146.  rad Jr Univ.  rad Jr Univ.  r Chayberger  to major hi  cytotoxic T-  immune disea.  pp; English.  pp; English.  rate shown.  are shown.  ent HIA-A2 e.  cifficities.
нанананана 	n; rept.	Jr Jay Lune Lune Lune Lune Lune Lune Lune Lune
111111446 77777448		17-VE-198; U00245. 30-JAN-1987; US-008846. Krensky AM, Parham P, Clayberger C; WPI; 88-235147/33. WPI; 88-235147/34. WPI; 88-235147/47. WPI; 88-23
	# # # # # # # # # # # # # # # # # # #	AA AA
777777	standard; 1990 (fill us sequent us sequent epitopes; plens. I	% 1002. % 1002
<b>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~</b>	T 1 P80911 standard; pr P80911; 18 SEP-1990 (first Consensus sequence alpha-3 regions of HLA-A2 epitopes; ex HTM-A2 epitopes; ex FROM region 1. region 7.	11-FUG-1988; U00245. 30-JAN-1988; U00245. 30-JAN-1987; US-0088. (STRD) Leland Stanfol Kensky AM, Parham P. WPI; 88-235147/33. New peptide corresp. Used for modulating transplants or auto-ised for modulating transplants or auto-ised for modulating the concensus sequences alpha-2 and alpha-3; peptides from different spectides from different sequences from different sequences from different sequences from different spectides from different spectides from different sequences.
	SUL 091	PD 11-AUG-1 PR 30-JAN-1 PA (GTRD) L KERSKY DR KERSKY DR WPI; 88- PT New PEPT PT UNEW PEPT PT LEARSPIA PT LEARSPIA PT LEARSPIA CC THE FOOT CC THE FOOT
	TH-"THEOREMAN	* " " " " " " " " " " " " " " " " " " "

```
7 RVDLGTLRGY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
R84876
                                                                                                                              R71441
g
                                                                                                                                                               õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                          Treatment of auto-immune disease by admin. of peptide(s) corresp. to major histocompatibility complex antigens - esp. for delaying onset of cilinical symptoms of insulin dependent diabetes by modulating T cell madiated attack on target cells

Claim 7: Page 20; 24pp; English.

Worstown and the invention. These sequences are based on a portion of the major histocompatability complex (MFC) class I antigen (see the major histocompatability complex (MFC) class I antigen (see worston). The method is for affecting the course of an autofmmune disease involving T-cell mediated destruction of tissue in mammals. These involving T-cell mediated destruction of tissue in mammals. These convolving T-cell mediated destruction of tissue in mammals. These convolving T-cell mediated destruction of tissue in mammals. These convolving T-cell mediated destruction of tissue in mammals. These convolving T-cell mediated destruction of tissue in mammals. These call in the calcarded to the disease. Other diseases that can be treated are mallitus, preferably being administered during the pre-clinical stage to delay onset of the disease. Other diseases that can be treated are multiple sclerosis. Theumatoid arthritis, postiasis, pemphidus vulgaris, signer's disease, thyroid disease, Hashimoto's thyroiditis, myasthenia gravis, etc. The peptides modulate T-cell mediated attack on autologous carget cells, and may also reduce inflammation, swelling, and release of cytokines, perforins, granzymes etc. associated with T cell activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4: Page 45: 103pp; English.

R71439-R71443 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
They were used to modulate interactions between MHC 1/HLA and cell surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human HIA A2-(62-85) antigen derived peptide.
Human HIA-A2-(62-85) antigen derived peptide; cell receptor;
interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goldstein A, Goodenow RS, Olsson L; WPI; 95-098577/13. Regulating cell surface receptor response - by modulating interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 44; DB 1; Length 10;
Pred. No. 0.0047;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R71439 standard; peptide; 17 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                             14 NOV-1996.
05-APR-1996; U04710.
12-MAY-1995; US-440504.
(SANG-) SANGSTAT MEDICAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-AUG-1994; U09189.
12-AUG-1993; US-105416.
(REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVDLRTLLGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-FEB-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-0CT-1995
                                                                                                                                                            Buelow R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT TRESULT TRESULT TRESULT TREE SULT TREE 
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
```

```
Mew cell-mediated immune-specific immunogenic compsns. - used in prophylaxis and treatment of cancer, microbial infections, viral infections and parasitic infestations infections and parasitic infestations Example 1; Page 62; 141pp; English.

A claimed cell-mediated immune (CMI)-specific immunogenic compsn. comprises a conjugate of a primary antigen bearing a primary epitope, with an immunomodulatory peptide (IP), i.e. the present peptide. The IP comprises an allopeptide moiety of at least 5 anino acids, whose sequence corresponds to a polymorphic region of a MHC encoded polymorphic Class I or II antigen. The compsn. can be used to elicit a CMI-specific response which is prophylactic, or therapeutic for, e.g. microbial and viral infections, parasitic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surface receptors. Via competitive inhibition the peptides diminish the receptors response, this feature may be useful for the treatment of neoplasias, lupus erythematosus and arthritis.

Sequence 17 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 45; 103pp; English.
R71439-R71443 are human major histocompatibility complex class 1
(MHC 1) alpha 1 domain and HLA derived peptides and fusion peptides.
They were used to modulate interactions between MHC 1/HLA and cell
                                                                        Human MHC 1 and HLA fusion peptide Dk-(69-76)HLA-A2-(77-85).
Major histocompatibility complex class 1; MHC 1; cell receptor; alpha 1 domain; fusion peptide Dk-(69-76)HLA-A2-(77-85); interaction modulation; arthritis; neoplasias; lupus erythematosus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-MAY-1996 (first entry)
HIA AW68.1 61-84 immunogenic peptide.
Antigen; epitope; cell mediated; immune specific; cancer;
Infection; infestation; mucin-1; MUC-1; tumour; HLA AW68.1 61-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                          Goldstein A, Goodenow RS, Olsson L;
WPI; 95-099577/13.
Regulating cell surface receptor response - by modulating
interaction between MHC class I antigen and the cell surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infestations and cancer, partic. MUC-1 expressing tumour cellwhen the present peptide is the IP, and a MUC-1 epitope is the {\sf LP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1;
Pred. No. 0.0083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koganty RR, Longenecker BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R84876 standard; peptide; 24 AA. R84876;
R71441 standard; peptide; 17 AA.
R71441;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.3%;
90.0%;
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-APR-1995; U04540.
12-APR-1994; US-229606.
(BIOM-) BIOMIRA INC.
                                                                                                                                                                                                                                                 12-AUG-1994; U09189.
12-AUG-1993; US-105416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunogenic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 RVDLGTLRGY 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ding L, Koganty RI
WPI; 95-373528/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RVDLRTLRGY
                                                                                                                                                                           Homo sapiens.
WO9505189-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9527505-A1.
                                                 12-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-OCT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
```

ö

Gaps

ö

Score 44; DB 1; Length 17; Pred. No. 0.0083; 0; Mismatches 1; Indels

86.3%; 90.0%;

Query Match 86.3 Best Local Similarity 90.0 Matches 9; Conservative

1 RVDLRTLRGY 10

ŏ

ö

ö

Gaps

ö

ပ္ပင္တ

RESULT R84875

ö 셤

```
Example 13; Page 32; 80pp; English.

Example 13; Page 32; 80pp; English.

Example 13; Page 32; 803090-R83096 and R92907-R92913 represent fragments of class class I major histocompatibility complex (MHC) antigens. This sequence corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-A2. These sequences can be used to extend the period of The peptides are administered to a patient from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to administration for limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLA-A2 CTL modulating peptide (A2.1.60-84). Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-A2.
New peptide(s) based on Class I HLA antigen domains - used for modulating cytocoxic T-lymphocyte activity towards targets brample 13: Page 39; 61pp: English.

The peptide is used to modulate cytocoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL infection. The peptide can also be used for identifying CTLs which bind to it and removang subsets of CTLs from a T-cell composition. This peptide is derived from the HLA-A2.1 antigen and corresponds to the amino acid positions 60-84 of that antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%; Score 44; DB 1; Length 25; 90.0%; Pred. No. 0.013; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 1;
Pred. No. 0.013;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Parham P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R83074 standard; peptide; 25 AA.
R83074;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N95420 standard; peptide; 25 .
R95420;
12-NOV-1996 (first entry)
HLA-A2.1.60-84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clayberger C, Krensky AM,
WPI; 95-358582/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 RVDLGTLRGY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R95420
      à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME OF THE PART O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           822B
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ding L, Bloming INC.

Ding L, Koganty RR, Longenecker BM, Reddish MA;

WPI: 95-373528/48.

The Word oll-mediated immune-specific immunogenic compsns. - used in prophylaxis and treatment of cancer, microbial infections, viral infections and parasitic infestations.

Example 1: Page 62: 141pp: English.

Scample 1: Page 62: 141pp: English.

A claimed cell-mediated immune (CMI) *specific immunogenic compsn.

Comprises a conjugate of a primary antigen bearing a primary epitope, with an immunomodulatory peptide (IP), i.e. the present peptide.

Comprises an allopeptide moiety of at least 5 amino acids, whose sequence corresponds to a polymorphic region of a MHC encoded polymorphic class I or II antigen. The compsn. can be conded polymorphic class I or II antigen. The compsn can be coded polymorphic class I or II antigen. The compsn can be therepeutic for, e.g. microbial and viral infections, parasitic infestations and cancer, partic. MUC-1 expressing tumour cells when the present peptide is the IP, and a MUC-1 epitope is the
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-MAR-1994 (first entry)
Peptide fragment of HLA-A2.1 antigen.
Human leukocyte antigen: HLA, peptide; transplantation; neoplasia;
parasitic disease; oyfotoxic T lymphocyte; modulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-1996 (first entry)
HLA A2.1 61-84 immunogenic peptide.
Antigen: epitope; cell mediated; immune specific; cancer;
infection; infestation; mucin-1; MUC-1; tumour; HLA A2.1 61-84;
immunogenic peptide.
                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44; DB 1; Length 24; Pred. No. 0.012;
                                                                                                                                 Length 24;
                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                              Score 44; DB 1;
Pred. No. 0.012;
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-SEP-1993.
25-FEB-1993. U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R84875 standard; peptide; 24 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R41222 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86.3%;
90.0%;
                                                                                                                              86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krensky AM,
                                                                                                                              Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-001-1995; U04540.
12-APR-1994; US-229606.
(BIOM-) BIOMIRA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                            1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                          1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clayberger CA, Ki
WPI; 93-303134/38.
      primary epitope.
Sequence 24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
WO9317699-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R84875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primary
                                                                                                                                                                                                                                                                                                                                                                                                                         9
```

NAME OF THE PARTY OF THE PARTY

ò q ö

Gaps

ö

Length 25; 1; Indels N-PSDB; V30457

```
NEW STANDARD STANDARD
  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                            While Still State of Carlo and And State of Carlo and And State of Carlo and And State of State of Carlo and And State 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
HLA; p74; alphal-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC; B cell; calcium influx; cytocxic I lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W68385;
14-0CT-1998 (first entry)
Chimeric HLA-A2.1/Deta-2 microglobulin protein.
Antigen; major histocompatibility complex; MHC; lymphocyte; detection;
immobilisation; cytotoxic T-cell; tumour; leukaemia; lymphoma;
viral infection; chimeric; beta-2 microglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 1; Length 25;
Pred. No. 0.013;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "from human beta-2 microglobulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Abastado J, Kourilsky P, Langlade-Demoyen P, Lone Y;
WPI: 98-018653/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .302
/note= "from HLA-A2.1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-1997; F00892.
21-MAY-1997; F00892.
21-MAY-1996; US-651925.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="flexible linker" 313. 412
                                                                                                                                                          18-MAY-1995.
10-NOY-1994. U12985.
10-NOY-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W68385 standard; Protein; 412 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.3%;
90.0%;
                                                                                                                                                                                                                                                                        Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-194027/25.
                                                                                                                                                                                                                                                                     Clayberger C,
                                                                                                                                    WO9513288-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9744667-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 - NOV - 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
W68385
  ò
```

```
Percetion, purification and elimination of antigen-specific lymphocytes - for producing cytotoxic T cells for immuno-therapy of cancers and viral infection.

Example 2, Fig 10, 222pp; French.

Example 2, Fig 10, 222pp; French.

Example 2, Fig 10, 222pp; French.

Coetween antigen-specific lymphocytes comprises forming a complex complex of antigen-specific lymphocytes. Complex (MHC) molecules, immobilising the complex and binding samples containing the antigen-specific lymphocytes. Expression of the MHC molecule in a cell is detected by antibodies against the MHC molecule or by an antibody to a chimeric MHC-marker protein, e.g. an MHC/Deta-2-microglobulin chimeric protein and comprises the first 3 domains of the HLA-A2.1 heavy chain linked to human beta-2 microglobulin via a flexible linker. The method is also used to beta-2 microglobulin via a flexible linker. The method is also used to specific killing of tumour cells (solid tumours, leukaemia or lymphoma) by injection into a human or animal, but also for treating viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The patent claims epitopes of the HIV gpl60 protein which are immunologically monologous to at least one epitope of the HLA immunologically monologous to at least one epitope of the HLA.

The patent family, preferably the HLA class 1 protein heavy chains. The present sequence is a region of the heavy chain alpha-1 domain, cw4 allele, to which the epitopes are homologous. In particular, the epitopes are homologous to the sequences TQKKRQAQ and NLRKLRGYY.

The identification of HLV gpl60 epitopes homologous to HLA epitopes can be used to develop agents for vaccines and immunodiagnosis of HLY infection. The HLY publ60 epitopes homologous are able to induce anti-HLA autoantibodies and act as superantigens during the infection course, leading to a gradual and selective loss of certain T receptor families.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA epitope.
Epitope: immuno-homologue; HLA; heavy chain; alpha-1 domain; allele;
cw4; superantigen; immunodiagnostic; AIDS; HIV; immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 1; Length 412; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI: 93-386478/48.
HIV GP160 epitope(s) immunologically homologous to HLA -develop agents for immuno-diagnosis and vaccines for HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-MAY-1993; ITO049.
11-MAY-1992; IT-RM0350.
(SANR-) FOND CENT SAN ROMANELLO DEL MONTE TABOR.
(SUPE-) INST SUPERIORE DI SANITA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R44112 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l. .9
/label= epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JUL-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99 RVDLGTLRGY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beretta A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
```

ö

`

```
|| || || || || || || RVSLRNLRGY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RVDLRTLRGY 1:0
                                                                                  25 AA;
                                                                                                                                                                                                                                                                                                                                                            WO9513288-A1.
                                                                                                                                                                                                                                                                           12-NOV-1996
                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                              14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                              RESULT
R95418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                       ន្តន្តន្តន្តន្តន្ត
                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HLA-Bw46 CTL modulating peptide (Bw46.60-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-Bw46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 13; Page 32; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequent corresponds to residues 60-84 of the alpha-1 domain of the class I MHC HIA-BW46. These sequences can be used to extend the period of
                        Gaps
                                                                                                                                                                                                                                                                                              Mew peptide(s) based on class I HLA antigen domains - used for modulating cytocoxic T-lymphocyte activity towards targets claim 9; Page 53; 61pp; English.

The peptide (or a fragment of at least 10 amino acids, joined at at least one terminus to a sequence other than that of wild type HLA antigen) is used to modulate cytocoxic T-lymphocyte (CTL) activity, either by inhibition or stimulation. It can be used for inhibiting CTL toxicity in transplantations, for inducing CTL activity in parasitic diseases and meoplashs and in studies on viral infection. The peptide can also be used for identifying CTLs which bind to it and removing subsets of CTLs from a T-cell composition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                      unmatched
recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                        ö
Score 40; DB 1; Length 22;
Pred. No. 0.071;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40; DB 1; Length 25;
Pred. No. 0.081;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Extension of acceptance period of transplants from MHC donor hosts - using Class I B75-84 MHC antigen of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
                                                                                                                                                                                                                           16-SEP-1993.
25-FEB-1993; U01758.
02-MAR-1992; US-844716.
(STRD ) UNIV LELAND STANFORD JUNIOR.
CLAYDETGER CA, Krensky AM;
WPI; 93-303134/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R83072 standard; peptide; 25 AA.
78.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 80.0،
المالية Similarity 80.0،
            Best_Local Similarity 80.0 Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1995; U04349
                                              1 RVDLRTLRGY 10
                                                             12 RVNLRKLRGY 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 RVSLRNLRGY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R83072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
R83072
AC R83072
DT 16-MAY
DE HA-BWN
KW LIMPNOON
KW LAMPNOON
KW LAMPNOON
KW LAMPNOON
KW CYLCUC
KW CACC
CLAYBE
CLAYBE
CLAYBE
CRASS
CC CLASS
CC CLASS
                                                                                                       RESULT
R41206
ID R4:
                                                                    g
                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

```
While String lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example Page 91, 29pp. English.

Example Page 91, 29pp. English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the LHA-Bw46.60-84. These sequences can be used to isolate the protein p74 from a r-cell lysate. P74 is a r-cell surface membrane protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly expressed on B and T cells. And tan be isolated by lysis of a suitable cell with an amphoteric detergent, and then passed through an affinity column containing a covalently bound HIA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HIA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compound and p74.

Compositions of CTL differentiation or cytolysis. Candidate compound and p74.

Composition of CTL activity can be inhibited in a cellular composition of containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIA-Bw46.60-84.
HIA-Bw46.10-84.
HIA-10-14. alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CTL; differentiation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 40; DB 1; Length 25; Pred. No. 0.081; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                           78.4%; Score 40; DB 1;
80.0%; Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R95418 standard; peptide; 25 AA. R95418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.4%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                    Krensky AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 RVSLRNLRGY 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clayberger C, Kre
WPI; 95-194027/25
```

```
Disclosure; Page 7; 26pp; English.
Antibodies able to detect both epitopes of HIV gpl60 and epitopes of beta-2-microglobulin free Class I HLA ree heavy chains are pref.
prepd. using gpl20-C5 and HLA alpha-1 peptides (R71628-29) which respectively include peptides HIV-26 and HLA-22.
                                                                                                HIV; gpl20; HLA; beta-2-microglobulin; HLA; passive immunization human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Use of antibodies reactive with HIV and HLA molecules - for detection of HIV infection and for providing passive immunity against HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 78.4%; Score 40; DB 1; Length 45; Best Local Similarity 80.0%; Pred. No. 0.15; Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                   16-MAR-1995.
06-SEP-1994; IT0146.
10-SEP-1993; IT-RM0613.
(SANR-) FOND CENT SAN RAFFAELE DEL MONTE TABOR.
                                                                                                                                                                                                          Location/Qualifiers
16. .37
/label- HLA-22
                              R71629 standard; peptide; 45 AA.
                                                    R71629;
21-SEP-1995 (first entry)
HLA-alpha-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           95-123513/16.
                                                                                                                                                                                                                                                                                             WO9507465-A.
                                                                                                                                                                                                                                           peptide
R71629
ID R7
AC R7
```

ö

Gaps

ö

Search completed: February 8, 2000, 04:05:45 Job time: 9362 sec

1 RVDLRTLRGY 10 ||:|| ||||| 27 RVNLRKLRGY 36

q ŏ

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Run on:

February 7, 2000, 18:04:42; Search time 111.22 Seconds
(without alignments)
4.241 Million cell updates/sec

US-08-653-294-37 51 1 RVDLRTLRGY 10 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database :

pirl:\* pir2:\* pir3:\* PIR\_62:\*
1: pir1:
2: pir2:
3: pir3:
4: pir4: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	MHC class I histoc	MHC H-2K1-k - mous		RT1.A(u) alpha cha	- 22		MHC class I protei	lass I	class I histocompa	H	MHC class I histoc	class I	MHC class I histoc	class I		cell su	lass	s I hist	ass I	MHC class I histoc	class I histocompa	MHC class I histoc	s I hist	38 I	class I	lass I	ss I hist	lass I	class I	MHC class I protei
ΩI	350	544	S52367	160331	G02922	S18197	I61867	B27638	JH0538	I54548	HLHU28	HLHUAW	нгниев	HLHU10	S06424	170694	I36965	S18198	148160	A45845	S03535	HLHUA2	JH0534	JH0536	137477	137482	S01171	JL0135	76	I84432
DB	7	~	~	~	7	~	7	~	~	7	Н	~	Н	Н	7	7	~	~	7	7	7	ч	7	7	~	~	7	~	7	7
Length	371	243	344	344	353	354	359	361	362	365	270	273	273	275	332	337	357	357	361	362	364	365	365	365	365	365	365	365	365	365
% Query Match	0.0	90.2	0.5	0.2	0.2	0.2	0.2	0.2		0.2	e. 3		٠. م	6.3	•				6.3			3						<del>ن</del>		.3
& Out	100	ā	90	ā		ā		ō	ā	6	õ	æ	æ	ã	æ	ã	æ	æ	æ	æ	æ	æ	æ	æ	æ	æ	æ	æ	æ	8
Score	51		46				46			46			44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44	44
Result No.	7	7	ю	4	2	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30

A11.2 - human HLA-Aw33.1, HLA-Aw	MHC class I histoc MHC class I protei	HLA-Aw661 antigen HLA-Aw34.2 antigen	gene HLA-A-0203 pr MHC HLA-A2.4a chai	MHC class I histoc gene HLA-A-0205 pr	gene HLA-A-6802 pr MHC class I histoc	HLA-A30.3 precurso MHC class I histoc	-A*0210
183063 172171	172170 136961	137480 137483	I38443 I61857	I37542 I38442	I38441 I38519	I56039 I38610	137470
00	00	0 0	~ ~	~ ~	0 0	~ ~	7
365 365	365 365	365 365	365 365	365 365	365 365	365 365	365
86.3	86.3 86.3	86.3 86.3	86.3 86.3	86.3 86.3	86.3	86.3 86.3	86.3
<b>7 7 7</b>	4 4 4 4	4 4 4 4	4 4 4 4	4 4 4 4	4 4 4 4	4 4 4	44
31 32	3 3 4	32 30	37	39 40	4 4 2 2	4 4 4 4	. 45

## ALIGNMENTS

•
---

Gaps ö Length 371; Query Match 100.0%; Score 51; DB 2; Length 37 Best Local Similarity 100.0%; Pred. No. 0.0065; Matches 10; Conservative 0; Mismatches 0; Indels

1 RVDLRTLRGY 10 ŏ

ö

셤

C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 02-Aug-1996
C; Accession: 154459
R; Watts, S.; Davis, A.C.; Goodenow, R.S.
Immunogenetics 29, 355-357, 1988
Immunogenetics 20, 355-357, 1988
Immunog MHC H-2K1-k - mouse

Gaps ö Query Match 90.2%; Score 46; DB 2; Length 243; Best Local Similarity 90.0%; Pred. No. 0.045; Matches 9; Conservative 1; Mismatches 0; Indels

ö

1 RVDLRTLRGY 10

ò

```
Class I histocompatibility antigen Gogo-A3 alpha chain - gorilla (fragment)
C; Species: Gorilla gorilla (gorilla)
C; Species: Gorilla gorilla (gorilla)
C; Species: Gorilla gorilla (gorilla)
C; Stacession: S18197
R; Watkins, D.I.; Chen, Z.W.; Garber, T.L.; Hughes, A.L.; Letvin, N.L.
Immunogenetics 34, 185-191, 1991
A; Title: Segmental exchange between MHC class I genes in a higher primate: recombinat A; Reference number: S18197; MUID:91372865
A; Accession: S18197
A; Molecule type: nucleic acid
A; Residues: I-354 <WAT>
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC class I histocompatibility antigen alpha chain precursor (BL3-7) - bovine C; Species: Bos primigenius taurus (cattle)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHC class I protein - orangutan (fragment)
C;Species: Pongo pygmaeus (orangutan)
C;Species: Pongo pygmaeus (orangutan)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 23-Jul-1999
C;Accession: 161867
C;Accession: 161867
A;Pithe: Comparison of class I MHC alleles in humans and apes.
A;Reference number: 136961; MUID:90201944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross references: EMBL:X54375; NID:922889; PIDN:CAA38250.1; PID:922890 C; Superfamily: class I histocompatibility antigen; immunoglobulin homology F; 212-277/Domain: immunoglobulin homology <IMM>
                                                            I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M30681; NID:g342845; PIDN:AAA88836.1; PID:g342846
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 354;
                                                                                                                                                          Length 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 359
                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-359 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 2;
Pred. No. 0.067;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 46; DB 2;
Pred. No. 0.068;
1; Mismatches
                                                                                                                                                       Score 46; DB 2;
Pred. No. 0.067;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.2%;
90.0%;
                                                                                                                                                          90.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 90.0.
                                                                                                                                                       Query Match 90.2
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.2
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                        91 RVNLRTLRGY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RVDLRTLRGY 10
                              A;Gene: Lero-G
C;Superfamily: class
   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S18197
                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                             C;Accession: $52367
R;Joly, E.; Clarkson, C.; Howard, J.C.; Butcher, G.W.
submitted to the EMBL Data Library, October 1994
A;Bescription: Isolation of a functional cDNA encoding the RTI.A(u) MHC class I heavy ch
A;Reference number: $52367
A;Accession: $52367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHC class I Lero-G*01 - golden lion tamarin (fragment)
(Species: Leontopithecus rosalia (golden lion tamarin)
C;Species: Leontopithecus rosalia (golden lion tamarin)
C;Date: 04 Sep-1997 #sequence_revision 04-Sep-1997 #text_change 23-Jul-1999
C;Accession: 602922
C;Accession: 502922
C;Accession: 502922
C;Accession: 602922
C;Ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: 160331
R;Joly, E.; Clarkson, C.; Howard, J.C.; Butcher, G.W.
Immunospenetics 41, 326-328, 1995
A;Title: Isolation of a functional cDNA encoding the RT1.Au MHC class I heavy chain by A;Reference number: 160331; MUID:95237903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-353 <CAD>
A; Cross-references: EMBL:U59642; NID:g1389930; PIDN:AAB97485.1; PID:g1389931
                                                                                                                                                          RTI.A(u) protein alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C.Species: Rattus norvegicus (Norway rat)
C.Date: 02-Aug_1996 #sequence_revision 02-Aug-1996 #text_change 23-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-344 <JOLD-
A;Cross-references: EMBL:X82106; NID:g1228090; PID:g1228091
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: RT1.A(u)
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A/Accession: I60331
A/Status: preliminary: translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-344 <RES>
A/Cross-references: EMBL:X82106; NID:9836643; PID:9836644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 2;
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.2%; Score 46; DB 2;
llarity 90.0%; Pred. No. 0.065;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: G02922
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RT1.A(u) alpha chain - rat (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 90.vv
96 RVNLRTLRGY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|||||||
75 RVNLRTLRGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

```
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 02-Sep-1997
C; Accession: A02187
R; Lopez de Castro, J.A.; Strominger, J.L.; Strong, D.M.; Orr, H.T.
Proc. Natl. Acad. Sci. U.S.A. 79, 3813-3817, 1982
A; Title: Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA A; Reference number: A93919; MUID:82247941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A/Gene: GDB:HLA-A
A/Cross-references: GDB:119310; OMIM:142800
A/Map position: 6p21.3-6p21.3
C/Superfamily: class I histocompatibility antigen; immunoglobulin homology
C/Steywords: duplication; qlycoprotein; heterodimer; membrane protein; transplantation
F;1-90/Domain: alpha-1 <EX1>
F;91-182/Domain: alpha-2 <EX2>
F;91-182/Domain: alpha-2 <EX2>
F;96-261/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC class I histocompatibility antigen HLA-Aw68 alpha chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             class I histocompatibility antigen HLA-A28 alpha chain - human (fragment)
A; Accession: I54548
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-365 < RES>
A; Residues: 1-365 < RES>
A; Cross-references: EMBL: X82669; NID: 9642266; PIDN: CAA57986.1; PID: 91000514
C; Genetics: 1
A; Genetics: 22/1; 112/1; 204/1; 296/1; 339/1; 349/1; 365/1
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Holmes, N.; Parham, P.
EMBO J. 4, 2849-2854, 1985
A;Title: Exon shuffling in vivo can generate novel HLA class I molecules.
A;Reference number: A91021; MUID:86055720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F:196-261/Domain: immunoglobulin nomology /LEW | P:196-261/Domain: immunoglobulin nomology /LEW | P:101-164,203-259/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Length 270;
Pred. No. 0.13;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                            Length 365
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                      Score 46; DB 2;
Pred. No. 0.069;
1; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 6p21.3-6p21.3
A; Introns: 89/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 1-270 <LOP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1111 | 1111 | 75 RVDLGTLRGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-273 <HOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: A24671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: A2467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                              J. Immunol. 141, 642-651, 1988
A:Title: Molecular cloning of bovine class I MHC cDNA.
A:Reference number: A92826; MUID:88258075
A:Reference number: Application of the class I histocompatibility antigen; Immunoglobulin homology
C:Reywords: heterodimer: transmembrane protein
F:1-24/Domain: signal sequence 4status predicted <SIG>F:25-561/Froduct: MHC class I histocompatibility antigen, BoLA alpha chain (BL3-7) #stat
F:20-285/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ajintrons: 25/1; 115/1; 207/1; 299/1; 338/1; 349/1
C:Superfamily: class I histocompatibility antigen; immunoglobulin homology
C:Keywords: transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-362/Product: class I histocompatibility antigen heavy chain, Gogo-Oko #status predi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RiLawlor, D.A.; Warren, E.; Taylor, P.; Parham, P.
J. Exp. Med. 174, 1491-1509, 1991
A;Title: Gorilla class I major histocompatibility complex alleles: comparison to human A;Reference number: JH0534; MUID:92078860
A;Accession: JH0538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenetics 41, 332, 1995
A;Title: Genomic organization and sequence of the rat major histocompatibility complex A;Reference number: 154548; MUID:95237905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   class I histocompatibility antigen Gogo-Oko heavy chain precursor - lowland gorilla C;Species: Gorilla gorilla (lowland gorilla)
C;Bate: 30-Jun.1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: JH0538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 16-Feb-1997 C;Accession: B27638 R;Ennis, P.D.; Jackson, A.P.; Parham, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  major histocompatibility complex class I - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-bug-1996 #sequence_revision 02-bug-1996 #text_change 23-Jul-1999
C;Accession: I54548
R;Walter, L.; Tiemann, C.; Heine, L.; Gunther, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1.362 <LAW>
A;Residues: 1.362 <LAW>
A;Cross_references: EMBL:X60692; NID:922908; PIDN:CAA43100.1; PID:922909
A;Experimental source: EBV-transformed B cell
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;25-114/Domain: alpha-1 <ALL>
F;115-206/Domain: alpha-2 <ALZ>
F;207-208/Domain: alpha-3 <ALZ>
F;207-285/Domain: alpha-3 <ALZ>
F;299-362/Domain: intracellular #status predicted <INT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90.2%; Score 46; DB 2;
90.0%; Pred. No. 0.069;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 2;
Pred. No. 0.068;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 90.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
I54548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
```

```
Search completed: February
Job time: 22208 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                      ò
                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Davidson, W.F.; Kress, M.; Khoury, G.; Jay, G.
J. Biol. Chem. 260, 13414-13423, 1985
J. Biol. Chem. 260, 13414-13423, 1985
A:Title: Comparison of HLA class I gene sequences. Derivation of locus-specific oligonud A:Reference number: A92500; MUID:86033791
A;Accession: B24512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6P21.3-6P21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen
F;130-195/Domain: immunoglobulin homology <IMM>
F;20/Binding site: carbohydrate (Asn) (covalent) *status predicted
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Keywords: glycoproteth; heterodiamer: transmembrane protein; transplantation antigen F:155-260/Domain: immunoglobulin homology <a href="mailto:rimmunoglobulin">rimmunoglobulin</a> homology <a href="mailto:rimmunoglobulin">rimmunoglob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: class I histocompatibility antigen; immunoglobulin homology skeptords: glycoprotein; heterodimer; transmembrane protein; transplantation antigen 195-260/Domain: immunoglobulin homology clMAP
(85/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Class I histocompatibility antigen HLA-Aw69 alpha chain - human (fragment) Species: Homo sapiens (man)
Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Sep-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHC class I histocompatibility antigen HLA-A10 alpha chain - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Species: Homo sapiens (man)
C:Date: 31-Dec.1988 *sequence_revision 31-Dec-1988 *text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:HOlmes, N.; Parham, P.
EMBO J. 4, 2849-2854, 1985
A.Title: Exon shuffling in vivo can generate novel HLA class I molecules.
A;Reference number: A91021; MUID:86055720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 1-275 <DAV>
A;Cross-references: GB:M11887; NID:g184157; PIDN:AAA52656.1; PID:g184158
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                               Score 44; DB 1; Length 273;
Pred. No. 0.13;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 273;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
0.13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 44; DB
Pred. No. 0.13
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
A;Map position: 6p21.3-6p21.3
                                                                                                                                                                                                                                                                    86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 90.v.
9, Conservative
                                                                                                                                                                                                                                                                                                                                                                 9; Conservative
                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1111 | 1111 | 74 RVDLGTLRGY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-273 <HOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111 | 11111
74 RVDLGTLRGY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession: B24512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: B24671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
```

7, 2000, 18:04:42

Length 275;

DB 1;

Score 44;

86.38;

```
N'Alternate names: MHC ChlA chain
C'Species: Pan troglodytes (chimpanzee)
C'Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 23-Jul-1999
C'Accession: S06424; I36959
R'Lawlor, D.A.; Ward, F.E.; Ennis, P.D.; Jackson, A.P.; Parham, P.
Nature 335, 268-271, 1988
A):Title: HIA-A and B polymorphisms predate the divergence of humans and chimpanzees.
A):Reference number: S06424; MUID:88319000
                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                       MHC class I histocompatibility antigen Ch25 alpha chain precursor – chimpanzee
                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PID:9553155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.3%; Score 44; DB 2; Length 332; 90.0%; Pred. No. 0.16;
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                          A; Accession: S06424
A; Molecule type: MRNA
A; Residues: 1-33 Z-LAM>
J. Tamunol. 142, 3937-3950, 1989
A; Titte: Diversity and diversification of HLA-A,B,C alleles.
A; Reference number: 136956; MUID: 89235215
A; Accession: 136959
                 ä
Pred. No. 0.13;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
90.06;
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 9; Conserv
                                                      1 RVDLRTLRGY 10
                                                                              9 RVDLGTLRGY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
```

```
February 8, 2000, 01:26:02; Search time 68.63 Seconds (without alignments) 4.352 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                       OM protein - protein search, using sw model
```

Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 US-08-653-294-37 51 1 RVDLRTLRGY 10 Title: Perfect score: Sequence: Scoring table:

82229 segs, 29864866 residues Searched:

82228 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 08 Listing first 45 summarles

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	rattus	homo s		g.	bos	PIU316 homo sapien p10313 homo sapien	canis	gorill		g	ğ	gori	pan	pan	рошо	уошо	homod	homo	рошо	рошо	homo	рошо	mus ก		bos t		рошо		Ď	pan t	gor	30500 homo	03
SUMMARIES 3 ID	¦	HLAE	HLAE	TOK	HALE	1 1Ab9_HUMAN	HA19	1A01_		1A01_				1 <b>A</b> 0	1A1:	1A3(	1A3.	1A33	1A34	1A66			_	1A03_	_		1B4		100			1002_	_
Length DB	371	œ (	<b>a</b> (	~ .	<b>.</b>	2/3	. ~	2	'n	Ŋ	ιc.	'n	'n	'n	'n	'n	ın	ın	ın	ın	ın	'n	ል	0	0	~	~	ın	'n	'n	ıo	ıo	10
8 Ouery Match	100	٠. د			٠,	86.3	٠.	ė.	è.	ė.	ė.	ė.	ė	ė.	ė.	ώ.	ů.	Ġ.	ů.	ė.	Ġ	ė	ė.	o.	ö	78.4	ω.	·.	æ.	œ.	78.4	78.4	78.4
Score	:	46	<b>4</b> •	94	0.4	<b>7 7 7</b>	44	44	44	44		44				44			44	44		44				40						40	
Result No.		0.0	m -	4° L	n v	9 1	- σο	0	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

P30501 homo sapien P30387 gorilla gor P30502 homo sapien P04222 homo sapien P30503 homo sapien P30504 homo sapien	homo homo homo homo
1C03_HUMAN 1C04_GORGO 1C04_HUMAN 1C05_HUMAN 1C06_HUMAN 1C07_HUMAN	1C11_HUMAN 1C12_HUMAN 1C13_HUMAN 1C14_HUMAN 1C15_HUMAN
ананна.	ннннн
, a a a a a a	300
444444	4 4 4 4 4
44.87	7 2 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8
44444	44444 00000
8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	4444 4443 1443

## ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HIA class I gene.";

1. Immunol. 140:4024-4030(1988).

(2) SEQUENCE FROM N.A. (E*0102).

MEDLINE: 88285691.

MEDLINE: B.H., GERAGHTY D.E., SHIMIZU Y., DEMARS R., ORR H.T.;

"HIA-E. A novel HiA class I gene expressed in resting T lymphocytes.";

J. Immunol. 141:897-904(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 98325367.
O'CALLAGHAN C.A., TORNO J., WILLCOX B.E., BRAUD V.M., JAKOBSEN B.K., STUART D.I., WCMICHAEL A.J., BELL J.I., JONES E.Y.;
STUART D.I., WCMICHAEL A.J., BELL J.I., JONES E.Y.;
STUCKLURA! features impose tight peptide binding specificity in the nonclassical MHC molecule HLA-E.";
MOI. Cell 1:31-541(1998).
-!- FUNCTION: PREFERBLY BINDS TO A PEPTIDE DERIVED FROM THE SIGNAL SEQUENCE OF MOST HLA-A, -B, -C AND -G MOLECULES.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN E E*0101/E*0102.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                              01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN E E*0101/E*0102
PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (E*0101).
MIZDLONS: WRAPAL J.A., KOLLER B.H., DUPONT B., YANG S.Y.;
MISOLATION and nucleotide sequence of a cDNA clone encoding a novel
                                        ö
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   100.0%; Score 51; DB 1; Length 371; 100.0%; Pred. No. 0.002;
                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 22-295.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A3277; A3277.
PIR; A28834; A28834.
HSSP; P03899; IHSA.
MIN; 143010; --
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL 1 2 358 HLA CLASS I HISTC
                                                                                                                                                                                                 358 A.A.
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M20022; AAA52655.1; -. EMBL; M21533; AAA59835.1; -.
Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                        HLA-E OR HLAE OR HLA-6.2.
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                              99 RVDLRTLRGY 108
                                                                          1 RVDLRTLRGY 10
                                                                                                                                                                                               HLAE_HUMAN
P13747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                              RESULT 2
HLAE_HUMAN
                                                                                                           g
                                                                                                                                                                                                                   ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entlies requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE; 90201944.

LAMLOR D.A., WAREN E., WARD F.E., PARHAM P.;

"Comparison of class I MHC alleles in humans and apes.";

Immunol. Rev. 113:147-185(1990).

-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, E-1 ALPHA CHAIN PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                Score 46; DB 1; Length 358;
Pred. No. 0.023;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E-1 ALPHA CHAIN.
EXTRACELLUIAR ALPHA-1.
EXTRACELLUIAR ALPHA-2.
EXTRACELLUIAR ALPHA-3.
CONNECTING PEPTIDE.
CONNECTING PEPTIDE
                                                                                                                              S -> L (IN E*0102)
/FTId-VAR_004394.
                                                                                                                                                                          G -> R (IN E*0102)
/FIId=VAR_004395.
3D79F233 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
;; 55E15638 CRC32;
                                           CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM: PF00047; 19; 1.
PFAM: PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
NON_TER 1 1
SIGNAL <1 18
                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                      40130 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ξ.
Έ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M30681; AAA88836.1; -.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                       90.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40409
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
305
329
3329
185
107
                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THE IMMUNE SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                      ||:|||||||
96 RVNLRTLRGY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119
221
104
359 AA;
                                                                                                                                                                                                                      358 AA;
                                                                                                                                                                                                                                                                                                                                                                            1 RVDLRTLRGY 10
296
3306
122
107
                                                                                                                                                                             104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HLAE_PONPY
P16212;
                                                                DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
DISULFID
CARBOHYD
SEQUENCE
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                             VARIANT
                                                                                                                                 VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 3
HLAE_PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                      g
82444444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HIDD BELLE STEET STEET
```

ò g

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC.
SIGNIFICANT WITH IMMUNOGLOBULIN C-REGION
DOMAINS AND BETA-2-MICROGLOBULIN.
                                                        01-5AN-1990 (Rel. 13, Created)
01-5AN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 13, Last annotation update)
BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BL3-7 PRECURSOR.
BOS taurus (BOVINE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE; 88258075.
ENNIS P.D., JACKSON A.P., PARHAM P.;
MOJECULAR CLONING OF BOYINE CLASS I MHC CDNA.";
J. Immunol. 141:642-651(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1A69_HUMAN STANDARD; PRT; 273 AA.
P10316;
01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-7UL-1998 (Rel. 36, Last annotation update)
HIA CLASS I HISTOCOMPATIBILITY ANTIGEN, AW-69(A-28) ALPHA CHAIN
                                                                                                                                                                                                                                                                                                 THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 46; DB 1; Length 364;
Pred. No. 0.023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALPHA CHAIN BL3-7.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.;
A27F581C CRC32;
                               364 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41513 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M21043; AAA30641.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR, B27638; B27638.
HSSP; P30460; 1AGB.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1117
2209
3301
331
364
301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 RVDLNTLRGY 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                 MICROGLOBULIN)
                                                                                                                                                                       Bovinae; Bos
                            HA1B_BOVIN
P13753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
SIMILAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
1A69_HUMAN
ID : 1A69_HU
AC P10316;
DT 01-MAR-
DT 15-JUL-
DE HLA CLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                 01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CLASS I HISTOCOMPATIBILITY ANTIGEN, GOGO-OKO ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland gotilla)
ELWATYOLA: Metacoa: Chocata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
CLASS I HISTOCOMPATIBILITY ANTIGEN,
GOGO-OKO ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                             Length 359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 362; 0.023;
                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                          Score 46; DB 1;
Pred. No. 0.023;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD795172 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 46; DB :
Pred. No. 0.02:
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60692; CAA43100.1; -.
PIR; JH0538; JH0538.
HSSP; P30460; JAGB.
PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; 19; 1.
MHC I; Transmembrane; Glycoprol SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.2%;
llarity 90.0%;
Conservative (
                            90.2%;
             40755
                                                                                                                                                                                                     STANDARD;
                                                                                                          MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||||| |||||
RVDLETLRGY 108
                                                                                         1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                     10KO_GORGO
P30388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
SEQUENCE
```

ö

ö

DOMAIN DOMAIN

CHAIN

DOMAIN

Н 66

ò g us-08-653-294-37.rsp

```
HA19_CANFA
P18466;
                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                          DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HA19_CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation for European Bioinformatics Institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 86033791.
DAVIDSON WF., KRESS M., KHOURY G., JAY G.;
"Comparison of HLA class I gene sequences. Derivation of
locus-specific oligonucleotide probes specific for HLA-A, HLA-B, and
                                                              SEQUENCE FROM N.A. (A*6901). , MEDILINE; 86055720.  
MEDILINE; 86055720.  
"Exon shuffling in vivo can generate novel HLA class I molecules.";  
"Exon shuffling in vivo can generate novel HLA class I molecules.";  
EMBO J. 4:3849-2254(1985).  
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM..
                                                                                                                                                                POLYMORPHISM: THE ONLY ALLELE OF AW-69 KNOWN IS A*6901 WHICH IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-NV-1997 (Rel. 35, Last annotation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-10 ALPHA CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            -!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB 1; Length 273; Pred. No. 0.044;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEBFB366 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                     EMBL; X03158; -; NOT_ANNOTATED_CDS.
EMBL; X03159; -; NOT_ANNOTATED_CDS.
PIR; B24671; HLHU69.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW.
                                                                                                                                                                                                                                                                                                                                             PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   85
163
258
273
                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                        HSSP; P01892; 1AQD.
MIM; 142800; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1111 | 1111
74 RVDLGTLRGY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                              SHOWN HERE.
          HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1AXX_HUMAN
P10313;
 (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID
                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1AXX_HUMAN
õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                원
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV'1990 (Rel. 16, Created)
01-NOV'1990 (Rel. 16, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
DLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A9/A9 ALPHA CHAIN PRECURSOR.
Canis familiaris (Dog).
HLA-C genes.";
J. Biol. Chem. 260:13414-13423(1985).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                    THE IMMUNE SYSTEM.
SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE; 90316611.
**SAMIENTO U.M., STORB R.;
**Nucleotide sequence of a dog class I cDNA clone.";
Immunogenetics 31:400-404(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 1;
Pred. No. 0.045;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY.
8B232F3C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  362 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; B24512; HLHU10.
HSSP: P01892; 1HHH.
MIM; 142800; -.
FROSITE: PS00290; IG_MHC; 1.
PFRM; PF00047; 19; 1.
PFRM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30548 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M11887; AAA52656.1; -. PIR; B24512; HLHU10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                    MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 RVDLGTLRGY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RVDLRTLRGY 10
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 92078860.
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
LAWLOR D.A., WARREN E., TAYLOR P., PARHAM P.;
"Gorilla class I chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-: FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1401_GORGO STANDARD; PRT; 365 AA.
P30375;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                           DLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A9/A9 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X60258; CA442810.1; -.
PIR: JH0554; JR0534.
HSSP: P01891; ZHLA.
PROSITE: P800209: IG_MHC; 1.
PFAM; PF00129; MHC_I; 1.
PFAM; PF00129; MHC_I; 1.
SIGNAL BY SIMILARITY.
CHAIN 25 365 CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.3%; Score 44; DB 1; Length 362; 90.0%; Pred. No. 0.061; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
D5250E8D CRC32;
                                                                                                                                                                                                                         PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
SIGNAL 1
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40462 MW;
                                                                       EMBL; M32283; AAA30865.1; -.
                                                                                                                                                                                     PS00290; IG_MHC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 90.۰۰
کتر 9; Conservative
                                                                                                              PIR; A45845; A45845.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
115
208
300
330
125
228
110
362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99 RVDLDTLRGY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1A01_GORGO
CCC
CCC
CCC
DDR
DDR
ET
FT
FT
FT
FT
FT
FT
FT
SO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT TAR BAR A PAT TAR A PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ద
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1401. PANTR STANDARD; PRT; 365 AA.
P16209;
01-APR-1990 (Rel. 14, Created)
01-APR-1993 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (All 25, Last annotation update)
Pan Krologoparibility Antigen, A-2 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanzee).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Putheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE; 90201944.
LAMLOR D.A., WARREN E., WARD F.E., PARHAM P.;
"Comparison of class I MHC alleles in humans and apes.";
Immunol. Rev. 113:147-185(1990).
-:- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                          86.3%; Score 44; DB 1; Length 365; 90.0%; Pred. No. 0.062; 1ve 0; Mismatches 1; Indels
GOGO-A0101 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A-2 ALPHA CHAIN.

EXTRACELLULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                                                              CXTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
7, 40682CC4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6ECSFF0E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM: PF00047: 19: 1.
PFAM: PF00129: MHC_I: 1.
MHC I: Transmembrane; Glycoprotein; Signal.
SIGNAL
                                                                                                                                                                                                                                                         .;
₩
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M30678; AAA87970.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P01892; 1HHH.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                         40829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40848
                                                                                                                                                                                                                                                                                                                            Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                            114
206
208
308
332
365
1188
110
                         255
1115
2007
2009
3309
125
125
110
365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                               1 RVDLRTLRGY 10
                                                                                                                                                 DOMAIN
DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                 DOMAIN
DOMAIN
DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
1A01_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
     STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                    ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              윱
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE THE TEST TO BE A PROPERTY OF THE STATE THE STATE OF THE STATE OF
```

```
90207291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 92269955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 82247941
                                                                                            HLA-A OR HLAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BIDDISON W.E.
                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseélsb-sib.ch).
                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 90201944.
LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.;
LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.;
"Comparison of class I MHC alleles in humans and apes.";
Immunol. Rev. 113:147-185(1990).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASS I HISTOCOMPATIBILITY ANTIGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1A02_HUMAN STANDARD; PRT; 365 AA.
P01892; P06338; P30514; P30444; P30445; P30446; Q29680; Q29899;
                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16-JUL-1999 (Rel. 38, Last annotation update)
Pongo pygmaeus (Orangutan).
                                                                                                                                                                                                                                                                                                                                                             Eukāryotā; Metazoa; Chordāta; Craniata; Vertebrata; Mammalia;
Eutheria; Prīmates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 1; Length 365;
Pred. No. 0.062;
0; Mismatches 1; Indels
                   Length 365;
                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A-1 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONNECTING PEPTIDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; FAD23315 CRC32;
                 Score 44; DB 1;
Pred. No. 0.062;
                                                                                                                                                                                                                                 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE: PS00290: II.
PFAM: PF00047; 1g; 1.
PFAM: PF00129; MHC_I; 1.
MHC_I; Transmembrane; Glycoprotein; Signal.
                                                       0; Mismatches
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .,
MM.
                 86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.3%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M30680; AAA88835.1; -.
Ouery Match
Best Local Similarity 90.۰۰
ایک Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                 STANDARD;
                                                                                                                    ||||| |||||
RVDLGTLRGY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227
110
365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILL FILLS TOB
                                                                                            1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 1A01_PONPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                                  P1621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1A02_HUMAN
                                                                                                                                  66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                g
                                                                                              à
                                                                                                                                                                                                                                                                                      PERSON NAME OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ENNIS P.D., ZEMMOUR J., SALTER R.D., PARHAM P.;
"Raptid cloning of Han-A,B cDNA by using the polymerase chain
reaction: frequency and nature of errors produced in amplification.";
Proc. Natl. Acad. Sci. U.S.A. 87:2833-2837(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOPEZ DE CASTRO J.A., STROMINGER J.L., STRONG D.M., ORR H.T.; "Structure of crossreactive human histocompatibility antigens HLA-A28 and HLA-A2: possible implications for the generation of HLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Comparison of amino acid sequences of two human histocompatibility antigens, HLA-A2 and HLA-B7: location of putative alloantigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DECINE SOLUTION OF THE STATE OF
21.-UUL-1986 (Rel. 01, Created)
13-AUG-1997 (Rel. 105, Last sequence update)
15--UUL-1999 (Rel. 38, Last annotation update)
HLA CLASS I HISTOCOMPATIBILLITY ANTIGEN, A-2 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 87306734.
MATISON D.H., HANDY D.E., BRADLEY D.A., COLIGAN J.E., COMAN E.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DNA sequences of the genes that encode the CTL-defined HLA-A2 variants M7 and DK1.";
Immunogenetics 26:190-192(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A. (A*0201).

MEDLINE; 85132727.

KOLLER B.H., ORR H.T.;

"Cloning and complete sequence of an HLA-A2 gene: analysis of HLA-A alleles at the nucleotide level.";

J. Immunol. 134:2727-2733(1985).
                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BELICH M.P., MADRIGAL J.A., HILDEBRAND W.H., ZEMMOUR J., WILLIAMS R.C., LUZ R., PETZL-ERLER M.L., PARHAM P., "Unusual HLA-B alleles in two tribes of Brazilian Indians."; Nature 357:326-329(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 85230571.
KRANGEL M.S.;
JUDUSUAL RNA Splicing generates a secreted form of HLA-A2 mutagenized B lymphoblastoid cell line.";
EMBO J. 4:1205-1210(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORR H.T., LOPEZ DE CASTRO J.A., PARHAM P., PLOEGH H.L.,
STROMINGER J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (A*0203/A*0205).
MEDLINE; 87252273.
HOLMES N., ENNIS P., WAN A.M., DENNEY D.W., PARHAM P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               roc. Natl. Acad. Sci. U.S.A. 76:4395-4399(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 79:3813-3817(1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 26-298 FROM N.A. (A*0202/A*0203).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (A*0201/A*0211/A*0212).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 39-365 FROM N.A. (A*0201).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (A*0201).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (A*0201).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 25-295 (A*0201).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REVISIONS (A*0201).
```

```
SEQUENCE FROM N.A. (A*0213)
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                             EZQUERRA A., DOMENECH N., VAN DER POEL J., STROMINGER J.L., VEGA M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 88113844.

DOMENECH N., EZQUERRA A., CASTANO R., LOPEZ DE CASTRO J.A.;

"Structural analysis of HLA-A2.4 functional variant KNE. Implications
for the mapping of HLA-2-specific T-cell epitopes.";

Immunogenetics 27:196-202(1988).
"Multiple genetic mechanisms have contributed to the generation of
the HLA-A2/A28 family of class I MHC molecules.";
J. Immunol. 139:936-941(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 88314183.

DOMENECH N., CASTANO R., GOULMY E., LOPEZ DE CASTRO J.A.;
Molecular analysis of HLA-A2.4 functional variant KLO: close structural and evolutionary relatedness to the HLA-A2.2 subtype.";
Immunogenetics 28:143-152(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 88186100.
CASTANO R., EZQUERRA A., DOMENECH N., LOPEZ DE CASTRO J.A.;
"An HAA-A2 population variant with structural polymorphism in the alpha 3 region.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CASTANO, A.R., LOPEZ DE CASTRO J.A.;
Structure of the HLA-A*0211 (A2.5) subtype: further evidence for
"Structure of the HLA-A*0211 (A2.5) subtype: further evidence for
selection-driven diversification of HLA-A2 antigens.";
Immunogenetics 35:344-346(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                        LOPEZ DE CASTRO J.A.; "Molecular analysis of an HLA-A2 functional variant CLA defined
                                                                                                    MEDLINE; 92033809.
CASTANO A.R., LOPEZ DE CASTRO J.A.;
Structure of the HLA-A*0204 antigen, found in South American Indians. Spatial clustering of HLA-A2 subtype polymorphism.";
Immunogenetics 34:281-285(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPSTEIN H., KENNEDY L., HOLMES N.; "An Oriental HLA-A2 subtype is closely related to a subset of Caucasoid HLA-A2 alleles.";
                                                                                                                                                                                                                     WATKINS D.I., MCADAM S.N., LIU X., STANG C.R., MILFORD E.L., LEVINE C.G., GARBER T.L., DOGON A.L., LORD C.I., GHIM S.H., TROUP G.M., HUGHES A.L., LETVIN N.L.;
"New recombinant HLA-B alleles in a tribe of South American Amerindians indicate rapid evolution of MHC class I loci.";
Nature 357:329-333(1992).
                                                                  DOMENA J.D.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                             PARRAM P., LAWLOR D.A., LOMEN C.E., ENNIS P.D.; "Diversity and diversification of HLA-A,B,C alleles."; J. Immunol. 142:3937-3950(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQÜENCE OF 9-365 FROM N.A. (A*0211).
MEDLINE; 92218010.
                                                                                                                                                                                                 SEQUENCE OF 9-365 FROM N.A. (A*0204). MEDLINE; 92269956.
                                                     SEQUENCE FROM N.A. (A*0203/A*0205).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     olytic T lymphocytes.";
Immunol. 137:1642-1649(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 29:112-116(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenetics 27:345-355(1988).
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (A*0206). MEDLINE; 89235215.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (A*0210). MEDLINE; 89122133.
                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE (A*0206).
MEDLINE; 86305811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE (A*0207).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL SEQUENCE (A*0208).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PARTIAL SEQUENCE (A*0209).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cytolytic T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15]
```

```
MEDLINE; 88014204.
BJORKWAN P.J., SAPER M.A., SAMRAOUI B., BENNETT W.S.,
STROMINGER J.L., WILEY D.C.;
"Structure of the human class I histocompatibility antigen, HLA-A2.";
Nature 329:506-512(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last sequence update)
CLASS I HISTOCOMPATIBLITY ANTIGEN, GOGO-A0401 ALPHA CHAIN PRECURSOR.
GOTILLA GOTILLA GOTILLA (Lowland GOTILLA).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BORDIGNON C.; "HLA-A*02 subtype distribution in Caucasians from northern Italy: identification of A*0220.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KASHTWASE K., TOKUNAGA K., ISHIKAWA Y., OOHASHI H., HASHIMOTO M., AKAZA T., TADOKORO K., JUJI T.:
"A new A2 sequence HLA-A2K from Japanese.";
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                           BAROUCH D., KRAUSA P., BODMER J., BROWNING M.J., MCMICHAEL A.J., "Identification of a novel HLA-A2 subtype, HLA-A*0216."; Immunogenetics 41:388-388(1995).
                                                                                                                                                                                                                                                                                                                                                                                                        "A novel subtype of A2 (A*0217) isolated from the South American Indian B-cell line AMALA.";
Tissue Antigens 45:343-347(1995).
                                                                                                                                                                                                                                                                                                                                                       SELVAKUMAR A., GRANJA C.B., SALAZAR M., ALOSCO S.M., YUNIS E.J., DUPONT B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 97161038.
FIEISCHHAUER K., ZINO E., MAZZI B., SEVERINI G.M., BENAZZI E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 1; Length 365;
Pred. No. 0.062;
0; Mismatches 1; Indels
                     DE CASTRO J.A.;
subtype: HLA-A*0213.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SZMANIA S., BAXTER-LOWE L.A.; "Nucleotide sequence of a novel HLA-A2 gene."; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF A*0201 MEDLINE; 91245570.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF A*0201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS)
MEDLINE; 94222455.
MEMBER D.:, FERNANDEZ J.M., LOPEZ Primary structure of a new HLA-A2 Immunogenetics 39:378-378(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tissue Antigens 48:673-679(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.38;
90.08;
                                                                                                                      SEQUENCE FROM N.A. (A*0216).
MEDLINE; 95278976.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (A*0218).
                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (A*0217).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A*0221).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (A*0220)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 86.3
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                  MEDLINE; 95381236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 RVDLGTLRGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-BLOOD;
                                                                                                                                                                                                                                                                                                          TISSUE-BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1A03_GORGO
P30377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
1A03_GORGO
AD 1A03_GORD
DT 01-APR
DT 01-APR
DE CLASS
OS GOTI11.
```

ö

```
EMBL; X13113; CAA31505.1; ALT_INIT.
                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                          86.3%;
                                                                                                                PIR; S03535; S03535.
HSSP; P01891; 2HLA.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                           40822
                                                                                                                                                                                                                                                                                                                                                   Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                             24
365
                                                                                                                                                                                                            25
1115
207
209
3309
1125
110
365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     99 RVDLGTLRGY 108
 MICROGLOBULIN)
                                                                                                                                                                                                                                                                                                                                                                                  1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
1A04_PANTR
ID 1A04_PANTR
AC P13749;
                                                                                                                                                                                                                                                                 DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
 ò
                                                                                                                                                                                                                                                                                                                                                                                                     셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                  MEDLINE; 92078860.
LAWLORD D.A., MARREL E., TAYLOR P., PARHAM P.;
LAWLORD D.A., MARREL
GOTILL Class I major histocompatibility complex alleles: comparison
to human and chimpanzee class I.";
J. Exp. Med. 174:1491-1509(1991).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
THE IMMUNE SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Nucleotide sequences of chimpanzee MHC class I alleles: evidence for trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988)
-i- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1403_PANTR STANDARD; PRI; 365 AA.
P13748;
01-3AN-1990 (Rel. 13, Created)
01-3AN-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
01-APR-1993 (Rel. 25, Last Pannotation update)
Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                            Glycoprotein; Signal.

BY SIMILARITY.

CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE: 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
KLEIN J.;
                                                                                            DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                               86.3%; Score 44; DB 1; Length 365; 90.0%; Pred. No. 0.062; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                           GOGO-A0401 ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                     CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                   Y SIMILARITY.

Y SIMILARITY.

Y SIMILARITY.

C34850E8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                  40933 MW;
                                                                                                                                                                                                           EMBL; X60257; CAA42809.1; -. PIR; JH0536; JH0536. HSSP; P01892; 1HHH.
                                                                                                                                                                                                                                          PROSITE; PS00290; IG_MHC; 1.
PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 90.vv
                                                                                                                                                                                                                                                                             MHC I; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMUNE SYSTEM
                                                                                           -!- SUBUNIT: DIMER ( MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
110
365 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RVDLRTLRGY 10
[1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 89030641.
                                                                                                                                                                                                                                                                                                                     25
207
209
309
333
                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1A03_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ద
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. The Three are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-126 ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LEIN J.;
Nucleotide sequences of chimpanzee MHC class I alleles: evidence for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         trans-species mode of evolution.";
EMBO J. 7:2765-2774(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pan troglodytes (Chimpanzee).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 89030641.
MAYER W.E., JONKER M., KLEIN D., IVANYI P., VAN SEVENTER G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE IMMUNE SYSTEM.

1. SUBDINIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A-108 ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; BC39DEDC CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
0.062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_1; 1.
MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB Pred. No. 0.060; Mismatches
```

```
DR EMBL; X13114; CAA31506.1; -.

DR PIR; $01171; $01171.

DR HSSP; PO1091; 2HLA:

DR PROSITE; PS00209; IG_MHC; 1.

DR PFAM; PF00047; ig; 1.

DR PFAM; PF00047; ig; 1.

KW MHC I; Transmembrane; Glycoprotein; Signal.

FT SIGNAL

FT CHAIN 25 114 EXTRACELLULAR ALPHA-1.

FT DOMAIN 25 114 EXTRACELLULAR ALPHA-2.

FT DOMAIN 207 298 EXTRACELLULAR ALPHA-2.

FT DOMAIN 333 365 CCYTOPLASNIC TAIL.

FT DOMAIN 333 365 CCYTOPLASNIC TAIL.

FT DOMAIN 333 365 CCYTOPLASNIC TAIL.

FT DISULFID 227 283 BY SIMILARITY.

FT CARBONYD 110 BY SIMILARITY.

FT CARBONYD 110 BY SIMILARITY.
```

Search completed: February 8, 2000, 01:26:03 Job time: 1563 sec

QY Db

ö

0; Gaps

Query Match

86.3%; Score 44; DB 1; Length 365;
Best Local Similarity 90.0%; Pred. No. 0.062;
Matches 9; Conservative 0; Mismatches 1; Indels

THIS PAGE BLANK (USPTO)

bos taurus homo sapien bos taurus bos taurus rattus norv

gorilla gor callithrix equus cabal pithecia pi

046746 046749 046749 029896 0298996 039831 0398531 0398531 039884 039884 043906 043906 043906 043906 043906 043906 043906 043906 043906 043906 043906 043906 043906 043906

0046452 0029896 0029896 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030 0078030

rattus norv homo sapien rattus norv

leontopithe leontopithe

rattus norv homo sapien homo sapien canis famil canis famil

ALIGNMENTS

us-08-653-294-37.rspt

```
1 RVDLRTLRGY 10
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                  RESULT
002949
002949 rattus norv
095567 rattus norv
P79599 rattus norv
070953 rattus norv
030441 callithrix
030421 ateles belz
030221 ateles belz
030221 ateles belz
03075 pithecia pi
046720 bos taurus
046734 bos taurus
046732 bos taurus
046734 bos taurus
046734 bos taurus
046731 bos taurus
                                                Search time 176.54 Seconds (without alignments)
3.927 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                 Description
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                      225878 seqs, 69334122 residues
                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                   8, 2000, 19:16:19
                                    sw model
                                                                                                                                                                                                    summaries
                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                               002949
095567
P79599
P70527
002953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  019744
062875
046720
046722
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q30441
Q31254
Q19243
Q30221
                                                                                                                                                                                                                                         sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                            sp_unclassified:*
                                                                                                                                                                                                                                                                                                                     sp_vertebrate:*
                                                                                                                                                                                                                                                                     sp_mhc:*
sp_organelle:*
sp_phage:*
                                    OM protein - protein search, using
                                                                                                                                                                                            Post-processing: Minimum Match 0%
Listing first 45
                                                                                US-08-653-294-37
                                                                                                                                                                                                                          sp_archea:*
sp_bacteria:*
                                                                                        51
1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                             sp_plant:*
sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 1000000
                                                                                                                                                                                                                                                                                                             sp_virus:
                                                   February
                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
Perfect score:
Sequence:
                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                51
51
51
51
51
51
51
51
51
51
51
```

Database :

Searched:

Run on:

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                             STRAIN-LEWIS. 1F; TISSUE-SPENCYTES;
STRAIN-LEWIS. 1F; TISSUE-SPENCYTES;
SOLMEL, LE NOLLE A.F., GONZALEZ A.L., MEHLING B., STEVENS J.,
COADWELL W.J., HUBNIG T., HOWARD J.C., BUTCHER G.W.;
CUIT. Biol. 0:0-0(0).
EMBL; Y13579; CAA73907.1; -.
HSSP: P01901; 1KBG.
PFAM; PF00047; 1g; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
002949 PRELIMINARY; PRT; 344 AA.
002949;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MATURE MHC CLASS I ALPHA CHAIN (FRAGMENT).
RT1.A2F.
RATUS norvegicus (Rat).
ENKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Entherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 7; 100.0%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 344 3417 MW; 7AB3EF04 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 345 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q95567 PRELIMINARY;
Q95567; P79601;
01-FEB-1997 (TrEMBLRE1. 02,
01-JUL-1997 (TrEMBLRE1. 04,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
Q95567
ID Q99
AC Q99
DT 01:
DT 01:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
```

Result

```
SEQUENCE FROM N.A.
STRAIN-NEDH; TISSUE-SPLENOCYTES;
STRAIN-NEDH; TISSUE-SPLENOCYTES;
SOLOWELL W.J., HUBLING T., GONZALEZ A.L., MEHLING B., STEVENS J.,
COADWELL W.J., HUBLIG T., HOWARD J.C., BUTCHER G.W.;
CULT. B101. 0:0-0(0).
EMBL; Y08532; CAA69848.1; -.
PERM; PF00047; 1g; 1.
PFAM; PF001047; 1g; 1.
NON_TER 1
SEQUENCE 345 AA; 38953 MW; 5A4ED67C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1999 (TrEMBLrel. 12, Last annotation update)
MCC CLASS I ALPHA CHAIN (FRAGMENT).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalia;
Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-LEW. IF (F HAPLOTYPE);
STRAIN-LEW. IF (F HAPLOTYPE);
COADWELL W.J., HUENIG T., HOWARD J.C., BUTCHER G.W.;
CULT. BIOL. (0:0-0(0)).
EWBL; Y14014; CAA74333.1; --
HSSP; P01901; IKBG.
                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 11; Length 345; 100.0%; Pred. No. 0.022; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 51; DB 7; Length 346; 100.0%; Pred. No. 0.023; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              030441 PRELIMINARY; PRT; 356 AA.
030441;
01-NOY-1996 (TEMBLrel. 01, Created)
01-NOY-1996 (TEMBLrel. 01, Last sequence update)
01-NOY-1999 (TEMBLrel. 12, Last annotation update)
MHC CLASS I CAJA-G*01 (FRAGMENT).
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PROTEIN INVOLVED IN PEPTIDE PRESENTATION (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER 1 1 SEQUENCE 346 AA; 39103 MW; FCAA4D64 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        346 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.(
Matches 10, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 RVDLRTLRGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   002953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
030441
ID 03(
AC 03(
DT 01
DT 01
DE ME
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MATURE ALPHA CHAIN OF MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I
ANTICEN (FRAGMENT).
RTI.A2.
                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-RT1(0); TISSUE-SPLEEN;
JOLY E., LE FROLLE A.F., GONZALEZ A.L., MEHLING B., STEVENS J.,
COADWELL W.J., HUENIG T., HOWARD J.C., BUTCHER G.W.;
CULT. B101. 0:0-0(0).
EMBL, X90372; CAA62022.1; -.
HSEP, PO1901; 1KBG.
PFAM; PF00129; MRC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-RILIOD; TISSUE-SPLEEN;
STRAIN-RILIOD; TISSUE-SPLEEN;
COADWELL W.J., HUENIG T., HOWARD J.C., BUTCHER G.W.;
CULT. B10.1. 0:0-0(1999).
EMBL; X90373; CAA62023.1; --
HSSP; P01900; 1B11.
                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
HISTOCOMPATIBILITY COMPLEX CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 51; DB 7; Length 345; Best Local Similarity 100.0%; Pred. No. 0.022; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 51; DB 7; Length 345; 100.0%; Pred. No. 0.022; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         1 1
345 AA; 39139 MW; 8E486EB4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER 1 1 SEQUENCE 345 AA; 39221 MW; 602EBF79 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C B70527; FEB-1997 (TEMBLEL. 02, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P79599 PRELIMINARY;
P79599; Q95564;
01-MAY-1997 (TrEMBLRE1, 03, Cx
01-MAY-1997 (TrEMBLRE1, 03, La
01-NOY-1999 (TREMBLRE1) 12, La
MATURE ALPHA CHAIN OF MAJOR HI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00047; 19; 1.
PFAM; PF00129; MHC_I; 1.
```

ANTIGEN (FRAGMENT).

1 RVDLRTLRGY 10 

ò

RESULT P79599

NON\_TER SEQUENCE

DDE READER READE

ö

Gaps

ö

ò

RESULT P70527

ö

Gaps

ö

```
CADAVID L.F., SHUFFLEBOTHAM C., RUIZ F.J., YEAGER M., HUGHES A.L., WATKINS D.I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evolutionary instability of the major histocompatibility complex class I loc1 in New World primates."; proc. Natl. Acad. Sci. U.S.A. 94:14536-14541(1997).
EMBL; U59648; AAB97491.1; --
HSSP; P01891; 2HLA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
Ateles.
                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                            94.1%; Score 48; DB 7; Length 364; 90.0%; Pred. No. 0.094; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                        SEQUENCE FROM N.A.
SULLIVAN J.A., OBTIINGER H.F., SACHS D.H., EDGE A.S.B.;
J. Immunol. 159:00-0(1997).
EMBL: AF014.004, AAB69339.1; -.
HSSP; P30685; 1A9E.
PROSITE: PS00299; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ateles belzebuth (Long-haired spider monkey).
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata:
Eutheria; Primates; Platyrrhini; Cebidae; Atelinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               030221 PRELIMINARY; PRT; 356 AA. 030221; 0302021; 01.NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1999 (TrEMBLrel. 12, Last annotation update) MMC CLASS I ATBE-B*01 (FRAGMENT).
  01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MHC CLASS I ANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 7;
Pred. No. 0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 1 356 AA; 39667 MW; 7C371D68 CRC32;
                                                                                                                                                                                                                                                                                                                                      364 AA; 40791 MW; BFC101BB CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                             PFAM; PF00047; 1g; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 RVDLQTLRGY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 98070787.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHC.
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
019744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
Q30221
    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25PP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WANGENTY STEPROWSKI S.M., TIAN L., LANGOWSKI J.L., YU J., KAHAN B.D.;
"Nucleotide sequences of three distinct clones coding for rat heavy
chain class I major histocompatibility antigens.";
Immunogenetics 43:318-320(1996).
EMBL: U38970; AAC22550.1;
HSSP; P01900; 1BII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Callithrix jacchus (Common marmoset).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHC CLASS I RT1.AB HEAVY CHAIN 35A9D3A8 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 51; DB 7; Length 356;
Best Local Similarity 100.0%; Pred. No. 0.023;
Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 51; DB 7; Length 367; Best Local Similarity 100.0%; Pred. No. 0.024; Matches 10; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    031254 PRELIMINARY; PRT; 367 AA.
031254;
01-NOV-1996 (TEMBLrel. 01, Created)
01-NOV-1999 (TEMBLrel. 12, Last sequence update)
01-NOV-1999 (TEMBLrel. 12, Last annotation update)
MHC CLASS I RT1.AB HEAVY CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                        356 AA; 40093 MW; 728A4997 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       364 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   019243 PRELIMINARY; PRT; 019243; 01-JAN-1998 (TrEMBLrel. 05, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-CONA STIMULATED SPLENOCYTES; MEDLINE; 96175158.

        SIGNAL
        1
        21
        Pr

        CHAIN
        22
        367
        M

        SEQUENCE
        367 AA;
        41471 MW;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00047; ig; 1.
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 RVDLRTLRGY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 RVDLRTLRGY 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; MHC.
SIGNAL
```

ô

Gaps

œ

ά g RESULT 019243 ID 0193 AC 0193 DT 01-3

ö

NON\_TER SEQUENCE

RESULT Q31254

g

õ

ö

Gaps

ö

```
D 046734 PRELIMINARY; PRT; 166 AA.

AC 046734;
DT 01-JUN-1998 (TEMBLEel. 06, Created)
DT 01-JUN-1998 (TEMBLEel. 06, Last sequence update)
DT 01-JUN-1998 (TEMBLEEl. 06, Last sequence update)
DT 01-JUN-1998 (TEMBLEEl. 10, Last annotation update)
DT 01-JUN-1999 (TEMBLEEl. 10, Last sequence update)
DT 01-JUN-1998 (TEMBLEEl. 06, Last
           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                           URAKAWA T., KODAMA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO08586; BAA24716.1; -.
PFAM: PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                URAKAWA I., KODAWA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: #8008589; BAA24719.1; -
PFAM: PF00129; MHC_I: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             046722;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
101-JUNY-1999 (TrEMBLrel. 10, Last annotation update)
MHC CLASS I HEATY CHAIN (FRAGMENT).
Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 46; DB 7;
Pred. No. 0.1;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 7;
Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                      1
166 166
166 AA; 19338 MW; F0563A5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1
166 166
166 AA; 19337 MW; 9321E1A4 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      166 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
9; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70 RVDLNTLRGY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1111 |||||
70 RVDLNTLRGY 79
                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=302D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                               Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   046722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ST TWENT OF STANTANT OF STANTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.
MEDILINE; 98211697.
KNAPP L.A. CADAVID L.F., WATKINS D.I.;
KNAPP L.A. CADAVID L.F., WATKINS D.I.;
"The MHC-E locus is the most well conserved of all known primate class in histocompatibility genes.";
J. Immunol. 166:189-196(1998).
EMBI: AF004922; AAC39880.1;
PFAM; PF00129; MHC_I; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                      "Polymorphism in the human class I MHC locus HLA-E in Japanese."; muniogeneetics 32:205-209(1990). EMBL; M32506; AAA63223.1; -- PFAM: PF00129; MHC_I? I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pithecia pithecia (White-faced saki).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Platyrrhini; Cebidae; Pitheciinae; Pithecia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
MHC HLA-E ALPHA-1 (FRAGMENT).
EA1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 16, Last annotation update)
MHC CLASS I HEAVY CHAIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 7;
Pred. No. 0.054;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        144 144
144 AA; 16535 MW; DC03E510 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90.2%; Score 46; DB 7; 90.0%; Pred. No. 0.088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C19D8182 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC CLASS I ANTIGEN (FRAGMENT).
                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-PERIPHERAL BLOOD;
MEDLINE; 91033943.
OHYA K., KONDO K., MIZUNO S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER 1 1
SEQUENCE 90 AA; 10505 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 90.2%;
Best Local Similarity 90.0%;
Matches 9; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 90.v.
Pre 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||:|||||||
75 RVNLRTLRGY 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 RVNLRTLRGY 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 046720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     062875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
062875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       046720
                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
```

ö

Gaps

ö

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   046743 PRELIMINARY; PRT; 166 AA.
046743;
041-JUN-1998 (TEMBLrel. 06, Created)
01-JUN-1998 (TEMBLrel. 06, Last sequence update)
01-MAT-1999 (TEMBLrel. 10, Last annotation update)
MHC CLASS I HEAVY CHAIN (FRAGMENT).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovinae; Bos.
                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                   90.2%; Score 46; DB 7; Length 166; 90.0%; Pred. No. 0.1; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
90.2%; Score 46; DB 7; Length 166;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=303F;
URAKAMA T., KODAMA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ABOO8616; BAA24745.1;
PFAM; PF00129; MHC_I; 1.
                             URAKAWA T., KODAWA M., MORITA M., IKEDA H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB008605; BAA24734.1; -.
PFAM; PF00129; MHC_I; 1.
                                                                                                                     1
166 166
166 AA; 19338 MW; F0563A5A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0B5B8001 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166
19236 MW;
                                                                                                                                                                                                   Query Match
Best Local Similarity 90.03
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
166 1
166 AA;
                                                                                                                                                                                                                                                                     1 RVDLRTLRGY 10
SEQUENCE FROM N.A. STRAIN=303F;
                                                                                                                                                                                                                                                                                        1 RVDLRTLRGY 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                  NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                     RESULT 15
046743
                                                                                                                                                                                                                                                                                                     q
   õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
```

Search completed: February 8, 2000, 19:16:20 Job time: 21507 sec

70 RVDLNTLRGY 79

g

THIS PAGE BLANK (USPTO)

```
U59641 Callithrix jaccus MH X79892 E.caballus EQMHCB4 m L02833 Bovine MHC class I r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="mature MHC class I alpha chain"
/product="mature MHC class I alpha chain"
/protein_id="CAA73907.1"
/brotein_id="CAA73907.1"
/db_xref="G1:1182090"
/db_xref="SPTREMEL:002949"
/translation="G8HSLRYEYTAVSRPGLGEPRYMEVGYVDDTQFVRYDSDAENPR
XEPRARWMEREGPEYWEEFTQKAKEGEDIXRVDLRTLRGYYNQSEGGSHTIQVMXGCD
YGSOSSLLKGYRQDAYDGRDYIALNEDLKTWTAADFAAQITRNKWEQTGYARERLRAYL
EGTCVEWLRRYLELGKETLLRSDPFBAHYTLHPRPEGDVTLRCWALGFYPADITLITWG
LNGEDLTQDMELVETRRAGGOTFQKWASVVVPLGKEQNYTCRYBHEGLPEFLGRREDE
SPSTNSNMETTYIXVVLGAIIGTLAIIGIVVAVVRRRRRNTGGKGDYTPAPAGRDSSQS
                                                                                                                               RNRTIA2F 1035 bp mRNA ROD 12-FEB-1998 Rattus norvegicus mRNA for mature MHC class I alpha chain. Y13579 Y13579.1 GI:2182089 MHC class I alpha chain; RTI.A2f gene. Norwey rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (03-JUN-1997) E. Joly, The Babraham Institute,
Submitted (03-JUN-1997) E. Joly, The Babraham Institute,
Immunology, Babraham Hall, Cambridge CB2 4AT, UK
3 (bases 1 to 1035)
Joly, E., Le Rolle, A.F., Gonzalez, A.L., Mehling, B., Stevens, J.,
Coadwell, W.J., Huenig, T., Howard, J.C. and Butcher, G.W.
molecules
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 1035)
Le Rolle, A.F., Hnig, T., Butcher, G.W. and Joly, E.
Unpublished
2 (bases 1 to 1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 100.000
  1071
1074
1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="RT1.A2f"
/function="antigen presentation"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                iol. In press
Location/Qualifiers
1. 1035
/organism="Rattus norvegicus"
/strain="lewis.lF"
/db_xref="taxon:10116"
/germline
0.6496
0.6514
0.6570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /haplotype="RT1(f)"
/clone_lib="8-21"
/dev_stage="adult"
/tissue_type="spenocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
160.44
160.41
160.35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene-"RT1.A2f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDVSLPDCKA"
  46.00
46.00
46.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 C
                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: RNRT1A2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-37.x RNRT1A2F
                                                                                                                                                           seq_documentation_block:
LOCUS RNRT1A2F
                                                                                                      seq_name: gb_ro:RNRT1A2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Curr. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   229
gb_pr3:CJU59641
gb_om:ECMHCB4
gb_om:BOVMHCIB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                      SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Documentation ...

1 X13579 Rattus norvegicus mRNA | AJ249705 Rattus norvegicus mRNA for F X90372 R. norvegicus mRNA for F X90372 R. norvegicus mRNA for F X14014 Rattus norvegicus mRNA for F X14014 Rattus norvegicus mRNA for F 1055637 Callithrix Jacchus MHC U38970 Rattus norvegicus MHC NAFO1404 Sus scrofa MHC class 105648 Ateles belzebuth MHC class 105548 Ateles belzebuth MHC class 105548 Ateles belzebuth MHC class 105548 Ateles belzebuth MHC class 105545 B. taurus MHC class 1 gen M32505 Human (Wongoloid) MHC HI X97645 B. taurus MHC class 1 gen AB008569 Bos taurus mRNA for MH AB008569 Bos taurus mRNA for MH AB00852 Bos taurus gene for MH AB008605 Bos taurus gene for MH AB008610 Bos taurus gene for MH AB00861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U59642 Leontopithecus rosalla
U59643 Leontopithecus rosalla
X54375 G.gorilla MHC Class I A
AJ249700 Rattus norvegicus par
                                                                                                                                                                                                          -MODEL=frame+p2n.model -DEV=xlp
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.2
-Q=/Cgn1_1/USPTO_spool/US08653294/runat_04D00 -GAPD=12.000 -GAPDEXT=4.000
-QB-CENTEND -CFMT—fastap -SUFFIX=rege -GAPDP=12.000 -GAPDEXT=4.000
-QGAPDEXT=0.100 -LOOPCI=0.000 -LOOPCIT=0.000 -FGAPDP=4.500
-GAPDEXT=0.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAPDEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-UIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTPWT=pfs -NORM=ext -MINLER+0 -MAXIELEN-1000000 -USER=US08653294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Documentation
                                                                                                         software, version 4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           out_format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESCOTE L
0.0478
0.0478
0.0478
0.0478
0.0486
0.0486
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
0.0738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2989
2989
4176
4176
4188
4188
4200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4212
5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5068
5068
5314
6273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6291
6291
                                                                                                         About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28Core
180.81
180.79
180.79
180.75
180.75
180.54
177.40
177.40
177.90
171.90
171.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
1641.4
16
     GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database sequences: 821193
Database length: -1518192014
Search time (sec): 10176.920000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       t0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
                                                                                                                                                                                       Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strd
  OM Of: US-08-653-294-37
                                                       Date: Feb 8, 2000 10:26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query: US-08-653-294-37
Query length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9D_ro: RN0249705
9D_ro: RNN2140106
9D_ro: RNNT14014
9D_ro: RNNT14014
9D_ro: RND1490104
9D_ro: RND38970
9D_ro: RND38970
9D_ro: RND38970
9D_ro: RND38970
9D_pr3: CUU59633
9D_pr3: RSHUAE012
9D_pr1: HSHUAE012
9D_pr1: RSH008609
9D_pr1: RSH008609
9D_pr1: RSH008609
9D_pr2: SGU52118
9D_pr2: SGU52118
9D_pr2: SGU52118
9D_pr2: SGU52118
9D_pr2: SGU52118
9D_pr2: SGU52117
9D_pr2: RNRT1ALCG
9D_pr3: LRU59643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_prl:GGGGGGA3
gb_ro:RNO249700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_ro:RNRT1A2F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                score_list:
Sequence
```

Mammalia; Eutheria; Rattus.

LOCUS DEFINITION

ACCESSION VERSION

KEYWORDS

ORGANISM

SOURCE

```
'Product-"Mature alpha chain of major histocompatibility complex class I antigen"

'Protein_id="CAA6203.1"

'Protein_id="CAA6203.1"

'Ab_xref="G1:1971633"

'Ab_xref="G1:1971633"

'Ab_xref="GFIREMBL:P79599"

'Ab_xref="G1:1871633"

'Ab_xref="G1:1871633"

'Ab_xref="G1:1871633"

'Ab_xref="G1:1871633"

'Ab_xref="G1:187163"

'Ab_xref="Ab_xref="G1:187163"

'Ab_xref="G1:187163"

'Ab_xref="G1:187163"

                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (27-37L-1995) E. Joly, The Babraham Institute, Babraham, Cambridge, CB2 4AT, UK
Cambridge, CB2 14T, UK
3 (bases I to 10.38)
Joly,E., Le RolleA.F., Gonzalez,A.L., Mehling,B., Stevens,J.,
Coadwell,W.J., Huenig,T., Howard,J.C. and Butcher,G.W.
Co-evolutation of rat tap transporters and MHC class 1 R11-A
                                                  790373.1 GI:1871632
alpha chain; class 1 antigen; major histocompatability complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Curr. Biol. In press
On Mar 10, 1997 this sequence version replaced gi:940822.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 100.000
   norvegicus mRNA for RT1.A1(0) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      800
                                                                                                                 Norway rat.

Status norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
I (bases 1 to 1038)
Joly,E., Gonzalez,A.L. and Butcher,G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
/strain="R71(0)"
/isolate="88(1) 29.6.92"
/db_xref="taxon:10116"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="spleen"
/cell_type="splenocyte"
1...1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 CGAGTGGACCTGAGGACCTGCGCGCGTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        352 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="RT1.A1(0)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="RT1.A1(0)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex-"Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSDVSLPDCKA"
                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1038)
Joly, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1038 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: RNRTlA10G
                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-37 x RNRT1A10G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_ro:RNRT1A20G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS RNRT1A20G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
DEFINITION
                                                                                                                                                                                                                                      REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16-SEP-1999) le Rolle A.F., Cellular Immunology Program,
The Babraham Institute, CB2 4AF, Cambridge, UNITED KINGDOM
Location/Qualifiers
1. 1038
/organism="Rattus norvegicus"
/strain="BUF"
/db_xref="taxon:10116"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="GSHSLRYFETAVSRPGLGEPRYMEVGYVDDTQFVRYDSDAENPR
MEPRARWIEREGREYWEQQTQNAKGHEQVNRVDLRTLRGYYNQSEGGSHTIQRWHGCD
VGTDGSLLRGYEQHAYDGRDYIALNEDLKTWTAADFAAQITRNKWDQAGAAERSRAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGTCVEWLRRYLEHGKETLLRSDPPEAHVTLHPRPEGGŸTLRCWALGFYPADITLTWQ
LNGEDLTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCRVEHEGLPEPLSQRWEP
SPSTNSNMETTVIYVVLGAIIGTLAIIGIVVAVVRRRRRNTGGKGGNYAPAPGRDSSQ
                                                                                                                                                                                                                                                                                                                                 major histocompatibility complex; MHC class IA antigen; RT1-A2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. 1 (bases 1 to 1038) Eutcher, G. EROlle, A. Joly, E. and Butcher, G. Characterisation of the rat MHC class I molecules
                                                                                                                                                                                29-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-FEB-1998
                                                                                                                                                                             RNO249705 1038 bp mRNA ROD 29-NOV-19
Rattus norvegicus partial mRNA for MHC class Ia A2b antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /standard_name="MHC class Ia antigen"
/function="antigen presentation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB56216.1"
/db_xref="G1:5912596"
223 CGAGTGGACCTGAGGACCCTGCGCGCGTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: RNO249705 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /haplotype="RT1b"
/clone="Bb+8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="RT1-A2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene="RT1-A2b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                  AJ249705.1 GI:5912595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSDVSLPDCKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1038 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 1038)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           280 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . .1038
                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-37 x RNO249705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                         (RT1-A2b gene).
AJ249705
                                                                                        seq_name: gb_ro:RNO249705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_ro:RNRT1A10G
                                                                                                                                              seq_documentation_block:
LOCUS RNO249705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS RNRT1A10G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
```

BASE COUNT

ORIGIN

source

PEATURES

gene

JOURNAL REFERENCE AUTHORS TITLE

JOURNAL

AUTHORS TITLE

REFERENCE

12-FEB-1998

```
<1. .1041
/codon_atart=1
/product="MHC class I alpha chain"
/protein_id="CAA7433.1"
/protein_id="CAA7433.1"
/db_xref="Gar7433.1"
/db_xref="Gar7433.1"
/db_xref="Gar7433.1"
/db_xref="Gar74225995"
/db_xref="Gar74225995"
/db_xref="Gar74225995"
/db_xref="Gar74225995"
/db_xref="Gar74225995"
/db_xref="Gar74225995"
/db_xref="Gar74225995"
/db_xref="Gar74225995"
/db_xref="Gar74225995995"
/db_xref="Gar74225995"
/db_xref="Gar74235995"
/db_xref="Gar74225995"
/db_xref="Gar742259"
/db_x
                                                                                                                                                                                                                                                                                                     Submitted (17-JUN-1997) Mehling B., Universitaet Wuerzburg, Institut fuer Virologie und Immunbiologie, Versbacherstr. 7 97078 Wuerzburg, GERMANY
2 (bases 1 to 1041)
Joly, E., LeRolle, A., Gonzalez, A.L., Mehling, B., Stevens, J., Coddwell, W.J., Huenig, T., Howard, J.C. and Butcher, G.W. Co-Evolution of rat TAP transporters and MHC Class I RTI-A molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    % (bases 1 to 1041)
Joly.B., Le Rolle,A.F., Gonzalez,A.L., Mehling,B., Stevens,J.,
Joly.B., Le Rolle,A.F., Gonzalez,A.L., Mehling,B., Stevens,J.,
Coadwell,W.J., Huenig,T., Howard,J.C. and Butcher,G.W.
Co-evolutation of rat tap transporters and MHC class 1 RT1-A
molecules
Coration/Qualifiers
Location/Qualifiers
1. 1041
/organism="Rattus norvegicus"
/strain="LEW-1F" (f haplotype)"
/db_xref="taxon:10116"
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1041)
        Rattus norvegicus mRNA for MHC class I alpha chain, partial.
Y14014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="alpha 1-domain"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      271. .546
/note="alpha 2-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       547. .822
/note="alpha 3-domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    823. .957
/note="transmembrane"
/number=5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     958. .987
/note="cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /number=6
988. .>1041
/note="cytoplasmic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         349
                                                            Y14014.1 GI:2225994
MHC class I alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            281 c
                                                                                                                                                                                                                                                 Mehling, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'number=3
                                                                                                                   Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             number≖4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /number=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-37 x RNY14014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
     DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                    AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Mature alpha chain of major histocompatibility
complex class I antigen"
/protein.id="CaA62021."
/db_xref="GI:1811637"
/db_xref="SPTREMBL:095567"
/db_xref="SPTREMBL:095567"
/translation="GSHSLRYFYIAVSREGIGEPRYMEVGYVDDTQFYRYDSDAENPR
YEPRARWHEREQPEWREREQGAREGEQIYRDLTLRGYYRQSEGSHIIQEMYGCD
VGSDGSLLRGYRQDAYDGRDYIALNEDLKTWTAADFAAQITRRKWERRERIEMYCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EGICVESLRRYLELGKETLLRSDPPEAHVTLHPRPEGDYTLRCWALGFYPADITLTWQ
LNGEDLTQDMELVETRPAGDGTFQKWASVVVPLGKEQNYTCRVEHEGLPEPLSQRWEP
SPSTNSNMETTVIYVVLGAIIGTLAIIGIVVAVVRRRRRNTGGKGGNYAPAPGRDSSQ
                                                                                                                                                                                                                                                                                                                                                                                               E. Joly, The Babraham Institute, Babraham,
                                                                                                                                                                                                                                                                                                                                                                                Lorder John State Combridge, CB2 4AT, UK
Cambridge, CB2 4AT, UK
E 3 (bases 1 to 1038)
S John E., Le Rolle.A.F., Gonzalez,A.L., Mehling,B., Stevens,J.,
Coadwell,W.J., Huenig,T., Howard,J.C. and Butcher,G.W.
Co-evolutation of rat tap transporters and MHC class 1 RT1-A
molecules
Curr. Biol. In press
On Mar 10, 1997 this sequence version replaced g1:940828.
Location/Qualifiers
ce /organism="Rattus norvegicus"
                            X90372 .
X90372.1 GI:1871636
alpha chain; class i antigen; major histocompatability complex.
                                                                                                                                                           Mammalia; Eutheria;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 100.000
     norvegicus mRNA for RT1.A2(0) alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        800
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata;
Rodentia; Sciurognathi; Muridae; Murinae;
I (bases 1 to 1038)
Joly.E., Gonzalez,A.L. and Butcher,G.W.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="RT1(0)"
/isolate="88(1) 29.6.92"
/db_xref="taxon:10116"
/chromosome="20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="spleen"
/cell_type="splenocyte"
1. 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 CGAGTGGACCTGAGGACCTGCGCGGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <i. .1038
/gene="RT1.A2(0)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="RT1.A2(0)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSDVSLPDCKA"
                                                                                                                                                                                                                                                                                                        (bases 1 to 1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1041 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /germline
                                                                                                                Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to: RNRT1A20G
                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-37 x RNRT1A20G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS RNY14014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_ro:RNY14014
                                                                                                                                                                                                                                                                                                                                  Joly, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                         JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
```

```
US-08-653-294-37 x RNPEPPRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product_protein involved in peptide presentation"
//protein_id="CaA69481"
/db_xref="G1:131631"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P70527"
/db_xref="SPTREMBL:P7057"
/db_xref="SPTREMBL:P707"
/db_xref
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 (bases 1 to 1047)
Joly, E., Le Rolle, A.F., Gonzalez, A.L., Mehling, B., Stevens, J.,
Coadwell, W.J., Huenig, T., Howard, J.C. and Butcher, G.W.
Co-evolutation of rat tap transporters and MHC class 1 RT1-A
molecules
                                                                                                                                                                                                                                                                           RNPEPPRES 1047 bp mRNA ROD 12-FEB-1998
R.norvegicus mRNA for protein involved in peptide presentation.
Y08532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="splenocytes"
/note="identical sequence obtained from PC12 cells'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curr. Biol. In press
On Mar 10. 1997 this sequence version replaced g1:1619331.
Location/Qualifiers
1. 1047
/Organism.=Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-0CT-1996) E. Joly, The Babraham Institute,
Immunology, Babraham Hall, Babraham, Cambridge CB2 4AT,
3 (bases 1 to 1047)
Joly, E., Gonzalez, A.L. and Butcher, G.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0 Gaps: 0 Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Vertebrata, Rodentia, Sciurognathi, Muridae, Murinae, 1 (bases 1 to 1047)
Le Rolle, A. F., Butcher, G. W. and Joly, E. Unpublished
2 (bases 1 to 1047)
                                  to: 1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="NEDH"
/db_xref="taxon:10116"
/chromosome="20"
                                                                                                                                                        223 CGAGTGGACCTGAGGACCCTGCGCGCTAC 252
                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                              Y08532.1 GI:1871630
peptide presentation protein.
                                                                                             1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /germline
/haplotype="RT1g"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350
                               Align seg 1/1 to: RNY14014 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <1. .1038
<1. .1038
/gene="RT1.Ag"
/codon_start=1</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="RT1.Ag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .1038
                                                                                                                                                                                                                   seq_name: gb_ro:RNPEPPRES
                                                                                                                                                                                                                                                                              seq_documentation_block:
LOCUS RNPEPPRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Joly, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
```

```
/translation-"GSHSLRYFTTAVSRPGLGEPRFISVGYVDDTEFVRYDSDAENPR
PEPRRAMERGPEYWEOGYPTIAKENSOVNRVDLETLIKGYTWOSEGGSTTIQEMEGCD
VGSDGSLLRCYEQHAYDGRDYIALREDENDYRTHAGATTRSKWEBARYARRILAYL
EGTCYEMLRRYLEHRYDGRDYIALREDENFAHVTLHPRPEGDVTLRCWALGFYPADISLSWO
SLGREDLYGDELVETRRAGGOTFQKRASVVVPLGKEQNYTCRYEHEGLEFLEGRWEP
SLGREDSNMETYYTVYLGAVAIIAAVYINARRRRNTGGKGGVYTPAPGGRDS
GSSDVSLPDGKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases I to 1056)
Le Rolle, A.F.
Direct Submission
Submitted (16-SEP-1999) le Rolle A.F., Cellular Immunology Program,
The Babraham Institute, CB2 4AF, Cambridge, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              major histocompatibility complex; MHC class IA antigen; RT1-Alb
                                                                                                                                                               KNO249704 1056 bp mRNA ROD 29-NOV-1999 Rattus norveglcus partial mRNA for MHC class Ia Alb antigen (RTI-Alb gene).
                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; P
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I
(bases 1 to 1055)
LeRolle, A., Joly E. and Butcher, G.
Characterisation of the rat MHC class I molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /standard_name="MHC class Ia antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /function="presentation antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"/strain="BUF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 1056
to: 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB56215.1"
/db_xref="GI:5912594"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10116"
/chromosome="20"
/haplotype="RTlb"
/clone="Ba8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           223 CGAGTGGACCTGAGCCTGCGCGCTAC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                          223 CGAGTGGACCTGAGGACCCTGCGCGCGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354 g
                                             1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <i. .1041
/gene="RT1-Alb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="RT1-A1b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                        AJ249704.1 GI:5912593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 C
  to: RNPEPPRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: RNO249704
                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x RNO249704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                      seq_name: gb_ro:RNO249704
                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                              Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
```

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL MEDLINE

TITLE

REFERENCE AUTHORS JOURNAL

DEFINITION

ACCESSION VERSION

```
Chases 1 to 1588)
Wand, M. Tlan, L., Langowski, J.L., Stepkowski, S.M. and Kahan, B.D.
Direct Submission
Direct Submission
Submitted (20-007-1995) M. Wang, Division of Immunology & Organ
Transplantation, Department of Surgery, University of Texas Medical
School, 6431 Fannin Street MSB 6.255, Houston, TX 77030, USA
1. 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/product="MHC class I RT1.Ab heavy chain precursor"
/product="MHC class I RT1.Ab heavy chain precursor"
/protein_id="AAC52550.1"
/db_xief="G1:1263198"
/translation="MARRTLLLLIAAALAPTQTRAGSHSLRYFYTAVSRPGLGEPRFI
svgrVDDTEFYRYDSDAENPRYEPRARWMEREGPEYWEOQFRIAKENEOVNRYDLRTL
RGYYNOSEGGSHTIQEMFGCDVGSDGSLLRGYEQHAVDGRDYTALNEDLKTWTAADFA
AQITEKWERARYAERLRAYLEGGTCVEWLRRYLEHGKETLLRSDPPRAHVTHPRPREG
DYTLRCWALGFYPAD1SLSWQLNGEDLTQDMELVETRPAGDGTFQKWASVVVPLGKEG
NYTCRVEHEGLPEPLSQRWESSLSTDSNMETYVIYVVLGAVAIIAAVITAAVTVRR
                                                                                                                                                                             Nucleotide sequences of three distinct clones coding for rat heavy chain class I major histocompatibility antigens Immunogenetics 43 (5), 318-320 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RATMECRT 1590 bp mRNA ROD 11-MAR-1997
Rattus norvegicus MHC class I RT1.Aa alpha-chain precursor mRNA, complete cds.
M31018
M31018.1 GI:1877415
M31018.1 GI:1877415
FRI.Aa alpha-chain; cell surface antigen; cell surface alpha-chain; class I gene; integral membrane protein; major histocompatibility complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Norway rât.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 1590)
                                                 Eukaryota; Métazoa; Chordata; Cranlata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. .
1 (bases 1 to 158)
Wang,M., Stepkowski,S.M., Tian,L., Langowski,J.L., Yu,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/haplotype="RT1.Ab"
/tissue_type="ConA stimulated splenocytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product-"MHC class I RT1.Ab heavy chain"
426 c 484 g 332 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRRNTGGKGGVYTPAPGRDSSQSSDVSLPDCKA"
64. .1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286 CGAGTGGACCTGAGGACCTGCGCGCGTAC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: RNU38970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-37 x RNU38970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS RAIMHCRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_ro:RAIMHCRI
                                                                                                                                                       Kahan, B.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
ORGANISM
                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDTQFVRFDSDAANPRMEPRAPWVEQEGPEYWEEQTRRAKAHAQTDRVDLRTLKGYYN GSDAGSHT JOWMSGCWYGDDRYDDRYDGYDAYDGYDY TALMEDLLSSYTAADMAAQITQ KWEAANAAEEMRAYLEGECLEWLHRYLENAKETLQRAEPPRTHYTHPVSDHEATLR CWALGFYPAEITLLYMORDGEDGYTQDMELWETRPTGDRTFCOKWAAVVPSGEBERYTCH VQHEGLPEPLTLRWEPPSQPTIPIMGIVAALAITGAVGGAVVVAVMWRKKSSDKKGGS YSQAARSESAQGSDYSLTACKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="LLLLLSGALVLTETWAGSHSMRYFYTSVSRPGRGEPRFIIVGYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (31-MAY-1996) Wisconsin Regional Primate Research Center, University of Wisconsin-Madison, 1220 Capitol Court, Madison, WI
                                                                                                                                                                                                                            Callithrix jacchus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Platyrrhini; Callitrichidae; Callithrix.

1 (bases 1 to 1071)
Cadavid,L.F., Shufflebotham,C., Ruiz,F.J., Yeager,M., Hughes,A.L. and Watkins,D.I.
Evolutionary instability of the major histocompatibility complex class I loci in new world primates
Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14536-14541 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RNU38970 1588 bp mRNA ROD 16-MAY-1996
Rattus norvegicus MHC class I RT1.Ab heavy chain precursor, mRNA, complete cds.
U38970.1 GI:1263197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 1071)
Cadavid, L.F., Shufflebotham, C., Ruiz, F.J., Yeager, M., Hughes, A.L.
and Watkins, D.I.
                                                 CJUS9637 1071 bp mRNA PRI 22-JAN-1998 Callithrix jacchus MHC class I (Caja-G*01) mRNA, partial cds. US9637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="MHC class I caja-G*01"
/protein_id="AAB97480.1"
/db_xref="G1:1389921"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. 1071
/organism="Callithrix jacchus"
/db_xref="taxon:9483"
1. 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <i. .1071
/gene="MHC class I Caja-G"
/note="Allele: 01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MHC class I Caja-G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271 CGAGTGGACCTGCGGACCCTCCGCGGCTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                366 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
                                                                                                                                                       U59637.1 GI:1389920
                                                                                                                                                                                                           Callithrix jacchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                321 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x CJU59637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: CJU59637
seq_name: gb_pr3:CJU59637
                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_ro:RNU38970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
```

source

FEATURES

gene

BASE COUNT ORIGIN

DEFINITION

ACCESSION

VERSION

MEDLINE REFERENCE AUTHORS TITLE JOURNAL

JOURNAL

AUTHORS

TITLE

AUTHORS TITLE REFERENCE

JOURNAL

REMARK FEATURES

COMMENT

```
RFIAVGYVDDTOFVRFDSDARNPRMERRAPWIEKEGOEYWDRETGIORDTSOTYRVDL
KTLROYYNGSEAGSHTLQSMYGCYLGPDGLLLRGYROFAYDGADYLALNEDLRSWTAA
DMAAQISKRKWEAANAAEQERSYLGGRCVEWLRRYLEMGKDTLQRAEPPKTHVTRHPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDLGVTLRCWALGFYPREISLTWORRGODOSODMELVETRPSGDGTFOKWAALVVPPG
EEQSYTCHVQHEGLQEPLTLRWDPPQPPVPIVGIIVGLVLVLVAGAMVAGVVIWRKRR
SGEKGGSYTQAAGSDSAQGSDVSLTKDPRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MRVRGPQAILILLSGALALIGTRAGPHSLSYFYTAVSRPDLGDS
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 1095)
Sullivan,J.A., Oettinger,H.F., Sachs,D.H. and Edge,A.S.B.
Analysis of polymorphism in porcine MHC class I genes: Alterations in signals recognized by human cytotoxic lymphocytes
J. Immunol. 159 (1997) In press
2 (bases 1 to 1095)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 1071)
Cadavid, L.F., Shufflebotham, C., Ruiz, F.J., Yeager, M., Hughes, A.L.
and Watkins, D.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 1071)
Cadavid,L.F., Shufflebotham,C., Ruiz,F.J., Yeager,M., Hughes,A.L.
and Watkins,D.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evolutionary instability of the major histocompatibility complex class I loci in new world primates
Proc. Natl. Acad. Sci. U.S.A. 94 (26), 14536-14541 (1997)
98070787
                                                                                                                                                                                                          Direct Submission
Submitted (16-UTL-1997) Molecular and Cellular Biology, Diacrin
Inc., Building 96, 13th Street, Charlestown, MA 02129, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU59648 1071 bp mRNA PRI 22-JAN-1998
Ateles belzebuth MHC class I (Atbe-B01) mRNA, partial cds.
U59648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Platyrrhini; Cebidae; Atelinae; Ateles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="NHC class I antigen"
/protein_id="AAB69339.1"
/db_xref="G1:2352986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295 CGAGTGGACCTGAAGACCCTGCGGGGTAC 324
                                                                                                                                                                                                                                                                                                        1. .1095
/organism="Sus scrofa'
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        long-haired spider monkey. Ateles belzebuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                   /gene="PC14"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PC14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U59648.1 GI:1389908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 c
                                                                                                                                                                                                                                                                                                                                                                                                                    .1095
                                                                                                                                                                                                                                                                                                                                                                           .1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 4.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AF014004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-37 x AF014004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_pr3:ABU59648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS ABU59648
                                                                                                                                                                                         Edge, A.S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                        AUTHORS
TITLE
                                                                                                                                           JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                             gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
REFERENCE
                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
Rada,C., Lorenzi,R., Powis,S.J., van den Bogaerde,J., Parham,P. and
Howard,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"MEAMAPRTLLLLLAAALAPTQTRAGSHSLRYFYTAVSRPGLGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFIAVGYVDDTEFVRFDSDAENPRMEPRARWMEREGPEYWEQOTRIAKEWEQIYRVDL
RTLRGYYNOSEGGSHTIOEMYGCDVGSDGSLLRGYRODAYDGRDYIALNEDLKTWTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DFAAQITRNKWERARYAERLRAYLEGTCVEWLSRYLELGKETLLRSDPPEAHVTLHPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEGDVTLRCWALGFYPADITLTWQLNGEDLTQDMELVETRPAGDGTFQKWASVVVPLG
KEQNYTCRVEHEGLPKPLSQRWEPSPSTDSNMETTVIYVILGAVAMIGAVAIIGAMVA
                                                                                                                                                                                                       Submitted (21-DEC-1990) The Institute for Genetics, University of Cologne, Cologne, 50674, Germany (bases 1 to 1590)
                                                                                                                                                                                                                                                                                                                             ō
                                                                                                                                                                                                                                                                           Howard, J.C.
Direct submission
Submitted (10 MAR-1997) The Institute for Genetics, University of Cologne, Cologne, 20674, Germany
Sequence update by submitter
On Mar 11, 1997 this sequence version replaced g1:205421.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AF014004 1095 bp mRNA MAM 03-SEP-1997
DEFINITION Sus scrofa MHC class I antigen (PC14) mRNA, complete cds.
ACCESSION AF014004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product-"MHC RT1.Aa alpha chain signal peptide"
82. .1122
                                                            histocompatibility complex of murine rodents

Proc. Natl. Acad. Sci. U.S.A. 87 (6), 2167-2171 (1990) 90192768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/product="MnR RT1.Aa alpha-chain precursor"
/protein_id="AAB49324.1"
/db_xref="GI:1877416"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male"
/tissue_type="spleen and lymph node"
/coll_line="40 hour ConA blast cell line"
10. .1125
                                                  Concerted evolution of class I genes in the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="5' end could be at nucleotide 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVVRRKRRNTGGKGGDYAPAPGRDSSOSSDVSLPDCKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82. 1122
/product="MHC RT1.Aa alpha chain"
/558. 1564
1 423 c 493 g 338 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Rattus norvegicus"
/strain="DA"
/db_xref="taxon:10116"
/clone="3.3/1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1 to: 1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF014004.1 GI:2352985
                                                                                                                                             (bases 1 to 1590)
                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 51.00
Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: RATMHCRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-653-294-37 x RATMHCRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_om:AF014004
                                                                                                                                                                   Howard, J.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
```

source

CDS

ORIGIN

VERSION KEYWORDS SOURCE ORGANISM

```
(bases 1 to 254)
lasczyk, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /map="p21
                                                                                                                                                                                                                                                                                                                              alignment_block:
US-08-653-294-37 x HSHLAE012
                                                                                                                                                                                                                                                                                                                                                                                to: HSHLAE012
                                                                                                                                                                                                                                                         Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_prl:HSHLAE1E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS HSHLAE1E2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blasczyk, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
AUTHORS
                                                                                                       exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                       /translation="LLLLLSGALALTQTRAGSHSMRYFYTSVSRPGRGEPRFIAVGYV
DDTOFVRFDSDAAIPRMEPRALMMEQBGPEYWEBGYRRVKAAAQTDRVDLQTLRGYYN
OSEAGSHTJOTMYGCDVGPEGRFLRGYRQDAYDGYDIALDLRSWTRADMAAQNTK
RWRAANVAEQLRAYLEGKCQESLRRYLENGKEDPPRTHYHPPVSDHEATLR
CWALGFYPTEITLIANDEDGOTODDELWERPRAGGGTFGKWAAVVPCSGEBGRYTCY
VQHEGLPEPLTLRWEPSSQLIIPVGIIAGLAVLVAVVIGAAVTAVWMRRKSSGGKGGS
YSQAACSDSAQGSDVSLIACKA"
Submitted (31-MAY-1996) Wisconsin Regional Primate Research Center,
University of Wisconsin-Madison, 1220 Capitol Court, Madison, WI
53715, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (31-MAY-1995) R. Blasczyk, Bloodbank, Dept of Internal
Medicine, Div. of Hematology & Oncology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
3 (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (07-DEC-1995) R. Blasczyk, Bloodbank, Dept of Internal
Madicine, Div. of Hematology & Oncology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
On Dec 8, 1995 this sequence version replaced 91:871291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSHLAEO12 254 bp DNA PRI H.saplens HLA-E*01C230), exon 2. x87678 X87678 alpha chain; HLA-E*01; MHC class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                       /product="MHC class I Atbe-B*01"
/protein_id="AAB97491.1"
/db_xref="GI:1389909"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blasczyk, R., Forstmann, G. and Salama, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 254)
                                                             1. .1071
/organism="Ateles belzebuth"
/db_xref="taxon:9507"
                                                                                                                                                                                                                                                                                                                                                                                                    173 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .254
/organism="Homo sapiens"
/isolate="940459"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 CGAGTGGACCTGCAGACCTGCGCGGCTAC 300
                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                                      363 g
                                                                                                                                                                                        'note="Allele: 01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: ABU59648 from: 1
                                                                                                                                                         <1. .1071</li>/gene="Atbe-B"
                                                                                                                                       /gene="Atbe-B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                                                                                  319 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 47.00
Ratio: 4.700
Percent Similarity: 100.000
                                                                                                                     .. .1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-653-294-37 x ABU59648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_pr1:HSHLAE012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS HSHLAE012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blasczyk, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blasczyk, R
                                                                                                                                                                                                                                                                                                                                                                                                  216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
                                                                                                                       gene
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                  FEATURES
                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
```

```
Direct Submission
Submitted (31-MAY-1995) R. Blasczyk, Bloodbank, Dept of Internal
Medichine, Div. of Hematology & Oncology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
3 (bases 1 to 254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (07-DEC-1995) R. Blasczyk, Bloodbank, Dept of Internal
Medicine, Div. of Hematology & Oncology, Virchow-Klinikum,
Humboldt-Univ. Berlin, Augustenburger Platz 1, 13353 Berlin, FRG
On Dec 8, 1995 this sequence version replaced gi:871293.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo saplens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 254)
Blasczyk,R., Forstmann,G. and Salama,A.
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="alpha chain MHC class I glycoprotein"
77 c 90 g 41 t
                                                                                                                                                                 /product="alpha chain MHC class I glycoprotein"
78 c 90 g 40 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.sapiens HLA-E*01 variant (HLA-E*01t230), exon 2. X87680
                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note-"allele HLA-E*01T230"
                      'note-"allele HLA-E*01C230'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X87680.1 GI:1109760
alpha chain; HLA-E*01; MHC class I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/isolate="940637"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 CGAGTGAACCTGCGGACGCTGCGCGGCTAC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgValAspLeuArgThrLeuArgGlyTyr
                                                                                                                                                                                            ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA
                                        17. .254
/gene="HLA-E*01"
17. .>254
/gene="HLA-E*01"
/number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="HLA-E*01"
/number=3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HLA-E*01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 bp
/map="p21.3
```

us-08-653-294-37.rge

```
Direct Submission
Submitted (31-0CT-1997) Steffensen R., Aalborg Sygehus, Department
of Clinical Immunology and Blood Transfusion, 9000 Aalborg, DENMARK
2 (bases 1 to 270)
Steffensen, R., Christiansen, O.B., Bennett, E.P. and Jersild, C.
HLA-E polymorphism in patients with recurrent spontaneous abortion
99110147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    confirmed by sequence analysis"
/codon_start=3
/protein_id="CAA05526.1"
/db_xxef="GI:3929739"
/tab_xxef=ion="SHSLKYFHTSVSRPGRGEPRFISVGYVDDTQFVRFDNDAASPRM
VPRAPMMEQEGSEYWDRETRSAPTAIFRVNLRTLRGYYNGSEA"
85 c 92 g 44 t
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutherla;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 270)
                                                                                                                                                                                                                                                                                                                 19-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HLA-E"
/note="PCR product derived from human genomic DNA,
                                                                                                                                                                                                                                                                                                                   PRI
               Quality: 46.00 Length: 10
Ratio: 4.600 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                           AJ002533.1 GI:3929738
HIA-E gene; human leukocyte antigen.
human.
                                                                                                                                                to: 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: HSAJ2533 from: 1 to: 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .270
/organism="Homo sapiens"
/db_xref="taxon:9606"
1. .270
                                                                                                                                                                                                                       206 CGAGTGAATCTGCGGACGCTGCGCGGCTAC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 CGAGTGAACCTGCGGACGCTGCGCGCGTAC 251
                                                                                                                                                                                                                                                                                                             HSAJ2533 270 bp DNA
Homo sapiens HLA-E gene exon 2.
AJ002533
                                                                                                                                                                                  1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                              Align seg 1/1 to: HSHLAE1E2 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'gene-"HLA-E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene-"HLA-E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'number=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                        alignment_block:
US-08-653-294-37 x HSHLAElE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x HSAJ2533
                                                                                                                                                                                                                                                           seq_name: gb_pr1:HSAJ2533
                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                 LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL
MEDLINE
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
```

```
Human neuronal calcium chan
Human neuronal calcium chan
Human mitosin gene. Purifie
Mitosin nucleic acid sequen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detection, purification and elimination of antigen-specific
Tymphocytes - for producing cytotoxic T cells for immuno-therapy of
Tymphocytes and viral infection
Example 2; Fig 10; 222pp; French.

Example 2; Fig 10; 222pp; French.

Control of antigen-specific lymphocytes comprises forming a complex
Control of antigen-specific lymphocytes comprises forming a complex
Control of antigen-specific lymphocytes compatibility complex (MHC) molecules,
Immobiliasing the complex and binding samples containing the
Control of antigen-specific lymphocytes. Expression of the MHC molecule in a cell
Control of antigen-specific lymphocytes, an MHC/Deta-2-microglobulin chimeric
Conformarker protein, e.g. an MHC/Deta-2-microglobulin chimeric
Conforms the first 3 domains of the HLA-A2:1 heavy chain linked to human
Conformation with a flexible linker. The method is also used to
Conform the first 3 domains of the HLA-A2:1 heavy chain linked to human
Conformation of tumour-specific T-cells and to generate CTC for
specific killing of tumour cells (solid tumours, leukaemia or lymphoma)
Conformation or animal, but also for treating viral
                                                                                                                                                                                                                                                                                                                                                                               14-00T-1998 (first entry)
Chimeric HLA-A2.1/beta-2 microglobulin coding sequence.
Antigen; major histocompatibility complex; MHC; lymphocyte; detection; immobilisation; cytotoxic T-cell; tumour; leukaemia; lymphoma; viral infection; chimeric; beta-2 microglobulin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product- "chimeric HLA-A2.1/beta-2 microglobulin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human leukocyte antigen; probe; major histocompatibility complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-NOV-1997,
21-MAY-1997; F00892.
21-MAY-1996; US-651925.
(INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
(INSP ) INST PASTEUR.
Abastado J, Koutilsky P, Langlade-Demoyen P, Lone Y;
WPI; 98-018653/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
   .6e+03
.6e+03
.3e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .1239
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 CGAGTGGACCTGGGGACCCTGCGCGGCTAC
   88.25
88.18
86.31
86.31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: V30457 from: 1
                                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
ID Q12116 standard; DNA; 1101
AC Q12116;
                                                                                                                                                                                                                                                                       seq_documentation_block:
ID V30457 standard; DNA; 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-1991 (first entry)
HLA-C exon Cb-1.
   33.00
33.00
33.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:Q12116
                                                                                                                                                                                               seq_name: N_Geneseq_36:V30457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-37 x V30457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
Percent Similarity:
N_Geneseq_36:Q84662
N_Geneseq_36:Q84663
N_Geneseq_36:Q86851
N_Geneseq_36:V09076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo saptens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                       V30457;
                                                                                                                                                                                                                                                                                                                   NEW MARKET DATE OF THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KERGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T. ovis vaccine candidate antiginate paragraphy.

Taenia ovis antigenic polypeptilipase modulating factor gene, inpase modulating factor gene, inpase/lipase modulator fusion sequence encoding enzymes which sequence encoding enzymes which shodococcus rhodochrous desult in bNA encoding enzymes capable of DNA encoding an enzyme capable in the encoding an encoding an encoding an encoding 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 | Amycolatopsis mediterranei ri

10 | Streptococcus pneumoniae genc

15 | Streptococcus pneumoniae genc

16 | Sorangium cellulosum soraphen

18 | Sorangium cellulosum soraphen

19 | The soraphen biosynthesis genc

10 | Swine HEV ORF | DNA. New isola

10 | Swine HEV ORF | DNA. New isola

10 | Continuation (7 of 10) of

10 | Continuation (8 of 10) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! Chimeric HLA-A2.1/beta-2 micrd
! HLA-C exon Cb-1. HLA-C gene, D
! HLA-C exon Cb-2. HLA-C gene, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence of amylase gene and u
Tumour rejection antigen precu
Tumour rejection antigen precu
Sequence of Heliothis amigera
Calcium channel alpha-1E subun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Hereditary haemochromatosis
| Hereditary haemochromatosis
| Mouse NF-AT Interacting Protein
| Human secreted protein gene 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human calcium channel 27980/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! Hereditary haemochromatosis
                                                                                                                                                                                                                                                                                                           -WODEL-frame-pan.model -DEV-xlp
-Q-Cqqnl_J/OSPTO_SDOOL/VG808653294/runat_04022000_160701_15807/app_query.fasta.2
-DB=N Geneseq_36 -OFMT-fastap -SUFFIX-rng -GAPOP=12.000
-GAPEXT=4.000 -NINMATCH=0.100 -LOOPEL-0.000 -LOOPEXT=0.000
-GAPEXT=4.000 -NINMATCH=0.100 -LOOPECL-0.000 -VGAPEXT=0.500
-FGAPOP=6.000 -FCAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FGAPOP=6.000 -DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500
-FTANS-human40.01 -LOOPECT=7.000 -START=1 -MATRIX=blosum62
-ALIGN=15 -MODE-LOCAL -OUTPWT=Pfs -NORM-ext -MINLEN-0
-MAXLEN-15 -MODE-LOCAL -OUTPWT=Pfs -NORM-ext -MINLEN-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Taenia ovis antigenic
                                                                                                                                                       About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1032
22118
25533
5533
5535
5535
134525
134525
1816
1816
1816
1816
1816
1816
1816
           out_format :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1284
11101
11101
11101
11101
112665
28598
28958
49377
7207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.06
11.63
11.63
11.63
11.63
2.3e+03
642.11
742.49
1.8e+03
1.9e+03
1.9e+03
1.9e+03
1.9e+03
1.9e+03
1.9e+03
1.6e+04
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
116.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EScore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   695.21
697.71
1.4e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.9e+03
2.5e+03
       N_Genesed_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZSCOTE

143.87

130.37

130.37

189.07

98.00

97.96

90.86

190.75

192.13

45

92.14

93.17

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10

93.10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121.56
117.11
117.11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112.39
106.12
97.75
97.75
97.75
97.75
101.23
101.23
101.23
101.23
101.23
101.23
102.75
94.99
94.99
94.99
96.75
96.75
96.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.75
97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           999.44
98.89
98.47
93.10
92.69
88.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database sequences: 311585
Database length: 125096042
Search time (sec): 873.190000
       OM of: US-08-653-294-37 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search information block:
Query: US-08-653-294-37
Query length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Genesed_36:*
                                                                                                                                                                                                                                                                           Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_36:x23031 -
N_Geneseq_36:x23032 -
N_Geneseq_36:x20248_06 -
N_Geneseq_36:x20248_07 -
                                                                               Date: Feb 8, 2000 7:32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:V21187
N_Geneseq_36:V52305
N_Geneseq_36:V52305
N_Geneseq_36:T06769
N_Geneseq_36:T089956
N_Geneseq_36:T089958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:Q44282
N_Geneseq_36:Q55131
N_Geneseq_36:Q55132
N_Geneseq_36:T58971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
N_Geneseq_36:V30457
N_Geneseq_36:Q12116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_36:T17935
N_Geneseq_36:Q72739
N_Geneseq_36:T17934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:X15615
N_Geneseq_36:X15616
N_Geneseq_36:Q04525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Geneseq_36:012117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:V57926
N_Geneseq_36:V57903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:T93045
N_Geneseq_36:X04354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _Geneseq_36:008510
_Geneseq_36:V69717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Geneseq_36:083735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_36:T90899
N_Geneseq_36:Q12115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:T90895
N_Geneseq_36:Q75974
N_Geneseq_36:Q75973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36:Q29268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genesed_36:07889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _Geneseq_36:T9669(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N_Geneseq_36:Q58522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N_Geneseq_36:Q1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _Genesed_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database:
```

us-08-653-294-37.rng

```
HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 2; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and produ. of monoclonal antibodies specific for the HIA-C antimals and produ. of sequence and 101112486 and J03112487.

Sequence 1101 BP; 215 A; 335 C; 379 G; 172 T;
                                                                                                                                                                                                      HIA-C gene, DNA probe and transformant cells - for immunisation of animals and monoclonal antibody development.

Claim 1; Page 1; 13pp; Japanese.

Probes comprising part of the sequence can be used to identify class I genes. The DNA can be expressed for immunisation of animals and prodn. of monoclonal antibodies specific for the HIA-C animals and prodn. of monoclonal antibodies specific for the HIA-C sequence 1101 BP; 211 A; 337 C; 377 G; 176 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human leukocyte antigen; probe; major histocompatibility complex; MHC; class I; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 40.00 Length: 10
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                 Quality: 40.00 Length: 10
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: Q12116 from: 1 to: 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 CGAGTGAGCCTGCGGAACCTGCGCGGCTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
1. .1101
/*tag= a
                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID Q12117 standard; DNA; 1101 BP.
AC Q12117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1991.
22-SEP-1989; 247695.
22-SEP-1989; JP-247695.
(OLVU ) OLYMPUS OPTICAL KK.
WPI; 91-182969/25.
                                                                                                                                     22-SEP-1989; JP-247695.
(OLYU ) OLYMPUS OPTICAL KK.
WPI; 91-182989/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                  /*tag= a
                                                  .1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:012117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-37 x Q12116
                                                                                                    14-MAY-1991.
22-SEP-1989; 247695.
MHC; class I; ss.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLA-C exon Cb-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; R12466.
                                                                                                                                                                                           P-PSDB; R12465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                    J03112485-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J03112485-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
```

alignment\_block: US-08-653-294-37 x Q12117

```
PER 18-AUG-1997; E04495.

18-AUG-1997; EP04495.

PAUG-1997; EP-810551.

RANOYS ) NOVARTIS AG.

PI Engel N. Schupp T. Toupet C;

RANOS ) NOVARTIS AG.

PI Engel N. Schupp T. Toupet C;

RANCISTORIA WESB45-WESB60.

PT PESDB; WESB45-WESB60.

PT COPTOCHER TERMINICIN analogues

CIAIM 4; Page 53-102; 205pp; English.

The present sequence represents a Amycolatopsis mediterranei rifamycin and rifamycin analogues

CIAIM 4; Page 53-102; 205pp; English.

CIAIM 5 And Fragment Comprises a DNA region involved directly or indirectly or modifying genes (luster, and functional or indirectly or modifying genes involved in ansamycin or indirectly or modifying genes involved in ansamycin or indirectly or completely deleted. The ONA fragment can be used for assembling a library of polyketide or synthesis gene cluster has been partly or completely deleted. The DNA fragment can be used for assembling a library of polyketides.

CIAIM 5789 BP; 6707 A; 19183 C; 20504 G; 7395 T;
                                                                                                                                       seq_documentation_block:

DV21187 standard; DNA; 53789 BP.

AC V21187.

AC V21187.

AL JUL-1998 (first entry)

DE Awycolatopsis mediterranei rifamycin synthesis gene cluster fragment.

KW Amycolatopsis mediterranei; rifamycin; synthesis; gene cluster;

KW polyketide synthase; actinomycete; ansamycin; ds.

OS Awycolatopsis mediterranei.
                                                                                                                                                                                                                                                                         Location/Qualiflers
1825. 15543
/*tag= a
/label= ORF_A
/product= "polyketide synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag- e
/label- ORF_
/product- "polyketide synthase"
51713. .5293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "ttay-
/label- ORF_C
/~~^duct- "polyketide synthase"
                                                                                                                                                                                                                                                                                                                                                                                                        /label- ORF_B
/product- "polyketide synthase"
30895. .36060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "polyketide synthase"
 to: 1101
                                                        295 CGAGTGAGCCTGCGGAACCTGCGGGGTAC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= ORF_D
/product= "polyketide
                                      1 ArgValAspLeuArgThrLeuArgGlyTyr 10
to: Q12117 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36259. .41325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41373. .51614
                                                                                                          seq_name: N_Geneseq_36:V21187
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag=
 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDS
```

3

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E E E E
                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes a computer readable medium which has the nucleotide sequences SEQ ID NO:1 to 391 (V52134 to V52524) recorded on it, or a representative fragment or a sequence at least 958 identical to SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391. The nucleotide sequences depicted in SEQ ID NO: 1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the Spneumoniae genome (SEQ ID NO:1 to 391) where the nucleic acid molecule is produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEQ ID NO:1 to 31, identifying members of the library which contain sequences that hybridise to the target sequence and isolating the nucleic acid molecules from the members: or (b) isolating mRNA, DNA or CDNA produced from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fragment of the S. pneumoniang genome to prime the amplification and isolating the amplified sequences. The computer readable medium can be used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical sequence 11770 BP; 3673 A; 1919 C; 2574 G; 3603 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptococcus pneumoniae genome fragment SEQ ID NO:172.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-0CT-1997; U19588.
31-0CT-1996; US-029960.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Chol GH, Dillon PJ, Dougherty BA, Fannon M,
Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to reverse of: V52305 from: 1 to: 11770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Gaps: 0
Percent Identity: 75.000
                       Length: 9
Gaps: 0
Percent Identity: 77,778
                                                                                                                                                                                                 to: V21187 from: 1 to: 53789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 1094-1101; 1409pp; English.
                                                                                                                                                                                                                                                                                                   20272 AAGCTCGACCTGCGGACGCTGCGCGGC 20298
                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                   V52305 standard; DNA; 11770 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x V52305/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus pneumoniae.
                                                  Ratio: 4.222
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:V52305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 4.625
Percent Similarity: 100.000
                       38.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.00
                                                                                                                         alignment_block:
US-08-653-294-37 x V21187
                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1998.
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                    Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1
```

```
The present invention describes a computer readable medium which has
The present invention describes a computer readable medium which has
The present invention describes a computer readable medium which has
The nucleotide sequences SEQ ID No.: 1 to 391 (752134 to V52524) recorded
The nucleotide sequences are general to sequence depicted in SEQ ID No.:
To 391 (V52134 to V52524) are genomic fragments from Streptococcus
The present invention also describes an isolated nucleic acid
molecule encoding a homologue of any of the fragments of the S. pneumoniae
The present invention also describes an isolated nucleic acid
molecule encoding a homologue of any of the fragments of the S. pneumoniae
The present invention also describes an isolated nucleic acid
molecule encoding a homologue of any of the sequences in SEQ ID No::
That hybridise to the target sequence and isolating the nucleic acid
molecules from the members; or (b) isolating mRNA, DNA or CDNA produced
from an organism, amplifying nucleic acid molecules whose nucleotide
Sequence is homologous to amplification primer the amplification and
isolating the amplified sequences. The computer readable medium can be
used in a computer-based system for identifying fragments of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computer readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae genome fragment SEQ ID NO:134.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-YAY-1998.
30-OCT-1997; U19588.
(HUNA-) HUMAN GENOME SCI INC.
BATASH SC, Chol GH, Dillon PJ, Dougherty BA, Fannon M, Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2890 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to: 12665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ss for S. pneumoniae.
3902 A; 2431 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-OCT-1996 (first entry)
Sorangium cellulosum soraphen gene cluster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: V52267 from: 1
                                                                         11503 GATATGAGGACGTTAAAAGGTTAC 11480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12528 GATATGAGGACGTTAAAAGGTTAC 12505
3 AspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                  V52267 standard; DNA; 12665 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 AspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID T06769 standard; DNA; 28598 BP.
AC T06769;
                                                                                                                                                                                                                                                                                                                                            23-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compositions and vaccines
Sequence 12665 BP; 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-37 x V52267/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.625
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:T06769
                                                                                                                                                   seq_name: N_Geneseq_36:V52267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.00
                                                                                                                                                                                                                                 seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
```

```
alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                                                                           Protecting plants against pathogens with genetically transformed biological control agant - which expresses all polypeptide(s) biological control agant - which expresses all polypeptide(s) and pyrolnitrin biosynthetic pathway as 1 biological control agant - which expresses all polypeptide(s) and pyrolnitrin biosynthetic pathway as 16; Column 104-128; 88pp; English.

This genomic DNA sequence encodes the Soraphen gene cluster. This sequence encodes two open reading frames (ORF's), the positions of which are not given in the specification. ORF's, the positions of which size and encodes 5 biosynthetic modules homologous to the erythromycin genes of Saccharopolyspora erythraea. Each module contrains character of CKR) and an acyl carrier protein (ACP domain. ORF2 is immediately adjacent to ORF1 and is thought to contain 3 modules. Soraphen is a type I polyketide synthase (PKS), which has antiblotic activity. Transgenic plants containing such antipathogenic genes like those actack by phytopathogens. Shoraphen cluster should have enhanced resistance to attack by phytopathogens.
                                                                                The state of the s
                                                                                                                                                                                                                                                                                                                                                                             4601 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAR-1998 (first entry)
Sorangium cellulosum soraphen gene cluster genomic DNA.
Soraphen; polyketide synthase; PKS; antipathogenic; antibiotic;
transgenic plant; phytopathogen; resistance; ss.
Sorangium cellulosum.
Antipathogenic substance; soraphen; phenylpyrrole; antibiotic; fungicide; pesticide; myxobacterium; ss. Sorangium cellulosum.
W095333818-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 28598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lam ST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 10 Gaps: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , Hill DS,
Uknes SJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to reverse of: T06769 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3978 AGGGTCGATGCCCGCACGCTCGAAGGCTTC 3949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hammer PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beck JJ, Gaffney TD, Hammer PE.
Ligon JM, Ryals JA, Schupp T,
WPI; 97-447901/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
ID T89956 standard; DNA; 28958 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-653-294-37 x T06769/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-SEP-1997.
01-JUN-1995; 457342.
20-JUL-1990; US-570184.
02-JUL-1992; US-908284.
31-AUG-1992; US-937648.
08-JUN-1994; US-258261.
(CIBA.) CIBA. GEIGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.00
4.111
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: N_Geneseq_36:T89956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JS5662898-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block
```

```
927. .19874
/*tag= b
/product= SorA
/note= "gene product is highly homologous to
/note= product is highly homologous to
type I PKSs that are known to be involved
in the synthesis of polyketide compounds"
                                                                                                                                                                                                                                                                                                                11-MAY-1998 (first entry)
The soraphen biosynthesis gene cluster from Sorangium cellulosum.
The soraphen biosynthesis gene cluster from Sorangium cellulosum.
Polyketide synthase; PKS; biosynthesis; soraphen; SorR; SorB;
SorM; biosyntheric module; beta-kercacyisynthase; acyltransferase;
ketoreductase; beta-ketone processing domain; cytostatic agent;
antimicrobial agent; phytopathogenic fungl; transgenic plant;
Sorangium cellulosum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
383. 760
/*tag= a
/product= SorR
/note= "gene product highly homologous to the reductase domains of type I PKSs such as eryA from Saccharopolyspora erythraea"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "gene product is highly homologous
type I PKS genes"
19870. .24556
                                                                                                                           from: 1 to: 28958
Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= d //note= "module 2 of SOTA" | 13455. 19616 | .*tag= e //note= "module 3 of SOTA" | 19871. .46318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "module 1 of SorB" .30820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SorB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SorB
                                                                                                                                                         /noté= "module 4 of S
40190. .46318
/*tag= 1
/note= "module 5 of S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /_rag= c
/note= "module 1 of
'203, .12884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "module 2 of 10881. .35446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   oŧ
                                                                                                                          Align seg 1/1 to reverse of: T89956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "module 3
                                                                                                                                                                                                                                                                  seq_documentation_block:
ID V05287 standard; DNA; 49377 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= g
/product= SorB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .. .46318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .40114
                                                                       alignment_block:
US-08-653-294-37 x T89956/rev
                     4.111
                                                                                                                                                                                                                              seq_name: N_Geneseq_36:V05287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
24638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-
35528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19871
   Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
```

```
P-PSDB; W93408
                                                                                                                                                      contamination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contamination
                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seguence
                                                                                                                                                                        Sequence
 88888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence contains a cluster of genes that encode polyketide synthases (PKSs) that are involved in the synthasis of soraphens in sorangham cellulosum. The proteins encoded by the present sequence are Sorangium cellulosum. The proteins encoded by the present sequence are Soran, Sorah, SorB and SorM. SorA and SorB contain biosynthetic modules which contain a beta-ketoacylsynthase, an acyltransferase, a ketoreductase and an acyl carrier protein domain, as well as beta-ketone processing domains. S. cellulosum soraphens are useful as a cytostatic and antimicrobial agent active against phytopathogenic fungi. Soraphen-producing transgenic plants or biological control agents can also be produced, which may reduce crop losses and nutritional deprivation for local populations in many parts of the world sequence 49377 BP; 19522 C; 14477 G; 8131 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated swine hepatitis E virus - used to develop products for the diagnosis, prevention and treatment of hepatitis E virus infection in mammals, particularly humans Example 1; Fig 6A-C; 70pp; English.

This invention describes a swine hepatitis E virus (HEV) and its natural mutants which are capable of cross-reacting with antibodies reactive with a human HEV strain or natural mutants. The HEV and the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Swine HEV ORF 1 DNA.
Swine hepatitis E virus; HEV; cross-reaction; antibody; human; therapy; vaccine; immunise; infection; detection; diagnosis; prevention; ss.
      foot...
/Product = SorM
/Product = SorM
/note= "gene product is homologous to the methyltransferase from Streptomyces methyltransferase from Streptomyces hygroscopicus that is involved in the synthesis of the polyketide rappamicin"
                                                                                                                                                                                                                                             DNA encoding Sorangium cellulosum polypeptide(s) - used for, e.g. blosynthesis of soraphen useful as antimicrobial agent against phytopathogenic fungi clusi 2: Columns 47-90; 64pp; English.
                                                                                                                                                                                                (NOVS ) NOVARTIS FINANCE CORP.

Beck JJ, Hill DS, Ligon JM, Neff S, Ryals JA, Schupp T;
WPI; 98-158369/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 49377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.00 Length: 10
4.111 Gaps: 0
90.000 Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: V05287 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20281 AGGGTCGATGCCCGCACGCTCGAAGGCTTC 20252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-JAN-1999: U14665. 18-JUL-1999: U14665. 18-JUL-1997: US-053069. (USH) US DEPT HEALTH & HUMAN SERVICES. Emerson SU, Meng X, Purcell RH; P-PSDB: W93408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID X23031 standard; DNA; 5127 BP.
.47891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          x23031;
11-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-37 x V05287/rev
                                                                                                     US5716849-A.
10-FEB-1998.
14-DEC-1996; 764233.
24-AUG-1993; WO-U07954.
08-UUN-1994; US-258261.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: N_Geneseq_36:X23031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hepatitis E virus. WO9904029-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores
```

```
The fight of the first than the first firs
can be used in vaccines for immunising against HEV infection. The swine HEV can be used in humans to prevent possible infection by human HEV. The swine HEV can also be used as a therapeutic treatment for infection by other strains of HEV. The swine HEV can also be used for the production of antibodies which can be used in therapy, detection and diagnosis. The products can also be used for determining the susceptibility of cells or organs to infection with swine HEV. The swine HEV is particularly useful for the development of agents for the prevention, treatment and detection of human HEV because it is not a human virus and thus can be handled both experimentally and clinically without fear of severe infection and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-JUN-1999 (first entry)
Swine HEV ORF I genomic DNA.
Swine hepatilis E virus; HEV; cross-reaction; antibody; human; therapy;
vaccine; immunise; infection; detection; diagnosis; prevention; ss.
Hepatilis E virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1892 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1328 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1880 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1383 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 0
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2126 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1480 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1999; U14665, 17-JUL-1998; U14665, 18-JUL-1999; U14665, (USSH) VS DEPT HEALTH & HUMAN SERVICES. Emerson SU, Meng X, Purcell RH; WPI; 99-132270/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1527 CGGGTCGACCTCAGAACCCTCATAGGC 1501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgValAspLeuArgThrLeuArgGly 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: X23031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1309 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   936 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-37 x X23031/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality: 36.00
Ratio: 4.500
Percent Similarity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.00
4.500
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: N_Geneseq_36:X23032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5127 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7207 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
```

```
Talministry Tage 22-24; 36pp; English.

The antigenic polypeptide encoded by this sequence, its fragments and variants can be used in a vaccine to protect against infection by a cestode parasite, particularly in ruminants. The nucleic acids (See also T17934) can be used to produce recombinant viral vaccines. The DNA (preferably this DNA sequence) can also be labelled and used as a probe to identify nucleic acids encoding a protective antigen of an Echinococcus or Taeniid parasite other than Taenia ovis. Sequence 360 BP; 98 A; 99 C; 86 G; 77 T;
                                                                                                         Taenia ovis antigenic polypeptide coding sequence.
Taenia ovis; antigen; vaccine; infection; cestode; parasite; probe;
viral vaccine; Echinoccus; Taeniid parasite; ss.
Taenia ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-1995 (first entry)
T. ovis vaccine candidate antigen.
T. ovis vaccine candidate antigen.
T. ovis vaccine; protective antigen; tapeworm; glutathione-S-transferase; fusion protein; Escherichia coli; pGEX-2T; ss.
Taenia ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lawrence SB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Taenia ovis antigenic polypeptide - used to develop vaccines protect against infection by a cestode parasite, partic. in ruminants.
                                                                                                                                                                                                                                                                                                                                                                                              Lawrence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.375 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 87.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 360
                                                                                                                                                                                                                                                                                                  31-JAN-1996.
07-ARR-1994; 002410.
07-ARR-1993; NZ-237361.
PITMAN MORE NZ LTD.
Dempster RP, Gauci C, Harrison GBL, Heath DD,
Lightowlers MW, Richard MD, Robinson CM;
PP-PSDB; R92832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-0CT-1994.
07-APR-1994, NZ0029.
07-APR-1999, NZ-247361.
(NZAP-1993) NZ-247361.
(NZAP-1998) NZ-247361.
(PITM ) PITMAN MOORE NZ LTD.
(PITM ) PITMAN MOORE NZ LTD.
Dempster RP, Gauci C, Harrison GBL, Heath DD,
Lightcowlers MW, Rickard MD, Robinson CM;
WPI; 94-333117/41.
                                                                                                                                                                                                                                        /*tag= a /product= Antigenic polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
10. .372
/*tag= a
                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to reverse of: T17935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 AGACTGGACTTGCGAACACTGAGA 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID Q72739 standard; cDNA; 600 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ArgValAspLeuArgThrLeuArg
                      seq_documentation_block:
ID T17935 standard; cDNA; 360
                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x T17935/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:Q72739
                                                                                                                                                                                                                  .360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
                                                                                  16-AUG-1996
                                                                                                                                                                                                                                                                                ZA9402410-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9422913-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1

        seq_documentation_block:

        Continuation (8 of 10) of X20248 from base 700001 (Borrella burgdorferi polynucleotide statements)

        WP Sequence split into 10 fragments LOCUS X20248 Accession X20248

        WP Fragment Name Begin Lincol
        End

        WP X20248_01
        100001

        WP X20248_02
        200001

        WP X20248_03
        300001

        WP X20248_04
        400001

        WP X20248_04
        400001

        WP X20248_05
        500001

        WP X20248_05
        500001

        WP X20248_05
        500001

        WP X20248_05
        500001

        WP X20248_05
        600001

        WP X20248_05
        800001

        WP X20248_07
        900001

        WP X20248_08
        800001

        WP X20248_09
        900001

                                                                                                                                                                                                                                        hase 600001 (Borrelia burgdorferi polynucleotide LOCUS X20248 Accession X20248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 110000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0 Gaps: 0 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: X20248_06 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from: 1
                                          to reverse of: X23032 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ArgValAspLeuArgThrLeuArgGlyTyr 10
|||:::||||::
1283 AGAATTGACATAGGAACTCTTGAGGGTTAT 1254
                                                                                                                                                                                                                                                                                                    1110000
210000
310000
510000
610000
610000
810000
910000
                                                                                                             1536 CGGGTCGACCTCAGAACCCTCATAGGC 1510
                                                                                                                                                                                                                               Continuation (7 of 10) of x20248 from bas WP Sequence split into 10 fragments LOCU WP Fragment Name Begin End NP X20248_00 100001 21000 WP X20248_02 200001 31000 WP X20248_03 300001 41000 WP X20248_04 4000001 81000 WP X20248_06 600001 71000 WP X20248_06 600001 71000 WP X20248_06 600001 71000 WP X20248_08 8000001 910000 WP X20248_08 8000001 910000 WP X20248_08 8000001 910000 WP X20248_09 900001 910001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: X20248_07
                                                                                    1 ArgValAspLeuArgThrLeuArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-37 x X20248_06/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-37 x x20248_07/rev
                                                                                                                                                                         seq_name: N_Geneseq_36:x20248_06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: N_Geneseq_36:x20248_07
US-08-653-294-37 x X23032/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.00
4.000
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:T17935
                                                                                                                                                                                                                    seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                          Align seg 1/1
```

```
New protective antigen from Taenia ovis - and related DNA vectors, transformed cells and antibodies, useful in vaccines, also for detecting homologous genes and proteins Disclosure; page 22-23; 37pp; English.

A T. ovis oncosphere lambda gill cDNA library was screened with rabbit antibodies raised against a 16 kDa protective antigen of T. ovis. The insert from a selected clone was subcloned into vector pGEX-2T and expressed as a glutathione-S-transferase fusion protein in Escherichia coli JMIOI. The DNA and predicted amino acid sequences of the T. ovis portion of the fusion protein were
                                                                                                                                                                                                                                  determined.
  P-PSDB; R62045.
```

alignment\_scores:

Quality: 35.00 Length: 8
Ratio: 4.375 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 87.500 alignment\_block: US-08-653-294-37 x Q72739/rev

132 T;

153 C; 121 G;

194 A;

Align seg 1/1 to reverse of: Q72739 from: 1 to: 600

THIS PAGE BLANK (USPTO)

NEE

```
Soares
Sugano
Sugano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.351
/organism="Rattus sp."
/organism="Rattus sp."
/db_xref="AtTCC (inhost):2004068"
/db_xref="AtTCC (inhost):2004068"
/clone="RpNaU72"
/clone="Tab="Rat PC-12 cells, NGF-treated (9 days)"
/clone="Tab="Tab"
/clone="Tab"
/clon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research 9712, Medical Center Drive, Rockville, MD 20850, USA 9712, Medical Center Drive, Rockville, MD 20850, USA Fax: (301)-838-0208
Email: nhlee@tigr.org
Exail: nhlee@tigr.org
Exail: nhlee@tigr.org
(tdb.nfo@tugr.org) TC (Tentative Consensus) numbers represent assemblies of ESTs.
   AA197564 mu22d05.rl
AI529689 ui81c04.yl
AI047292 ud64e05.yl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus sp.

Rattus sp.

Eukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 351)

Liee, N. H., Weinstock, K. G., Kirkness, E. F., Earle-Hughes, J. A.,

Fuldner, R. A., Marmaras, S., Glodek, A., Gocayne, J. D., Adams, M. D.,

Kerlavage, A. R., Fraser, C. M. and Venter, J. C.

Comparative expressed-sequence-tag analysis of differential gene
expression profiles in PC-12 cells before and after nerve growth
                                                                                                                                                                                                                                                       H35352 351 bp mRNA EST 02-APR-1998 EST109782 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA clone RPNAU72 similar to MHC class I, mRNA sequence. H35352 GI:980769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-APR-1997
5' end similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On May 8, 1995 this sequence version replaced g1:799766.
Other_ESTs: TC508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 92, 8303-8307 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS AA376928 113 bp mRNA EST
DEFINITION EST89412 Small intestine I Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 100.000
   727
754
816
   10.12
10.56
11.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: H35352 from: 1 to: 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
152.37
152.03
151.31
44.00
44.00
44.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 5.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_estl3:AA376928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-08-653-294-37 x H35352
                                                                                                                                                                                                                                   seg_documentation_block:
                                                                                                                                                       seg_name: gb_est4:H35352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95396786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84
   gb_est11:AA197564
gb_est28:A1529689
gb_est22:A1047292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA376928 EST89412 Small intesti

AA377133 EST89665 Small intesti

AA377133 EST89666 Small intesti

AA377133 EST89666 Small intesti

AA31847 EST185704 Colon carcin

AA31847 EST185704 Colon carcin

AA31847 EST185704 Colon carcin

AA176192 zp24907.rl Stratagene

AI214149 ap30e06.xl Schiller as

AI214126 ap30e06.xl Schiller as

AI102538 EST211827 Normalized r

AA313054 EST18381 Pancreas tum

AA158411 ud24e07.rl Scares 2NbW

AA158411 ud24e07.rl Scares 2NbW

AA14053 zo18911.rl Stratagene

AI666560 mul4008.rl Scares 2NbW

AA144053 zo18911.rl Stratagene

AI666560 mul4008.rl Scares 2NbW

AA764120 vv45b03.rl Scares 2NbW

AA764120 vv45b03.rl Scares 2NbW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA122653 zo21a05.rl Soares infant
AA122653 zo21a05.rl Stratagene
AA1916043 uj61f12.yl Sugano mous
AA199357 mul4h06.rl Soares ZNbM
AA709185 vv82e04.rl Stratagene
AA305941 EST176934 Jurkat T-cel
AA3175455 ms87h04.rl Stratagene
AA810833 vx46d06.rl Stratagene
AA017870 mh47h06.rl Stratagene
H23377 ym57e02.rl Soares mous
R59764 yh07c05.rl Soares infant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA02888 mh90604.r1 Soares mous AA396998 mx86e07.r1 Soares mous AA396998 mx86e07.r1 Soares mous AA386534 ab37606.y1 Stratagene A1365653 ac90601.x1 Schiller me AW012806 uc03a02.y1 Sugano mous AA640923 mc81b07.s1 NCI_CGAP_AA AA886072 uc72f11.y1 Sugano mous AA548636 nj38d02.s1 NCI_CGAP_AA A116479 ud74c02.y1 Sugano mous A1286941 u179a11.y1 Sugano mous A1785805 u178902.y1 Sugano mous A1785805 u178902.y1 Sugano mous A1785805 u178902.y1 Sugano mous
                                                                                                                                                                                                                                                                                                   -MODEL-frame+p2n.model -DEV-xlp
-Q=/cgnl_1/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.2
-Q=-cgnl_1/USPTO_spool/US08653294/runat_04000 -GAPEXT=4.000
-MINAAXCH=0.100 -LOOPCL=0.000 -LOOPCT=0.000 -GAPEXT=4.000
-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LISP=45 -DOCALIGN=200 -THR_SCORE=PCT -ALIGN=15 -MODE=LOCAL
-USP=45 -DOCALIGN=200 -THR_SCORE=PCT -ALIGN=15 -MODE=LOCAL
-UCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11113
3311113
3311113
331113
33113
33113
33113
33113
33113
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
3313
33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EScore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2850076
1185:08
1185:08
1195:09
1166:05
1166:05
1166:05
1166:05
1166:05
1167:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:09
1177:0
   EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query: US-08-653-294-37
Query length: 10
Database: EST:*
Database sequences: 4538634
Database length: 1887811982
Search time (sec): 7600.090000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      551.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
64.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              orig
   OM of: US-08-653-294-37 to:
                                                                               Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search information block:
                                                                                                                                                                                                                                                                   Command line parameters:
                                                                           Date: Feb 8, 2000 6:23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est12:AA313847
gb_est11:AA243092
gb_est23:A1750810
gb_est24:A1716192
gb_est24:A1214149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est11:AA199357
gb_est12:AA790185
gb_est12:AA305941
gb_est10:AA175455
gb_est20:AA880833
gb_est8:AA017870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est8:AA028838
gb_est14:AA396998
gb_est34:AI787144
gb_est15:AA488534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est13:AA376928
gb_est13:AA377133
gb_est26:AA900799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est26:AI102538
gb_est12:AA313054
gb_est23:AI158411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est10:AA134053
gb_est30:A1666560
gb_est19:AA764120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est10:AA132653
gb_est25:AI316043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est37:AW012806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est17:AA604923
gb_est21:AA986072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est16:AA548636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est26:AI365653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est23:AI116479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est34:AI785805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est25:AI286941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_est36:AI876777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est9:AA125323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
gb_est4:H35352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est9:C17443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_est2:R12066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est4:H23377
gb_est3:R59764
```

ORGANISM

REFERENCE AUTHORS

ACCESSION

VERSION KEYWORDS SOURCE

```
CE 1 (bases 1 to 128)

Radans, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Kelley, J.M., Kelley, J.C., Lui, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., L.J.Y.,
Badnarik, D.P., Cool, L., Kerzeck, Fischer, C., Hadson, P., Kim, A.K.,
Cool, D., Feng, D.-F., Ferrie, A., Coleman, T.A., Collins, E.J.,
Baymond, L., Wei, Y.F., Wingjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wingjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wingjun, J., Li, H., Meissner, P.S.,
Dillion, P.J., Fannon, M.R., Rosen, C.A., Haselline, W.A., Flelds, C.,
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of CDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
9712 Medical Center Drive, Rockville, MD 20850 USA
9712 Medical Center Drive, Rockville, MD 20850 USA
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression
For clone availability, additional sequence and expression
Information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                AA377<u>1</u>33 128 bp mRNA EST 21-APR-1997
EST89666 Small intestine I Homo sapiens CDNA 5' end similar to
similar to major histocompatibility complex, class I, E
                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12140200
On Sep 12, 1996 this sequence version replaced gi:1326664
Other_ESTs: THC117633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="ATCC (inhost):181551"
/db_xref="taxon:9606"
/clone_lib="small intestine I"
/clone_stage="adult"
/note="Organ: small intestine; Vestite="1: EcoRI; Site_2: XhoI"
a 35 c 44 g 20 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgvalAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 CGAGTGAATCTGCGGACGCTGCGCGGCTAC
                                                                                                                                   (GB:M20022), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kerlavage, AR
                                                                                                                                                                              AA377133.1 GI:2029461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-37 x AA377133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AA377133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioinformatics
seq_documentation_block:
LOCUS AA377133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores;
                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                              ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
                                                                                                                                                                                                                                                    KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                              Eukaryota: Metazoa: Chordata: Craniata; Vertebrata; Mammalla; Eukaryota: Metazoa: Catarrhini; Hominidae: Homo.

Eutheria: Primates; Catarrhini; Hominidae: Homo.

Adams.M.D., Kerlavage.A.R., Fleischmann.R.D., Fuldner.R.A.,

Bult.C.J., Lee.N.H., Kirkness, E.F., Weinstock, K.G., Man-Wal.G.,

Clayton.R.A., Cline.T.R., Cotton.M.D., Earle-Hughes, J.., Fine.L.D.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,

Glodek, A., Ghehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, F.S., Jr.,

Kelley, J.M., Kelley, J.C., Liu, L.I., Marmaros, S.M., Merrick, J.M.,

Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,

Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,

Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,

Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,

He, W.W., Hu, J.S., Greene, J.M., Gruber, C., Hastings, G.A.,

Kozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,

Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,

Fraser, C.M. and Venter, J.C.

Initial assessment of human gene diversity and expression patterns

based upon 83 million nucleotides of cDNA sequence

L. Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: arkerlavetigr.org
For clone availability, additional sequence and expression
for clone availability, additional sequence and expression
for clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="ATCC (inhost):181328"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="axon:9606"
/dov_stage="adult"
/dov_stage="adult"
/note="Organ: small intestine; Vector: pBluescript SK-;
Site_1: EcoRi; Site_2: XhoI"
a 33 c 35 g 18 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Sep 12, 1996 this sequence version replaced gi:1318560
   similar to major histocompatibility complex, class I, (GB:M20022), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kerlavage, AR
                                                                                                         AA376928.1 GI:2029245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other_ESTs: THC117633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-37 x AA376928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: AA376928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est13:AA377133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bioinformatics
                                                                                                                                                                                                               Homo sapiens
                                                                            AA376928
                                                                                                                                                                                  human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
```

JOURNAL MEDLINE

COMMENT

TITLE

Vector: pBluescript SK-;

81

Align seg 1/1

BASE COUNT

FEATURES

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL MEDLINE

```
seq_documentation_block: 377 bp mRNA EST 19-APR-1997
LOCUS AA313847 377 bp mRNA EST 19-APR-1997
DEFINITION EST185704 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5'
end similar to similar to major histocompatibility complex, class
ACCESSION AA313847
C17443 356 bp mRNA EST 02-OCT-1996
C17443 Human placenta cDNA (TFujiwara) Homo sapiens cDNA clone
GEN-547C05 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GEN-547C05"
/clone=llb="Human placenta cDNA (TFujiwara)"
/tissue_type="placenta"
/ 116 c 115 g 64 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1 to: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              271 CGAGTGAACCTGCGGACGCTGCGCGCGCTAC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA313847.1 GI:1966176
                                                                                    C17443
C17443.1 GI:1579046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: C17443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est12:AA313847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-37 x C17443
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                         human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source
                                                                                                                                                                    SOURCE
  LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /vsystain="sprague-Dawley"
/strain="sprague-Dawley"
/db_xxef="taxon:1016"
/clone="U1-R-E0"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.
Fatina Bonaldo, Ph.D. Clone distribution: clones will be available
through Research Genetics
                                                                            seq_documentation_block:
LOCUS AA900799 338 bp mRNA EST 05-FEB-1999
DEFINITION UI-R-E0-dn-h-09-0-UI.s1 UI-R-E0 Rattus norvegicus CDNA clone
UI-R-E0-dn-h-09-0-UI 3' similar to gill263201|gb|U38972|RW138972
Rattus norvegicus MHC class I RTI.Au heavy chain precursor, mRNA,
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodenita; Sciurognathi; Muridae; Murinae; Rattus. I (bases 1 to 318)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Apr 7, 1998 this sequence version replaced gi:3036153. Contact: Scares, MB Program for Rat Gene Discovery and Mapping University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 90.000

    .338
    /organism="Rattus norvegicus"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 CGAGTGAACCTGAGGACCTGCGCGCGTAC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ArgvalAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                  complete cds, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   primer: M13 Forward
                                                                                                                                                                                                                                                                                AA900799.1 GI:4233294
                                                                                                                                                                                                                                                                                                                                           Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AA900799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-37 x AA900799
                       seq_name: gb_est26:AA900799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est9:C17443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seg_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                             EST.
```

source

FEATURES

BASE COUNT

ORIGIN

```
Martin,J., Moore,B., Schellenberg,R., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ammur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                  TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORIGIN
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W. W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wei, Y.F., Wingjun, J., Li, H., Melssner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wingjun, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

Fraser, C.M. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 20850 USA 1912 Medical Center Drive, Rockville, MD 20850 USA 1918 90956 Eax: 3018699058 Example 3018699423 Email: arkerlavetigr.org Email: arkerlavetigr.org Email: arkerlavetigr.org information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:

LOCUS AA243092 420 bp mRNA

DEFINITION 2T25b01.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens

CDNA clone IMAGE:664393 5' similar to gb:MZ0022 HLA CLASS I

HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 420)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note-"organ: colon; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="ATCC (inhost):110041"
/db_xref="taxon:9606"
/clone_lib="Colon carcinoma (HCC) cell line II"
/tissue_type="colon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 5, 1995 this sequence version replaced g1:798157.
Other_Ests: THC169518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="KM12C"
/cell_line="KM12C(HCC)-parental human colon
carcinoma;Dukes B2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        . 69 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AA313847 from: 1 to: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            291 CGAGTGAACCTGCGGACGCTGCGCGCTAC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA243092
AA243092.1 GI:1873888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,118 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-37 x AA313847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est11:AA243092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                               2140200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ћитап.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

\*

```
/db_xref="footbased.gengers" / db_xref="footbased.gengers" / db_xref="footbased.gengers" / db_xref="footbased.gengers" / delastates | d
                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fig. 1 set@astson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1647 Std Error: 0.00
Seq primer: -28m13 rev1 ET from Amersham
High quality. sequence stop: 356.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AI750<u>010</u> 435 bp mRNA EST 22-JUN-1999 cn05902.xl Normal Human Trabecular Bone Cells Homo sapiens cDNA close NHTBC_cn05902 random, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Euraryotes, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
Jia,L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.T., Yang,L.M.,
Robey,P.G., Hotobkiss,R.N. and Francomano,C.A.
SGAP: The Skeletal Genome Anatomy Project
Unpublished (1997)
On Feb 18, 1999 this sequence version replaced gi:4296314.
Theising, B., White, Y., Wylle, T., Waterston, R. and Wilson WashU-NCI human EST Project Unpublished (1997)
On Dec 3, 1996 this sequence version replaced g1:975987.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medical Genetics Branch
National Human Genome Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .420
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284 CGAGTGAACCTGCGGACGCTGCGCGCTAC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AI750810.1 GI:5129074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-08-653-294-37 x AA243092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AA243092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est32:AI750810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
```

```
84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human .
                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 448)

Hillier, L. Lennon, G. Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hulthan, M., Kucaba, T., Lacy, M., Le, M., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            zp24g07.r1 Stratagehe neuroepithelium (#937231) Homo sapiens cDNA
clone IMAGE:610428 5' similar to gb:M20022 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Seq primer: -28M13 revo from Amersham
                                                                                                                                                                                                                                                                                                                                                                         /note-"Organ: Hip; Vector: pBluescript; Site_1: EcoRI"
138 c 144 g 77 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-DEC-1996
                                                                                        Health
    MD 20892-1267, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Sep 12, 1996 this sequence version replaced gi:1395431
Contact: Wilson RK
                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NHTBC_cn05902"
/clone_lib="Normal Human Trabecular Bone Cells"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63108
                                                             Email: librin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of
Intramural Sequencing Center (NISC).
Plate: 05 roguencing Conter (NISC).
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                      /tissue_type="Bone"
/cell_type="Trabecular Bone Cells"
/lab_host="SURE"
10/10C101, 9000 Rockville Pike, Bethesda,
Tel: 301-402-4877
Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAİ76192
AA176192.1 GI:1757314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        448 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: AI750810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-08-653-294-37 x AI750810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est10:AA176192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AA176192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sednence.
                                                                                                                                                                                                                                                                                                                                                                                                          92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                         FEATURES
```

```
'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ap30e06.x1 Schiller astronome Homo sapiens cDNA clone
IMAGE:1956698 3' similar to gb:M20022 HLA CLASS I
HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
High quality sequence stop: 339.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jost, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryotz, Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Metazoa; Catarrhini; Hominidae; Homo.

1 (bases 1 to 469)

2 (bases 1 to 469)

2 (bases 1 to 469)

3 (bases 1 to 469)

4 (bases 1 to 469)

4 (bases 1 to 469)

4 (bases 1 to 469)

5 (bases 1 to 469)

7 (bases 1 to 469)

7 (bases 1 to 469)

8 (bases 1 to 469)

9 (bases 1 to 469)

9 (bases 1 to 469)

9 (bases 1 to 469)

10 (bases 1 to 469)

11 (bases 1 to 469)

12 (bases 1 to 469)

13 (bases 1 to 469)

14 (bases 1 to 469)

15 (bases 1 to 469)

16 (bases 1 to 469)

17 (bases 1 to 469)

18 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1956898"
/clone_lib="Schiller astrocytoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .469
/organism="Homo sapiens"
/db_xref="taxon:9606"
High quality sequence stop: 110.
Location/Qualifiers
1. .448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence.
AI214149
AI214149.1 GI:3777750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AA176192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-37 x AA176192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_est24:AI214149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AI214149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
```

```
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                               /note="Organ: brain; Vector: pBluescript SK- (Stratagene); Ste_1: ECORI; Site_2: KhOi; Double-stranded cDNA was prepared from human astrocytoma using primer.
5'-GAGGAGAGAGAGAGAAACTAGTCTGAGT(18)-3'. An ECORI adaptor was used on the 5' end of the CDNA as follows: 5'-AATTGGGAGGAG.' The library was size-selected and went through one round of amplification. Average insert size is 1,7 kb, with a range from 0.4-12 kb. Tumor identification by consensus pathology. This library was University)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1214126 501 bp mRNA EST 21-OCT-1998 app30c6c.x1 Schiller astrocytoma Homo saplens cDNA clone IMAGE:1956874 3' similar to qb:M20022 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, E E*0101/E*0102 ALPHA (HUMAN);, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 501)

11 (Larses 2 to 501)

11 (Larses 2 to 501)

11 (Larses 3 to 501)

11 (Larses 3 to 501)

11 (Larses 4 to 501)

12 (Larses 4 to 501)

13 (Larses 5 to 501)

14 (Larses 5 to 501)

15 (Larses 5 to 501)

16 (Larses 5 to 501)

17 (Larses 5 to 501)

18 (Larses 5 to 501)

1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco
High quality sequence stop: 295.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
On Jan 17, 1998 this sequence version replaced gi:1900329.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism-"Homo sapiens"
/db_xref-"taxon:9606"
/clone-libacs:1956874"
/sclone-libacschiller astrocytoma"
/sex-"male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 t
/tissue_type="astrocytoma"
/dev_stage="44 years"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199 CGAGTGAACCTGCGGACGCTGCGCGGCTAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI214126
AI214126.1 GI:3777727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-37 x AI214149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AI214149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est24:AI214126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
```

```
AI102538 648 bp mRNA EST 08-JAN-1999
EST211827 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone
REMBO96 3' end, mRNA sequence.
                                                                                                                                    /note="Organ: brain; Vector: pBluescript SK- (Stratagene); Site_1: ECORI; Site_2: KhOI; Double-stranded cDNA was prepared from human astrocytoma using primer 5.-GAGNGAGAGAGAGAGAACTRGTCGAGT(AB)-3. An ECORI adaptor was used on the 5' end of the cDNA as follows: 5.-AATTCGGCAGGAG." The library was size-selected and went through one round of amplification. Average insert size is 1.7 kb, with a range from 0.4-12 kb. Tumor dentification by consensus pathology. This library was University).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
Rattus sp.
Rattus sp.
Evatrus s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT7T3Pac; Site_1: EcoRI; Site_2: NotI"
189 c 228 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
On Aug 21, 1998 this sequence version replaced gi:3704683.
Other_ESTs: TC51871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 90.000
/tissue_type="astrocytoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     199 CGAGTGAACCTGCGGACGCTGCGCGGCTAC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="REMB096"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                            /dev_stage="44 years"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AI102538
AI102538.1 GI:4134091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@ttgr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: M13-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 46.00
Ratio: 4.600
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AI214126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-37 x AI214126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Lee, NH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est26:AI102538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene Index
```

Length:

```
Euchards: Manualia;
Euchards: Metazoa: Chordata; Craniata; Vertebrata: Mammalia;
Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
Eutheria: Rodentia: Sciurognathi; Muridae; Murinae; Mus.
E 1 (Dases 1 to 344)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Gefsel,S., Kucaba,T., Lacy,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashD-HHMI Mouse EST Project

Unpublished (1996)

On Jan 19, 1998 this sequence version replaced gi:2284822.

Contact: Marra M/Mouse EST Project
WashD-HHMI Mouse EST Project
Fax: 314 286 1800

Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMMGE Consortium (info@lmage.linl.gov) for further information. MGI:920168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI158411 344 bp mRNA EST 30-SEP-1998 ud24e07.rl Soares 2NbMT Mus musculus cDNA clone IMAGE:1446852 5' similar to 9b:J00400 Mouse MHC class I H2-K gene (MOUSE);, mRNA
                                                                                                                         Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: -28ml3 rev2 ET from Amersham Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Soares 2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 344
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:1446852"
                                                                                                                                                                                                                                                                                                                    1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                     31 CGAGTGGACCTGGGGACCCTGCGCGGCTAC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AII58411
AI158411.1 GI:3686880
                                                                                                                    4.889
                                                                                                                                                                                                                                                                  Align seg 1/1 to: AA313054
                                                                                                                                                                                             alignment_block:
US-08-653-294-37 x AA313054
                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_est23:A1158411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence.
                                                                                                                         Ratio
                                                                                                                                         Percent Similarity
                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E 1 (Dases 1 to 245)
S Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Rirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S.,
Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
Moreno-Palanques, R.F., McDonald, L.A., Mquyen, D.T., Pelligrino, S.M.,
Phillips, C. A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Lik, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AA313054
DEFINITION EST183851 Pancreas tumor, subtracted (abundant clones) Homo saplens
CDNA 5' end similar to similar to major histocompatibility complex,
class 1, A3101, mRNA sequence.
ACCESSION AA313054
VERSION AA313054.1 GI:1965382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: arkerlar@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.html)
Seq primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="ATCC (1nhost):172202"
/db_xref="taxon:9666"
/clone_lib="Pancreas tumor, subtracted (abundant clones)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On May 8, 1995 this sequence version replaced gi:801299.
Other_ESTs: THC183330
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
               Gaps: 0 Gaps: 0 Percent Identity: 90.000
                                                                                                                                                                                             to: 648
                                                                                                                                                                                                                                                                     248 CGAGTGAACCTGAGGACCTGCGCGCGTAC 277
                                                                                                                                                                                                                                           1 ArgValAspLeuArgThrLeuArgGlyTyr 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                             from: 1
                                                                                                                                                                                             to: AI102538
                                            Ratio: 4.600
Percent Similarity: 100.000
                    46.00
                                                                                                                    alignment_block:
US-08-653-294-37 x AI102538
                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est12:AA313054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 3018699423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
alignment_scores:
                                                                                                                                                                                          Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
```

22

BASE COUNT

ď

54

BASE COUNT

```
AA125323 382 bp mRNA EST 18-FEB-1997 m080C08.17 SCARES 2NDMT MUS mUSCULUS CDNA CIONE INAGE:57534 5' similar to gb:x00492_cds1 HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-3 A*0301 ALPHA (HUMAN); gb:M69073 Mus musculus mRNA, complete cds (MOUSE);, mRNA sequence. AA125323.1 GI:1684491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 382)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gelsel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@lmage.llnl.gov) for further information.
MGI:350182
Seq primer: -28M13 rev2 from Amersham.
Locaton/Qualifiers
1. .382
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
The MashUrHMH Mouse EST Project
Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1282198.
Contact: Marra M/Mouse EST Project
WashUrHMH Mouse EST Project
WashIngton University School of MedicineP
H44 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
                                                                                                                                                                                                                                            to: 344
                                                                                  Length: 10
Gaps: 0
Percent Identity: 90.000
                                                                                                                                                                                                                                            Align seg 1/1 to reverse of: AII58411 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="IMAGE:575534"
/clone_lib="Soares 2NbMT"
/sex="male"
                                                                                                                                                                                                                                                                                      'tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="4 weeks"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain-"C57BL/6J
                                                                                                                                                                          alignment_block:
US-08-653-294-37 x All58411/rev
                                                                                     44.00
4.889
90.000
                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est9:AA125323
                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS AA125323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        house mouse
                                                                                                              Ratio:
Percent Similarity:
                                                                                       Ouality:
                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
ORIGIN
```

BASE COUNT 55 a 124 c 107 g 96 t ORIGIN

alignment\_scores:
Quality: 44.00
Ratio: 4.889
Percent Similarity: 90.000 Percent Identity: 90.000

alignment\_block: US-08-653-294-37 x AA125323/rev Align seg 1/1 to reverse of: AA125323 from: 1 to: 382

7

005385 buchnera ap 09xv35 caenorhabdi 09xv35 caenorhabdi 094274 streptomyce 09826 tilia kiusi 09218 arabidopsis 09x811 streptomyce 094013 caenorhabdi 092ap8 paenibacill 008781 gallus gall 042142 gallus gall 041313 solanum car 04733 schizosacch 09773 schizosacch 097731 sus scrofa P71966 mycobacteri

057883 pyrococcus 092b18 streptomyce 044214 anabaena sp 032477 pseudomonas 069350 rhodococcus

O9w661 pseudemys s O9w659 poephila gu P96676 bacillus su

```
STRAIN-CT3:

STRAIN-CT3:

STRAIN-CT3:

STRAIN-CT3:

STRAIN-CT3:

STRAIN-CT3:

SARAI W., HORIKAWA H., HAIKAWA Y., HINO Y.,

YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAMA A., NAGAI Y.,

SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,

FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,

AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrococcus horikoshii.
Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DAN Res. 5:55-76(1998).
EMBL; AP0000003; BAA1975-1; -
SEQUENCE 151 AA, 17160 MW; 11AACD59 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 37; DB 1; Length 151;
Pred. No. 4.8;
); Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-1998 (TrEMBLrel. 07, Created)
G-1998 (TrEMBLrel. 07, Last seq
N-1999 (TrEMBLrel. 09, Last ann
LONG HYPOTHETICAL FRXA PROTEIN.
                                                                                                                                                                                                                                 Q9Y7Q3
Q97931
P71966
Q51316
Q9W661
Q9W659
005385
Q9XV35
Q9X7V5
Q54274
Q98296
Q9ZT98
                                                                                                                                                                                                 Q41314
Q41313
                                                                                                                                                                                                                                                                                                                                                 P96676
057883
                                                                                                                                                                                                                                                                                                                                                                                                  044214
032477
069350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 75.5
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-JAN-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |||| ||||
96 RLLIELDER 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 RLLIRLDER 10
Q62157
Q62157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       058407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
058407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A PAC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      058407 pyrococcus
062157 mus musculu
033348 mycobacteri
055457 synechocyst
083484 treponema p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mycobacteri
caenorhabdi
homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chlorella v
caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 saccharomyc
bacillus an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amycolatops
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mycobacter;
mycobacter;
                                                                                                                                            (without alignments)
3.317 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            haemonchus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                           Search time 209.03 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9xj30 oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              016954
006421
061660
094942
0075872
P96419
                 4.5
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                              225878 seqs, 69334122 residues
                 GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                           8, 2000, 13:17:41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              summaries
                                                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q62157
Q55457
Q65457
Q833484
Q93330
Q4103
Q20152
Q9X058
Q9X058
Q02006
Q05006
Q05006
Q05032
                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              016954
006421
061660
094942
075872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          058407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sp_unclassified:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_human:*
sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_vertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sp_mhc:*
sp_organelle:*
sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_archea:*
sp_bacteria:*
sp_fungi:*
                                                                                                                                                                                       US-08-653-294-15
49
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Listing first 45
                                                                                                                                                                                                                                   1 YRLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 1000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPTREMBL_12:*
                                                                                                                           February
                                                                                                                                                                                                                                                                       BLOSUM62
                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB :
Maximum DB :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                       Sequence:
                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
```

151 AA

ö

Gaps

;

506 AA

```
1 YRLLIRLDE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-PCC6803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            083484
                                                                                                                                                                                                                                       055457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TP0471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ហ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                              LD DD T T T T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D T D 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g
   ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        õ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria: Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
COLE S.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An integrated map of the genome of the tubercle bacillus, Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.4%; Score 35; DB 11; Length 506; Best Local Similarity 77.8%; Pred. No. 40; Matches 7; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                           MURPHY L., HARRIS D.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
HYPOTHETICAL 10.2 KD PROTEIN.
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ZINC FINGER PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996)
EMBL: AL008883; CAA15528.1; -
Hypothetical protein.
SEQUENCE 87 AA: 10237 MW; 62B840DE CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               506 AA; 57882 MW; AEE397C3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding; Zinc-finger.
NON_TER 1 1 SEQUENCE 506 AA; 57882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 YRLLARLEE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 96181548.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRLLIRLDE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eprae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         033348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        033348
   SO DR RELEASE SO DR SO D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               음
```

```
STRAIN-PCC6803;
MEDLLINE, 97061201.
MEDLLINE, 97061201.
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
TABATA S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

EMBL; D64066; BAA10800.1; -.

Hypothetical protein.

SEQUENCE 132 AA; 15240 MW; 53B23658 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUGIURA M., TABATA S.,
"Sequence analysis of the genome of the unicellular cyanobacterium
"Sequence systis sp. strain PCC6803. I. Sequence features in the 1 Mb
region from map positions 64% to 92% of the genome.";
DNA Res. 2:153-166(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-PCC6803;
MEDLINE: 96127529.
KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE; 98332770.
FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN M., HICKEY E.K., CLAYTON R., KETCHUM K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 33; DB 2; Length 132; 66.7%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Treponema pallidum.
Bacteria, Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TIEMBLEB. 01, Created)
01-NOV-1996 (TIEMBLEB. 01, Last sequence update)
01-JAN-1999 (TIEMBLEB. 09, Last annotation update)
HYPOTHERICAL 15.2 FOR PROTEIN.
Synechocystis sp. (strain PCC 6803).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TIEMBLTE1. 08, Created)
01-NOV-1998 (TIEMBLTE1. 08, Last sequence update)
01-NOV-1998 (TIEMBLTE1. 08, Last annotation update)
HYPOTHETICAL 53.0 KD PROTEIN.
                                                                                                                                                                                                                                                                                      132 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           469 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || |:|||:
120 YRKLLRLDD 128
|||| |:|:
60 YRLLYRIDD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 YRLLIRLDE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
083484
1D 083484
AC 088
DJ 011
DD DJ 011
DD HY
GN TP
OC BA
CO BA
```

ö

ö

Gaps

ö

1; Indels

2; Mismatches

69.4%; Score 34; DB 2; Length 87; 66.7%; Pred. No. 11;

Query Match
Best Local Similarity 66.7
Matches 6; Conservative

```
MEDLINE: 97303241.
WAKASUGI T., NARGAI T., KAPOOR M., SUGITA M., ITO M., ITO S.,
WAKASUGI T., NARASHIMA K., TSUDZUKI T., SUZUKI Y., HAMADA A., OHTA T.,
INAMURA A., YOSHINAGA K., SUGIURA M.;
"Complete nucleotide sequence of the chloroplast genome from the green
alga chloralia unigatis: the existence of genes possibly involved in
chloroplast division.";
Proc. Natl. Acad. Sci. U.S.A. 94:5967-5972(1997).
EMBL; AB001684; BAA20659.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlorella vulgaris.
Chloroplast.
Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorellales;
                                                                                                                                                              STRAIN-DSM 5908;
MEDLINE: 97449857.
MEDLINE: 97449857.
MEDLINE: 97449857.
"Cloning and analysis of a peptide synthetase gene of the ballimycin producer Amycolatopsis mediterranei DSM5908 and development of a gene disruption/replacement system.";
J. Biotechnol. 56:115-128 (1997).
EMBL: X97860; CAA66454.1;
PROSITE: PSO0455; AMP_BINDING; 1.
PROSITE: PSO0455; AMP_BINDING; 1.
PRAM; PFO0501; AMP-Dinding; 1.
PFAM; PFO0509; DP-binding; 1.
                            Amycolatopsis mediterranei.
Bacteria: Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 32; DB 8; Length 52;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 33; DB 2; Length 132
Pred. No. 2.6e+02;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1324 1324
1324 AA; 142666 MW; 2C08588E CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74BE6B74 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-NOV-1998 (TrEMBLrel. 08, ORF52B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5985 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 70.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlorellaceae; Chlorella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0
Fra 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     969 YRVAGRLDER 978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : ||: ||||
17 FLLLVELDER 26
                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             020152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Y058
Q9Y058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
020152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09Y058
ID 09
AC 09
     SET THE PRESENCE OF THE PRESEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                              FRASER C.M., NORRIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
PRASER C.M., HORBIS S.J., WEINSTOCK G.M., WHITE O., SUTTON G.G.,
DODSON R., GWINN M., HICKEY E.K., CLAYTON R., FETCHUM K.A.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J.,
KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T.,
MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S.,
VENTER B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O.,
SODERGREN E., HARDHAM J.M., MCLEOD M.P., SALZBERG S., PETERSON J., KHALAK H., RICHARDSON D., HOWELL J.K., CHIDAMBARAM M., UTTERBACK T., MCDONALD L., ARTIACH P., BOWMAN C., COTTON M.D., FUJII C., GARLAND S. HARTCH B., HORST K., ROBERTS K., WATTHEY L., WEIDMAN J., SMITH H.O., VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                          'Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67.3%; Score 33; DB 10; Length 577; 60.0%; Pred. No. 1.2e+02; Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. NIPPONBARE;
TOZAWA Y., HASEGAWA H., TERAKAWA T., WAKASA K.;
TOZAWA Y., HASEGAWA H., TERAKAWA T., WAKASA K.;
TRICE CDNA encoding anthranilate synthase alpha subunit.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB022602. BAA82094.1; -.
SEQUENCE 577 AA; 63947 MW; 057FE09C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AE001223; AAC65460.1; -.
TIGR; TP0471; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       044103 PRELIMINARY; PRT; 1324 AA. 044103; 01-NOV-1996 (TEMBLrel. 01, Created) 01-NOV-1999 (TEMBLrel. 01, Last sequence update) 01-NOV-1999 (TEMBLrel. 12, Last annotation update) PEPTIDE-SYNTHETASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
ANTHRANILATE SYNTHASE ALPHA 1 SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ll protein.
469 AA; 52960 MW; F76800E7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 2;
Pred. No. 94;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                577 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.3%;
                                                                                                                                                                                                Science 281:375-388(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best Local Similarity 87,55
اجر 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
'-hnc 6; Conservē
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 || |:| |:|
81 YRCLVREDDR 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 YRLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 YTLLIRLD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRLLIRLD 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poaceae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical
                                                                                                                                                                      spirochete.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9XJ30,
```

φ

RESULT Q9XJ30

ò g ö

Gaps

ö

ö

Gaps

;; 0

7

RESULT 044103

ò g ID DI DI DE

```
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYSTEINE PROTEINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                             65.3%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 60.0 nes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 YRKLYRMDKR 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathway.
                                                                                                                                                                                                                                                                                                               NON_TER
CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q02895
Q02895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
Q02895
    DDE REPRESENT THE PROPERTY OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                       oţ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                            DEAN F.B., LIAN L., O'DONNELL M.; "CDNA cloning and gene mapping of human homologs for Schizosaccharomyces pombe rad17, rad1, and hus1 and cloning homologs from mouse, Caenorhabditis elegans, and Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                             65.3%; Score 32; DB 5; Length 267; 55.6%; Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 32; DB 4; Length 317;
Pred. No. 1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
BAUER C., WILLIAMS D.;
BAUER c., WILLIAMS D.;
"The sequence of Homo sapiens PAC clone DJ0669B10.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WATERSTON R.H.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL: AC004853; AAC64378.1; -. SEQUENCE 317 AA; 35293 MW; B32AE3AE CRC32;
  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-1999 (TrEMBLrel. 10, Created)
01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-WAY-1999 (TrEMBLrel. 10, Last annotation update)
WUGSC:H_DJ0669B10.1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                                                                           melanogaster.";
Genomics 54:424-436(1998).
EMBL: AF076843; AAC95525.1; -
SEQUENCE 267 AA; 29910 MW; A91CD2BF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            317 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65.3%;
87.5%;
01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 55.6
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 65.3
Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                              Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 99097342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                            RAD1-LIKE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||||||| |
47 LLIRLDSR 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WATERSTON R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                025032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
095006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            025032
ID 02
AC 02
DT 01
    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               요
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ŏ
```

```
"Cloning and sequence comparisons of four distinct cysteine proteases expressed by Remonorbus contortus adult worms.";
Mwol. Blochem. Parasitol. 51:209-218(1992).
EMBL; M80388; AAA29178.1;
HSSP; P07858; ICSB.
PFAM, PF00112; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE; 94019233.
SHIRAYAMA M., KAWAKAMI K., MATSUI Y., TANAKA K., TOH-E A.;
SHIRAYAMA a multicopy suppressor of mutants hyperactivated in the RAS-
CAMP pathway, encodes a novel HSP70 protein of Saccharomyces
Haemonchus contortus.
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Strongylida;
Trichostrongyloidea; Trichostrongylidae; Haemonchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 96009602.
WATANABE Y., IRIE K., MATSUMOTO K.;
"Yeast RLM1 encodes a serum response factor-like protein that may function downstream of the Mpk1 (Slt2) mitogen-activated protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE; 90078303.
DESHALES R.J., SCHEKMAN R.;
"SEG5 encodes a putative membrane protein required for protein translocation into the yeast endoplasmic reticulum.";
J. Cell Biol. 109:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                    MEDLINE; 92244291.
PRATT D., ARMES L.G., HAGEMAN R., REYNOLDS V., BOISVENUE R.J.,
COX G.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB 5; Length 341
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 89345597.
GAMPEL A., TZAGOLOFF A.;
"Homology of aspartyl- and lysyl-tRNA synthetases.";
proc. Natl. Acad. Sci. U.S.A. 86:6023-6027(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 341 CYSTEINE PROTEINASE.
341 AA; 38342 MW; 2520FB2D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last segu
01-NOV-1998 (TrEMBLrel. 08, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Biol. 15:5740-5749(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol. Gen. Genet. 240:323-332(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomycetaceae; Saccharomyces.
```

ö

,

```
RESULT
  SOWERTAN
                                                                                                                                                                                                                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
            A BUSSEY H., STORMS R.K., AHMED A., ALBERNANN K., ALLEN E., ANSORGE W., ARAUJO R., APARTOIO A., BARRELL B., BACCCK K., BENES V., BOSTEIN D., BOWMAN S., BRUCKNER M., CARPENTER J., CHERRY J.W., CHUNG E., CHUCKHER C., COSTER F., DAVIS R.W., DIETRICH F.S., CHURCHER C., COSTER F., DAVIS R.W., DIETRICH F.S., DELIUS H., DIPAOLO T., DUBOIS E., DUSTERHOFT A., DUNCAN M., FLOETH M., FRIEZE V., GOFFEAN A., HYMAN R., HEBLING U., ALEUMANN K., HILBERT H., HILLIER K., HOWICKE-SMITH S., HYMAN R., JOHNSTON M., KALMAN S., KLEINE K., KOMP C., KURDI O., LASHKARI D., LASHKARI D., MULLER H.W., MIRTIPATI S., MOESTL D., MULLER AUGR S., NAMATH A., PURNELLE D., SCHRFEN M., SCHARFE M., SCHREBS S., NAMATH A., SCHROEDER M., SDICU A.M., TETTELIN H., URRESTARZU L.A., USHINSKY S., WENDLER F., VISSERS S., VOSS H., WARLSH T.R., WANG Y., WANDLER F., WANG T., WANDLER F., WANG T., WANDLER F., WANG T., WANDLER F., WANG T., WANDLER F., VISSERS S., VOSS H., WANGETT E., ZONG W.W., ZOLLNER A., VO D.H., NAMANN R., WEDLER F., WINNETT E., ZHONG W.W., ZOLLNER A., VO D.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                          "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-STERNE;
OKINAKA R.T., CLOUD K., HAMTON O., HOFFMASTER A., HILL K.K., KEIM P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HALL J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.3%; Score 32; DB 3; Length 342; 70.0%; Pred. No. 1.1e+02; cive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. COLLINSON L.P., DAWES I.W.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. AVRAM D.A., BAKALINSKY A.T.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
HILL J.E., TZAGOLOFF A.A.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. WASSEY H., FORTIN N., FRIESEN J.D., I WANG Y., AMBED A., BUSSEY H., FORTIN N., FRIESEN J.D., I STORMS R.K., VO D.H., WINNETT E.; Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JIA Y., CHERRY J.M.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid virulence plasmid PX01.
Bacteria: Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U43281; AAB68211.1; -.
SEQUENCE 342 AA; 39682 MW; 9EAC1CD5 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRLLIRLDER 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 387:0-0(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9X314
Q9X314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9X314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RRAHRRA RRAHRA RA RRAHRA RRAHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WILSON R., AINSCORDER R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSETT T., COOPER J., COULSON A.,
BONFIELD J., BURTON J., CONNELL M., COPSETT T., COOPER J., COULSON A.,
GARDNER A., GREEN P., HAWRINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
JOHNSTON G., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY MIEG J., THOMAS K., VADIOIN M., VAUGHAN K., WATERSTON R.,
WATENSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
KOEHLER I., LAMKE G., KUMANO S., MAHILLON J., MANTER D., MARTINEZ Y., RICKE D.O., SVENSOND R., JACKSON P.J., if "The sequence and organization of pvJ., the large Bacillus anthracis plasmid harboring the Anthrax toxin genes.";
J. Bacteriol. 0:0-0(1999).
EMBL: AF065404; AAD32348.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 441;
                                                                                                                                                                                                                                                                                     Length 428;
                                                                                                                                                                                                                                                                                  Score 32; DB 2; Length 428
Pred. No. 1.4e+02;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 32; DB 5; Length 441
Pred. No. 1.4e+02;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAILMERISTOL N2;
WATERSTON N. S.
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC20376; ARC60986.1; -.
SEMBL; PF01362; DUF12; 1.
SEQUENCE 441 AA; 51624 MW; DE523A9B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-BRISTOL N2;
DAVIDSON S., WOHLDMANN P., BAUER C.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
SIMILARITY TO C4-TYPE ZINC FINGERS.
                                                                                                                                                                                                     428 AA; 50415 MW; FOFE581D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        441 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.3%;
50.0%;
                                                                                                                                                                                                                                                                                     Query Match 65.3%;
Best Local Similarity 55.6%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 50.00
S. Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R11G11.12.
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10
                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 YRMIARLDD 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-BRISTOL N2; MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLLIRLDE 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YRLLIRLDER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
016954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     016954
```

161 YRFLTKIDOR 170

15

```
1D 006421
D 01-3UL-1997 (TrEMBLEEL 04, Last sequence update)
DT 01-3UL-1997 (TrEMBLEEL 08, Last annotation update)
DT 01-10L-1997 (TrEMBLEEL 08, Last annotation update)
DT 01-10L-1997 (TrEMBLEEL 08, Last annotation update)
DT 01-NOV-1998 (TrEMBLEEL 08, Last annotation NA)
RP SEQUENCE FROM N.A.
RA BROWN D., CHURCHER C.M.;
RA SEQUENCE FROM N.A.
RA SEQUENCE FROM N.A.
RA SEQUENCE FROM N.A.
RA PARTAIN-HATANY
RA PARTAIN-HATANY
RA PALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA HALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA MYCODACTETIUM tuberculosis H37RV, and comparison with Mycobacterium
RI Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
DR EMBL: 29558; CAB08966.1;
SQUENCE 554 AA: 57835 MW; C42C89FC CRC32;
```

Search completed: February 8, 2000, 13:17:42 Job time: 32491 sec

ö

Gaps

ö

Query Match 65.3%; Score 32; DB 2; Length 554; Best Local Similarity 66.7%; Pred. No. 1.8e+02; Matches 6; Conservative 2; Mismatches 1; Indels

2 RLLIRLDER 10 || :|:||| 48 RLHVRIDER 56

9 9 충충충

```
Homo sapiens of Homo sapiens of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (03-A0G-1999) Production Sequencing Facility, DOE Joint Common Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA www.jgi.doe.gov.

**NOTE: This is a 'working draft' sequence. It currently consists of 93 contigs. The true order of the pieces

**is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

** as soon as if is available and the accession number will

** be preserved.
                                                                                                                     seq_documentation_block:
LOCUS ACO08537 187246 bp DNA HTG 02-SEP-1999
DEFINITION Homo sapiens chromosome 19 clone CIT-HSPC_490E21, *** SEQUENCING PROCESSES ***, 93 unordered pieces.
ACCESSION ACO08537 ***, 93 unordered pieces.
VERSION ACO08537.1 GI:5686530
SETWINDER HTG: HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 187246)
AC009643 H
AC004618 H
AC004670 H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            f unknown length
3 of 635 bp in length
unknown length
3 of 700 bp in length
f unknown length
of 263 bp in length
i onknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  f unknown length
9 of 675 bp in length
f unknown length
of 261 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    f unknown length
g of 400 bp in length
f unknown length
g of 40 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 647 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 273 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 257 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 73 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
182069
200000
200000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
f of 643 bp in len
f unknown length
g of 610 bp in ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
of 657 bp in len
unknown length
of 629 bp in len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
of 508 bp in ler
unknown length
of 648 bp in ler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
3.1e+04
3.4e+04
3.4e+04
                                                                                                                                                                                                                                                                                                                                                                    DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of contig cap of contig contig c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         651: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
  76.47
75.63
75.63
                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
2 (bases 1 to 187246)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8224:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2892:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3502:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4010:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6344:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6384:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7288:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1286:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1986:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2249:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4658:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5315:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5944:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6641:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7963:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8497:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8645:
  36.00
36.00
36.00
                                                                                   seq_name: gb_htg3:AC008537
                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8225
gb_htg4:AC009643
gb_htg2:AC004618
gb_htg2:AC004670
                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 U42835 Caenorhabditis elegans
1 U00050 Caenorhabditis elegans
1 Z68136 S. pombe chromosome I
1 AC010028 Drosophila melanogas
1 AC007167 Arabidopsis thalian
1 AC000815 Oryza sativa genomi
1 AC012259 Homo sapiens chromd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M57301 O.cuniculus UDP-N-acety
S68137 orf S' of mpal, mpal-Pu
M93021 Pasteurella haemolytica
J03474 Human serum amyloid A g
Y11829 A.thaliana hsp88.1 gene
                                                                                                                                      Command line parameters:
-MODEL-framet-p2n.model -DEV-x1p
-Q=/cgn1_1/GSPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-Q=/cgn1_1/GSPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-DB-Genemb1 -QFWT-fastap -SUFFIX-rge -GAPOP-12.000 -GAPEXT-4.000
-MINMATCH-0.100 -LOOPCI-0.000 -LOOPEXT-0.000 -GAPEXT-4.000
-GAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -PELOPOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.0500 -PELOPOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.0500 -DELOP-6.000
-DELEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.0500 -USER-US08653294
-NCPU-6 -ICPU-3 -NO.XLPXY -WAIT -THREADS-1
                                                                                 About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2253
2428
3000
4154
8646
14002
31482
34486
40252
83594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25083
32202
40242
94179
103874
129667
142418
    out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1710
1893
2485
2505
3460
4544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123.53
134.51
134.51
247.90
571.07
988.68
2.86+03
3.36+03
7.66+03
1.56+04
1.76+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. 4e+03
2. 7e+03
2. 7e+03
1. 2e+04
1. 6e+03
2. 3e+03
3. 3e+03
3. 3e+03
5. 6e+03
7. 8e+03
1. 0e+04
1. 9e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.2e+03
4.3e+03
5.5e+03
1.5e+04
1.6e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   152.13
170.79
232.81
234.95
240.30
339.36
462.82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1e+04
3e+04
6e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285,076
90,086
90,086
90,086
90,087
90,087
90,087
90,088
80,128
80,128
80,128
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
80,138
8
  GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Database: GenEmbl:*
Database sequences: 821193
Database length: -1518192014
Search time (sec): 11370.480000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
413.00
41
OM of: US-08-653-294-15 to:
                                                                                                                                                                                                                                                                                                                                                                                           Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strd
                                        Date: Feb 8, 2000 4:40
                                                                                                                                                                                                                                                                                                                                                                                                              Query: US-08-653-294-15
Query length: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                  GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_pl2:SPAC1F5
gb_htg4:AC010028
gb_pl2:ATAC007167
gb_pl2:ATAC006234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9b_htg2:AC006902
9b_htg4:AC010050
9b_htg4:AC00842
9b_htg3:AC003082
9b_htg2:AC006858
9b_htg2:AC006858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9b_pri: HUMM6PR
9b_pri: HSMPR465
9b_bal: THARG
9b_pli: AB011417
9b_bal: AE001251
9b_pli: SPBC2156
9b_pli: SPBC2166
9b_htg3: AC008847
9b_htg5: AC01643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pll:SPBC14C8
gb_inl:CELC24G7
gb_htg5:AC014106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_htg3:AC008537
gb_htg4:AC008591
gb_pr2:HS1106N18
gb_htg2:AC004965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_om:RABUDPNAA
gb_bal:S68137
gb_bal:PASMP
gb_pt2:HUMSAA
gb_pl1:ATHSP881
gb_in1:CELC04F6
gb_in1:CELC04F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_in1:AF026152
gb_p11:CS18SRN1
gb_p11:SPU45981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_p11:AP000815
gb_htg6:AC012259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_pr4:AC006581
gb_ba1:AP000003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 score_list:
Sequence
```

			÷
	-		
			•
•			
	•		
length the control of	igth ingth ingth igth ingth	h length h length h length h length h length h length h	length length th th th length length th th length th th length th
I bp in le to length bp in length bp in length bp in length bp in length to length	g the graph of the		58 bp in len Cook and a length 76 bp in length 125 bp in le Cook and length 126 bp in length 126 bp in length 126 bp in length 127 bp in lengt
bp in length bp in length bp in length length length length length length length length length bp in le length	len len len len len len len len	op i en con con con con con con con con con co	bp in le ob in le
of 651 bg unknown 1 of 189 bg unknown 1 of 189 bg unknown 1 of 595 bg unknown 1 of 595 bg unknown 1 of 695 bg unknown 1 of 692 bg unknown 1 of 692 bg unknown 1 of 625 bg	10 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	273 113 113 113 100wn 100wn 100wn 100wn 100wn 100wn 100wn	of 58 bp unknown of 76 bp unknown unknown of 564 bp unknown of 126 bp unknown of 126 bp unknown of 212 bp of 212 bp unknown of 23 bp unknown of 276 bp of 276 bp of 276 bp
chi	unknown length of 88 bp in length unknown length of 84 bp in length unknown length of 605 bp in length unknown length of 89 bp in length of 89 bp in length of 89 bp in length unknown length of 43 bp in length unknown length unknown length of 43 bp in length unknown length of 63 bp in length of 63 bp in length of 63 bp in length unknown length of 63 bp in length unknown length of 63 bp in length unknown length	unknown length of 573 bp in length unknown length of 613 bp in length unknown length of 609 bp in length unknown length of 64 bp in length unknown length of 681 bp in length unknown length unknown length unknown length of 645 bp in length unknown length of 6737 bp in length unknown length	oof 58 bp 1 of 76 bp 1 of 76 bp 1 of 76 bp 1 of 16 bp 1 of 16 bp 1 of 564 bp of 564 bp of 126 bp of 212 bp of 212 bp of 212 bp of 212 bp of 213 bp of 31 bp 1 of 31 bp 1 of 623 bp of 623 bp of 623 bp
tion to the tropa			<b>BU BU BU BU BU BU BU BU B</b>
continuo de contin	continuo con	continuous	contigory of the contig
9296: 9342: 9531: 0093: 0280: 0875: 1479: 2171: 2796:	2972: 3056: 3701: 4365: 4449: 4872: 4935:	15565: 16178: 16787: 17451: 18132: 18777: 19514:	20198: 20274: 20399: 20963: 21089: 21301: 21374: 21550: 22273:
93 93 100 102 108 114 121 121	2 6 6 4 4 4 4 4	155 161 167 174 181 187 195	2019 2027 2039 2096 2108 2130 2137 2137 2165 2227
446 97 443 332 94 81 76 77 72	15 57 00 07 66 50	93 66 79 88 88 88 78 78	ч
9297 9343 9532 10094 10281 10876 11480 12172	990768489	14993 15566 16179 16788 17452 18133 18778	20141 20199 20275 20400 20964 21090 21375 21375 21375 21375

* *	22850	24258:	gap of	unknown of 1409	length bp in length
* 1		6	ap o	nkno	ength
<b></b>	67 1	\$000 1000 1000 1000 1000 1000 1000 1000	ap	nknow	p in tengu ength
* *	25505	26750:	onti	f 12	م ۾
*	26751	27915:	onti	f 116	e d
* *	27916	28174:	ap o	unknown of 259 b	leng P in
* *	28175	30152:	ap o	ğπ	ength p in le
* *	30153	31646:	a b	unknown of 1494	ength p in leng
* *	164	3042	0.0	kno 13	ength p in leng
* *	304	4214	p o	know 117	ength p in leng
* *	421	L.	4	known 881	ength in lengt
* *	509	6881	p o	known 1786	length bp in len
* *	68	39070:	p o	know 218	ength P in leng
* *	39071	41053:	potio	know 198	engt p in
* * 1	41054	43362:	gap of	unknown of 2309	ength p in len
K #c 4	43363	45689:	otio	232	E 0.
k <b>4</b> k	45690	47736:	oti oti	204	i c
* *	47737	50962:	p o	know 322	engt p in
* *	50963	54510:	of i	85 35	eng o
* *	54511	57987:	otio	34 34	eng o i
* * *	57988	60620:	170	, 26 26	ä а.
* *	60621	64843:	otio	42 42	eng o 1
* *	64844	68934:	ti o	40 40	ength o in len
* *	893	2268	otio		ength o in leng
* *	226	6549	poti	kno 42	ength p in leng
* *	55	82005:	p o	kno 54	ength o in leng
* *	82006	86293:	ap	kno 42	E 0.
* *	86294	91795:	ap o	nkno f 55	eng i
* *	91196	98179:	ap o	nknow f 638	eng o
* *	98180	104674:	ap o	know 649	eng o
* * *	104675	114305:	gap of contig gap of		length bp in length length
t_sco	es: ality: Ratio: 4	2.00 667		Length Gaps	00
Percent Simil	y: 10	٥.	ercent	ťζ	100.0
alignment_bloc US-08-653-294	k: -15 x AC00	18537/rev	:		
Align seg 1/1	to rever	se of: AC	C008537	from: ]	1 to: 187246
. 2 Argle	uLeulleAr	gLeuAspGluAr	uArg 10		

```
op in length
length
                                                                                                                                                                          of 950 bp in length funknown length of 989 bp in length of 1495 bp in length of 1495 bp in length of 1895 bp in length of 1884 bp in length of 1884 bp in length funknown length
                                                                                                                                                                                                                                                                    f unknown length a of 1047 bp in length a of 1754 bp in length a of 1261 bp in length a unknown length a of 2951 bp in length a of 2924 bp in length
                                                                                                                                                                                                                                                                                                                                                                       f or ._.
f unknown length
g of 1847 bp in length
inknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g of 7184 bp in length f unknown length g of 7645 bp in length f unknown length
                                                                                          f unknown length of 1443 bp in length f unknown length of 1929 bp in length unknown length of 1035 bp in length f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                             of 1591 bp in length f unknown length of 3458 bp in length f unknown length of 3753 bp in length i unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 5377 bp in length unknown length of 3056 bp in length unknown length of 5499 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
length
bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
length
bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 11844 bp in length
unknown length
                                          f unknown length
g of 806 bp in length
t unknown length
of 136 bp in length
i unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bp in length
length
                                   of 201 bp in length
                        unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
of 3202 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
of 5377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 5451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown ]
of 5251 b
unknown ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 8227 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 8327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 2769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 4356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 6820
                                                                                                                                                                                                                                                                                                                                                                            gap of
contig
gap of
contig
gap of
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of t
                                  contig
gap of
gap of
contig
gap of
contig
gap of
                                                                                                                                                     contig
gap of
                                                                                                                                                                                                  contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
gap of
 gap of
contig
gap of
                                                                                                                             contig
gap of
                                                                                                                                                                            contig
gap of
                                                                                                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qap of
                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                        37384:
                                                                                                                                                                                                                                                                                                                                                                                                                                       42433:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48955:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57534:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70445:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82716:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87967:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102796:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      119350:
                                   16933:
                                                         17739:
                                                                                17875:
                                                                                                       19318:
                                                                                                                               21247:
                                                                                                                                                    22282:
                                                                                                                                                                           23232:
                                                                                                                                                                                                  24221:
                                                                                                                                                                                                                          25716:
                                                                                                                                                                                                                                               27600:
                                                                                                                                                                                                                                                                       28647:
                                                                                                                                                                                                                                                                                              30401:
                                                                                                                                                                                                                                                                                                                   31662:
                                                                                                                                                                                                                                                                                                                                          34613:
                                                                                                                                                                                                                                                                                                                                                                  35537:
                                                                                                                                                                                                                                                                                                                                                                                                                38975:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             46186:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52157:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60590:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77265:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95151:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111023:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129014:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140858:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154309:
                                                                              17740
                                                                                                                                                  21248
                                                                                                                                                                          22283
                                                                                                                                                                                                                                                                                                                                                                                        35538
                                                                                                                                                                                                                                                                                                                                                                                                                37385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46187
                                  16733
                                                        16934
                                                                                                      17876
                                                                                                                             19319
                                                                                                                                                                                                  23233
                                                                                                                                                                                                                         24222
                                                                                                                                                                                                                                               25717
                                                                                                                                                                                                                                                                       27601
                                                                                                                                                                                                                                                                                             28648
                                                                                                                                                                                                                                                                                                                   30402
                                                                                                                                                                                                                                                                                                                                          31663
                                                                                                                                                                                                                                                                                                                                                                 34614
                                                                                                                                                                                                                                                                                                                                                                                                                                       38976
                                                                                                                                                                                                                                                                                                                                                                                                                                                            42434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      111024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129015
                                                                                                                                                                                                                          LEST (bases 1 to 211769)

Submitted (0.3-Angu-1999) Production Sequencing Facility, DOB Joint Genome Institute.

LEST (bases 1 to 211769) Broduction Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON Oct 31, 1999 this Sequence version replaced gi:5686476.

* NOTE: This is a "working draft, Sequence. It currently tonsists of 60 contigs. The true order of the pieces is not known and their order in this Sequence record is arbitrary. Gaps between the contigs are represented as truns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                     DNA HTG 31-OCT-1999
5 clone CIT-HSPC_575N7, *** SEQUENCING IN
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 211769)
1005 Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                 s: contig of 518 bp in length
gap of unknown length
contig of 861 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
contig of 1027 bp in length
scontig of 1027 bp in length
gap of unknown length
contig of 1037 bp in length
gap of unknown length
gap of unknown length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 401 bp in length unknown length of 2117 bp in length unknown length of 1364 bp in length unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 167 bp in length
unknown length
of 526 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 1077 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  819 bp in length
known length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown length
of 296 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of 199 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 809 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 1407 bp in 1
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                       seq_documentation_block:
LOCUS AC008591 211769 bp DNA
DEFINITION Homo sapiens chromosome 5 clone CI
PROGRESS ***, 60 unordered pieces.
ACCESSION AC008591.2 GI:6165161
KEYWORDS HTG: HTGS_PHASE1.
contig
gap of
contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                                                                                                                     518:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3019:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4116:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4468:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8350:
                                                                                                                                                                                                                                                                                                                                                                                                                           1379:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9169:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1992:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4869:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10743:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11269:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13906:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .0576:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11921:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12533:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2829:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14914:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16489:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14105:
                                  seq_name: gb_htg4:AC008591
                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           519
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14915
                                                                                                                                         human.
                                                                                                                                                  ORGANISM
                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
RAUTHORS
TITLE
JOURNAL
                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                              COMMENT
```

```
Homo sapiens
     eature key
                                                                                                                                                                                                                                                                                                                                                                                                                ಥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                              37456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission

Submitted (30-OTT-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. Email enquiries: humquery@sanger.ac.uk CDne requests: clonerequest@sanger.ac.uk

On Oct 29, 1999 this sequence version replaced g1:6058975.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Ems., EMBL: Sw:, SWISSEROT: Tr:, TREMBL: Wp:, WORNPEP: Information on the WORNPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone 1106NLB. It may be shorter because we only sequence overlapping sections once, or the contrary and overlapping between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The true left end of clone 906P16 is at 142237 in this sequence. The true right end of clone d31193N1 is at 79367 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is amoltguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142336)
                                                                                                                                                                                                                                                                                                                                       others
164838: contig of 10529 bp in length gap of unknown length 177853: contig of 13015 bp in length 192072: contig of 14219 bp in length gap of unknown length 192072: contig of 14219 bp in length 211769: contig of 19697 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 211769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                            /clone="CIT-HSPC_575N7"
39430 c 40173 g 66628 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .211769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuLeuIleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: AC008591
                                                                                                                                                                                                                                                                                    /chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL035457.13 GI:6143575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-15 x AC008591/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete sequence. AL035457
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouality: 41.00
Ratio: 4.100
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_pr2:HS1106N18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submissions.
  154310
                                                    164839
                                                                                                                                                      192073
                                                                                                    177854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clark, G.
                                                                                                                                                                                                                                                                                                                                       64860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                              ORIGIN
```

```
Materaton, M.H.

Direct Submission

L. Submitted (12-JUN-1998) Genome Sequencing Center, Washington

L. Submitted (12-JUN-1998) Genome Sequencing Center, Washington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

* NOTE: This is a 'working draft' sequence. It currently

* consists of 42 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
           2 g
This sequence was generated from part of bacterial clone contigs of human chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGDP/Chr20 1106N18 is from the library RPCI-5 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpc.med.buffalo.edu/ VECTOR: pCYPAC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCUS AC004965 323792 bp DNA HTG 12-JUN-1998 DEFINITION HOMO Sapiens clone DJ1106H14, *** SEQUENCING IN PROGRESS ***,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 323792)
Materston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 142336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                f unknown length
g of 2301 bp in length
f unknown length
g of 1836 bp in length
f unknown length
g of 1844 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 1848 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.00 Length: 10
4.333 Gaps: 0
90.000 Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: HS1106N18 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                               32886 g 40076 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112966 TATAGACTGTGTATCAGGCTGGACCACAGG 112937
                                                                                                                                                                                                                              1. .142336
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="RPCI-5"
/clone="RP5-1106N18"
| 31918 c 32886 g 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1848: contig of 1867: gap of ud 4187: gap of ud 6023: contig of 6042: gap of ud 7865: gap of ud 7905: gap of ud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TyrArgLeuLeuIleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                  /map="q13.2-13.2"
                                                                                                                                                                                                                                                                                                                          /chromosome-"20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC004965.1 GI:3213032
HTG; HTGS_PHASE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 323792)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-15 x HS1106N18/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AC004965 323792 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unordered pieces. AC004965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_htg2:AC004965
```

```
g of 36012 bp in length
f unknown length
g of 89226 bp in length
f unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     f unknown length
g of 6761 bp in length
f unknown length
g of 9916 bp in length
f unknown length
g of 11386 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 12763 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 23551 bp in length
unknown length
of 28316 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17299 bp in length
                                           in length
                                                                                    in length
                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                        in length
                                                                                                                                                                                                                                                                                                                                                                               in length
                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                 op in l
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                 ength.
                                                                                                                                               ength.
                                                                                                                                                                                         ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                          ength.
                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                     length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                              ļ
                                                                                                                                                                                                                 ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
of 1664
                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
of 2829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
of 3483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 3939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
of 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
of 2808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
of 5050
                                                                                                                                                                                                                                                                                             2499
                                                                                                                                                                                                                                                                                                                                      3258
                                                                                                                                                                                                                                                 of 1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                           1900
                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 3836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 3745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 3480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 4311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 4768
  contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                           contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
gap of
contig
contig
gap of
contig
contig
contig
gap of
contig
contig
contig
gap of
contig
g
contig
contig
g
contig
g
contig
conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
gap of
contig
gap of
contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                      17678:
                                                                                                    13456:
15087:
15106:
17659:
                                                                                                                                                                                                                                                                                                                                                          27288:
30064:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61695:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80383:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40286:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             322060:
                                                                                                                                                                                                          19643
                                                                                                                                                                                                                                19662:
                                                                                                                                                                                                                                                                       21493:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70508:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46858
                                                                                                                                                                                                                                                                                                                  24011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67681
7906
9645
9645
111564
111564
113453
113453
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
115103
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80365
80364
820648
8282664
88828
88847
98763
98782
110187
1122969
140268
163838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    192173
192192
228204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318950
318968
320504
320522
```

```
Protein coding regions (CDS) have been predicted with the help of computer analysis using the Genefinder program in Pombase (an ACEDB database) with additional predictions for the branch-acceptor sites supplied by the program spisplice. CAUTION: It is possible that for any individual CDS we may have underestimated or overestimated the number of introns/exons or we may not have chosen the correct splice donor/acceptor sites. CDS are numbered using the following system eg SPBC25H2.Olc. SP (S. pombe). B (chromosome 2), c25H2 (cosmid name). Ol (first CDS), c (complementary strand). The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
IMPORTANT: This sequence MAX NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (27-WAR-1998) European Schizosaccharomyces genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 15A, E-mail: barrellesanger.ac.uk and Ratholieke Universiteit Leuven, Faculty of Agricultural and Ratholieke Baloigical Sciences, Laboratory of Gene Technology, Kardinaal Mercierlaan 92 Blok F, B-3001 Leuven, Belgium
(bases 18652 to 34051)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS
SPBC14C8 34051 bp DNA 19-OCT-1998
DEFINITION S. Prombe chromosome II cosmid c14C8.
AL022305.1 GI:3647356
KEYWORDS acetolactate synthase regulatory subunit; beta transducin; cdc18; cetolactate synthase regulatory subunit; beta transducin; cdc18; repeat; glucoamylase precursor; methionine aminopeptidase; pol5; protein import protein; ribosomal protein; RNA polymerase II subunit; rpb8; transcription factor; triacylglycerol lipase; WD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Department of Biological Sciences, University of Exeter, Perry Road, Exeter EX4 4QG, United Kingdom On Sep 25, 1998 this sequence version replaced gi:3006158. Notes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
1 (bases 1 to 34051)
Lyne,M., Rajandream,M.A., Barrell,B.G. and Volckaert,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                     775 others
11 322078: gap of unknown length
9 323792: contig of 1714 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 80.000
                                                                                                                                                                      /clone-"DJ1106H14"
81610 a 77790 c 79384 g 84233 t
                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgleuLeulleArgleuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xiang, Z. and Aves, S. Unpublished
                                                                                                                                                                                                                                                                                                                                                 39.00
4.333
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: AC004965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-15 x AC004965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fission yeast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seg_name: gb_pl1:SPBC14C8
322061
322079
                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain.
                                                                                                                                                                                                                                                                                                                           alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1
                                                                                                                                                                                                     BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
JOURNAL
REMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOURCE
```

```
/note="SPBC14C8.02, len:427, SIMILARITY:Saccharomyces cerevisiae, IM44 YEAST, mitochondrial import inner membrane translocase subunit tim44 precursor, (431 aa), fasta scores: opt: 893, E():0, (43.0% identity in 430 aa), /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLPRTMFSYGKENAFPVTPISNRNGTKGAGSKRAPLGSTKQSNA
SSYVPVPRTVLGKSTNYTSRFTSAPSYKKMSPMJISMDSPTILBPNGGGTSRSAVQER
SKRLSASPRRSLTDTPLPNELEDDIEYMPPPVHLDPLQSLGFDDVAIDCETLDPWPS
MQNKATSVTIRNTPASDFHVYKEFSDDPJIQFPLLSVDGDSPLTEKDTMLTTPATLKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              subunit precursor"
/protein_id="CAA18420.1"
/db_xxef="GI:3006160"
/db_xxef="SPTREMBL:060084"
/db_xref="SPTREMBL:060084"
/translation="MFLSRKITKNARTIVQCQRFFQTSIFSQNAAPQSPIKVFMDTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AELKKSOELODSVRALQDSSGSLSESDTFKRRPDATERARSGTTAASSFTGKTVGKAG
AKIGSYAQKAWESAPVQLSKKVISSTANTVATGVDTATKPVRETAFYKTIKQTMSDGS
TSSRYGFYADKEQRKKLREEFERRNRWFASSARIQPNEDVQSVVVHSNPSWKNKVEQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DPSENTEHFLQYLREYIVPEVTEAYVKGDKEVLKTWLSEAPFSVYETTTKEYAKHGVV
SVGKILDIRGVDIMSQRLLQPNDIPVFIVTFRTQEVHMFKDASSGELVAGKDDRIQOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MTSATTTEATAKDLQEKLSLKENDVVEDDGKVEENDAAEEGASN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEKKKKKKKKKKSSKKKKTPQEQTNPPTVGLSKIFVNKKYPVGEVCDYAEDNLMRTTDEE
KRALDRONFDQYNDLRRAAEVHRQARQYAQSVIKPGMSMMDVVNIIENTTRALVEEDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KNESRLVRKIQELKKSYQESEHPIVSSIRDMADSISGVWSRMFSETEASQVMRRFKEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="mitochondrial import inner membrane translocase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="SPBC14C8.03, len:426, SIMILARITY:Arabidopsis
thaliana, G3212871, putative translation initiation
factor., (431 aa), fasta scores: opt: 1697, E():0, (59.4%
identity in 416 aa)"
overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid c14C8 is overlapped at the 3' end by c15C4. Details of yeast sequencing at the Sanger Centre are available on the World Wide Web. (URL, http://www.sanger.ac.uk/Projects/S_pombe/)
During 1995 to 1996 about 66% of S. pombe chromosome I was sequenced by the Sanger Centre. The sequencing of the S. pombe genome is now being continued with funding from The European Commission. Fourteen European sequencing laboratories, including the Sanger Centre, are participating in the project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2261. .2284
/gene="SPBC14C8.02"
/note="PS00017 ATP/GTP-binding site motif A (P-loop)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"putative methionine metallopeptidase"
/protein_id="CAA18421.1"
/db_xref="G1:3006161"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product-"spindle pole body regulator"
/protein_id-"CAA18419.1"
/db_xref-"GI:3006159"
                                                                                                                                                                                                                                                                                                                                                                                            /organism="Schizosaccharomyces pombe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IYASVFTRVEDELDNPETRGWRIVDFARARAVDYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="SPBC14C8.01c, len:>220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:060085"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:4896"
/chromosome="II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="cosmid c14C8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(<1. .661)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1994. .3277
/gene="SPBC14C8.02"
1994. .3277
/gene="SPBC14C8.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4172. .5452
/gene="SPBC14C8.03"
4172. .5452
/gene="SPBC14C8.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(1. .661)
                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="cut2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="cut2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /map="IIR"
                                                                                                                                                                                                                                                                                                                                                                .34051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
```

```
PQYDNLLAAVKAATNKGIEEAGIDARLNEIGEAIQEVMESYEVEINGKTHQVKSIRNL
CGHNLDPYIIHGGKSVPIVKGGEEIKMEEGEIFAIETFGSTGRGVVHEDMECSHYAKI
PDAGHIPLRLPRAKALLNTITQNFGTLPFCRRYLDRIGESKYLLALNNLVSAGIVQDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="ttascattitttag, splice branch and acceptor"
complement(8460. 9812)
/gene="SPBC14C8.05c"
/gene="SPBC14C8.05c"
/note="SPBC14C8.05c, len:450, SIMILARITY:Aspergillus
/note="SPBC14C8.05c, len:450, Jucoamylase precursor, (639 aa),
fasta scores: opt: 797, E():0, (39.5% identity in 446 aa)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MSTPFNRVQRPKRHVFNCLVQNBPGVLSRLSGILAARGFNIDSL
VCATEVENENSRATIVLRGADEVVEQARRQIEDISUSVWAVLDVTGTSWPERELLAKV
SLLGPDHFOGHFERSEKVABSTNAKAKSDGEGVMNANALQILAASQLAAINQITTLFH
GRVADISTETIILELLTATPDRVDNFLSLLRPYGVLEACRTGTSAMTRAPHSNETEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product-"probable arp2-3 complex 41 kd subunit"
/protein_id="CAA1841."
/bb_xref="G1:3006164"
/db_xref="SPTREMBL:060088"
/translation="MATSQVLHILPRPSYEHAFNSQRIEFVTTTATNQVELYEQDGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"mrtywlflllggvvsaesllspwkrskeasmdewtdgokglamg
Hminnigdsgmhakdinpgcliaspstdspdytygwyrdsaltimtildrffeddkgl
Epiivkymdemyrlokypnpsgdfyagglgepkfnvdgtsydgdwgrpqndspalrai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKRAWODGTAFAKRIGAPDOAALYOFTIEPIDLKLGEFWDPGWGVIKGYKGRVDRSGL
DCSTLLASLYSNEFDHHILPTLKLQETWIRDYPVNGGWKQAMGRYFEDVYDGVSKSI
GNPWFICTSSAAEIIYKAIAYYDNKGLPELTEYNIHFFMKFAEFGDPYNWSVIRKNWH
TYADNFLKAVAEFQHPNGSMSEQFSRDDGHQKGARDLTWSYSSLLNAIYRREAIKGSV
LKSGIGFPTGVSLNHCAAHYTPNAGDTTILKEKDVMKVDIGVHVNGRIVDSAFTMSFD
                                                                                                                                                                                                                                                                                                                                                                                                                                     Join (7258. 7445,7526. 8036)
/gene="SPBC14C8.04"
/note="SPBC14C8.04, len:232, SIMILARITY:Saccharomyces
/note="SPBC14C8.04, len:232, SIMILARITY:Saccharomyces
servisiae, YCL009c, ILV6_YEAST, acetolactate synthase
small subunit precursor, (309 aa), fasta scores: opt: 513,
E():0, (49.4% identity in 243 aa),
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AFIKYMNYLFENGKEVHEVTVWIEAVLADLDYTANHWTEASFDLWEEIKDVHYFTLAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"acetolactate synthase small subunit precursor"
/protein_id="CAA18422.1"
/db_xref="GI:3006162"
                                                                                                                                                                                                                                                            4751. .4801
/gene="SPBC14C8.03"
/note="PS01202 Methionine aminopeptidase subfamily 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="SPBC14C8:05c".
/note="Pfam match to entry PF00723 glycosyl_hydr10, Glycosyl hydrolases family 15"
10878. .12058
/gene="Sop2"
join(10878. .10950,10998. .12058)
                                                                                                                                                                                                    /note="Pfam match to entry PF00557 pep_M24 metallopeptidase family M24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7446. .7451
/gene="spBC14C8.04"
/note="spBC14c8.04"
/511. .7511. .7525
                                                                                                                PPLCDIRGSYTAQFEHTI1LHPTQKEVVSRGDDY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"glucoamylase precursor"
/protein_id-"cab18423.1"
/db_xref-"gl:3006163"
/db_xref-"SPTREMBL:060087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    join(10878. .10950,10998. .12058)
/gene="sop2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="SPBC14C8.06, len:377"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref-"SPTREMBL:060086"
                                                                                                                                         4514. .5227
/gene="SPBC14C8.03"
                                                                                                                                                                                                                                                                                                                                                                                7258. .8036
/gene="SPBC14C8.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="SPBC14C8.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (8604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDDVEVEEVFLPPG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                signature"
7258. 803
                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
```

```
Rhabditina; Rhabditionary Sectionary Anderson, Recentinations, Recentinary Rhabditina; Roper, J., Burton, J., Copsey, T., Coper, J., Bonfield, J., Burton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Jones, M., Kershaw, J., Klisten, J., Hiller, L., Jones, M., Kershaw, J., Klisten, J., Laister, N., Jahthing, J., Lloyd, C., McMurray, A., Mortimore, B., O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Sanladon, N., Smith, A., Sonnhammer, E., Vaughan, K., Waterston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Walson, Sproat, J., and Wohldman, P., Weinstock, L., Wilkinson-Sproat, J., and Wohldnan, P.
WKHARTFSDHDKIVTCVDWAPKSNRIVTCSQDRNAYVYEKRPDGTWKQTLVLLRLNRA
ATFVRWSPREDKFAVGSGARVISVOYFEQENDWWSKHLKRPLRSTILSLDMHPNNVL
ALAGCADRKAYVLSAYVROVDAKPEASVWGSRLPFTNVCAEYPSGGWVHAVGFSPSGN
ALAYAGHDSSYTIAFPSAPEQPPRALITYKLSQLPLRSLLMANESAIVAAGYNYSPIL
LQGNESGWAHTRDLDAGTSKTSFTHTGNTGEGREEEGPVSFTALRSTFRNMDLKGSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Genetics, Washington University,
St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
                                                                                                                              SISSLPTVHONMIATLRPYAGTPGNITAFTSSGTDGRVVLWTL"
10951. .10956
/gene="sop2"
                                                                                                                                                                                                               /note="gtacag, splice donor sequence"
                                                                                                                                                                                                                                                                                        Length: 10
Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans strain-Bristol N2.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 46996)
Goola, D. and Wilson, R.
The sequence of C. elegans cosmid C24G7
Unpublished (1997)
3 (bases 1 to 46996)
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 34051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CELC24G7 46996 bp DNA
Caenorhabditis elegans cosmid C24G7.
U88310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21209 TATTCGCTCCTCATTGAATTAGACGAGAGG 21238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (03-FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U88310.1 GI:1825741
                                                                                                                                                                                                                                                                                      38.00
4.222
90.000
                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-08-653-294-15 x SPBC14C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: SPBC14C8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_in1:CELC24G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                           Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          elegans
                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOURCE
```

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions

Cambridge CB10 IRQ, England e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk

IROPTFSQPISEELESKYGK"

This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone

# NEIGHBORING COSMID INFORMATION:

cosmid is CO9D1, 13199 bp overlap;3' end lies in a gap. start of this cosmid is at base position 197 of CELC24G7; end is at 46996 of CELC24G7 The 5' Actual actual

#### NOTES:

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation). Location/Qualifiers 46996 FEATURES

### source

.17601, /organism="Caenorhabditis elegans" %strain="Bristol N2" /db\_xref="taon:6239" /chromosome="1" 15823. .24728 /gene="C24G7.5" join(15823. .158 /clone="C24G7"

> gene CDS

Join (1883. 1.5860,16237. .16593,16703. .16967,17315. .17601, 18125. .18246,18366. .18769,19326. .19526,20957. .21844, 21758. .22079,22455. .23239,23596. .23924,23983. .24201, 24248. .24487.24459. .24728). .24728. .22075,22457. .24728). .47281 .2448. .24487.2467. .24728). .47281 .24247. .24728

## /codon\_start=1

RIVQTHGKGAPKLQIDVLKSEIRLNVVSMPQKSTNQLGGISEESEEDSEARTANEDMK SNLQLQTDDPTGRPQIGGLKFKGRFSVIRDAVDSTTEGHAHCAVKIRHPSSEAISEYE FHIPETPVTVQSDMWGMGVVTFCLLAGFHPFTSEYDREEEIKENVINVKCDPNLIPVN ASQECLSFATWALKKSPVRRMRTDEALSHKFLSSDPSMVRRESIKYSASRLRKLAAM SLRDGQHENVQRLIAAFNNSNFLYLLSERLYEDVFSRFVFNDYYTEEQVALTMRQVTS **ALHFLHFKGIAHLDVNPHNIMFQSKRSWVVKLVDFGRAQKVSGAVKPVDFDTKWASPE** /protein\_id="AAB42336.1" /db\_xref="GI:1825742"

CDS

```
/db_xref="G1:1825743"

/tanslation="MIPTISKENTHOSTKSARKSSNESPYPSVTFRPNSSLSHLIIEV
/tanslation="MIPTISKENTHOSTKSARKSSNESPYPSVTFRPNSSLSHLIIEV
/tanslation="MIPTISKENTHOSTKSARKSSNESPYPSVTFRPNSSLSHLIIEV
ITQVCLIASNYLSKTVSDVSFLINEGGIOFPOITICNFTPIRTFVNEMNKTGOISD
NMINYIMHWFTEVPILIGSSNWQLLHEGNKDLQEYOKNNPNTTVGTFPIDAGFSCSDI
FRLCSPQGETPDCCSISTPVLFPLGKCYTLDLLESTKPSMHKOTFPGIOAGLAITLDA
HLEBOPDGSNGMDALFTNSYVNGFOYFVHPPHIPHLSSDEFTVTPNSVAYTAISSER
FELLPTNKWGNCTEHYPSGIKSDLPYLTGNCVSLCKAKFFMENCGCTPAVXNNERNLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA HTG 16-NOV-1999
*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (16 NOV-1999) Celera Genomics, 45 West Gude Drive,
Submitted (16 NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, ND, NSS and State (16 NOT-1998)
This sequence was identified as CDM:10211010 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* Cocation, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC014106
AC014106.1 GI:6437229
HTG: HTGS_PHASE2.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. [ (bases 1 to 63852) Adams, M. and Venter, J.C. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 46996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
12714 c 12710 g 19962 t
                                                                                                                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31327 TACAGGTTATTGATTCGTATGGAGCACAGA 31298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to reverse of: CELC24G7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-15 x CELC24G7/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63852 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                          38.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: AC014106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-15 x AC014106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_htg5:AC014106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_htg2:AC006902
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AC014106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18466 a
                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   jóin(43708. .43781,43825. .43858,44004. .44049,44094. .44202,44312. .44399,44447. .44678,44176. .45044,45323. .45488,45185. .45610,45653. .45815,46110. .46201,46250. .46395,46645. .46512,46563. .46686)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jóin(38014. 38120,38786. 38931,38976. 39021,39089. 39197,
39550. 39337,39384. 39515,40120. 40438,40757. 40922,
40978. 41046,41091. 41253,41342. 41433,41480. 41625,
41677. 41744,41862. 42000)
                                   join(28911. .28981,29343. .29464,29894. .30247,30296. .30386,
30573. .30894,30943. .31108,31289. .31944,32202. .32411)
/gene="C24G7.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWPEGYMENT TATAL THE COLOR OF THE COLOR OF THE CAPITAL TRANSMINION OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE CAPITAL 
                                                                                                                                                                                           /note="similar to degenerins; coded for by C. elegans cDNA CEMSH05F; coded for by C. elegans cDNA yk35e3.3; coded for /codon_start=1
                                                                                                                                                                                                                                                                                                                                                  /protein_id="Aab42340.1"
/db_xref="G1:1825746"
/db_xref="G1:1825746"
Kranslation="MFQKVFNSLLSSLGISAIFEIKAAANKQFANQLVIQVPVNSF-KNGKKIKGYGSAFFEIKHFSSTTTMHQPKRIFYGKGYARAFWALIVGHALAAMLCFQIF-ILLQMYFSKPTLSQVSFIVNEGGMDFPAVTVCNFNPIKKSYVRELNVSGDLTGETLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence-not_experimental
/protein_ide="AAB42339.1"
/db_xref="f01:1825745"
/translation="MKLLGMRKILPGDGWLGRLIIENEKWVLYANHHIQAQWIGEGQT
/translation="MKLLGMRKILPGDGWLGRLIIENEKWVLYANHHIQAQWIGEGQT
PILTQQPPXSEDISSEDSCWLLSRUYEGRESTEDRSYLQDKRYYFQHNNAQPYYTKHYKEDLAKGW
PILTQQPPXSPDISSEDCWLLSNLTGALRGRSFPTRENLQTDIELXFESLSAGFYRQGI
HKLNECWQDIVEHDGTYN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLEWLIMYSCSLGLLITQVFILASEYLSKPTYSDYSFLINEDGMDFPLITICNLNPIR
KTYVNEINKTGEVSPPMINYMMKWFTEIPTLIGGADRPTLHEGNEELKLYMKNHLNFT
VDSFFMNSGFSCPDIFKLCSFQGEIFDCCTLSTEVLTPLGKCFTLDLSSSTKASMHKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEPGIOAGLAITLDAHLEEQFDGSNGMDALFTNSFVNGFRYFVHPPNTIPHLSSDEFT
YSBYNTVAFSAS SSDRYVLLPHUMGMOTTBNFPOGIQSNLSTSSGSNCLEEKTAKRYMEN
CGCTPALYN TENNIKECTPVETTGLDNILARPNKEFGKIEFOTPNCKACAQGUNSLY
YRAYNSYGSQFSAGAFHYLKSINPEWTDGHMRANFOMINIFYRDMSYTEYNOVODASV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLOTNMDAMFLFSNLDRHNLKETHDEAETYFONHTDFOLIKFLRTAGYDCGEIFDCCK
YMKOKVTSLGKCWELDLRNLAPEWMRKOISPGSEAGLQIVVDAQLEEELKGENDDAKA
IFSDIYENGFRYFIHPPGTNAQLISEGISVSPSRTVYSAIKTVTHNLLNRGNWGNCSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MEPTLSPNYRNEAFEHDDSYLVNFVAGSSSGESSTPPPSFVFVKC
NFRYNOSRSQMIIEVPVAQLKKLRKLEGTVSIKRETQHFCETTTMHGPKRIFQGKRWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1QLLSDIGGNMGMFLGMSVITITEICLFFSKMFWLGFSKKRRDYMYSKRVNEKTHERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCETVEKMKA1ASQGNLSNLS1LKINKLKNYSEILNGSLVILSSKFTYPEHYFYIFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="c24G7.3"
join(33868. .32898.32979. .33141,33227. .33569)
/gene="c24G7.3"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to degenerins"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to degenerins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /evidence=not_experimental
/protein_id="AAB42338.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not_experimental
/protein_id="AAB42337.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GI:1825744"
28911. .32411
/gene="C24G7.4"
join(28911. .289
30573. .30894,30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38014. .42000
/gene="C24G7.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13708. .46686
/gene="C24G7.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polyA_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
               gene
```

CDS

CDS

CDS

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL REFERENCE

AUTHORS TITLE JOURNAL

COMMENT

```
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Metazoa; Arthropoda; Diptera; Brachycera;
Muscomorpha; Ephydroldea; Drosophilidae; Drosophila.

1 (Dases 1 to 11772)

8 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
Buchet, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Buyan-Rocha, S., Durbln, K.J., Ferantz, P., Gonesh, R., Gorrell, J., Gorcell, J., Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J., Gorrell, J., Forcum-Tansey, J., Frantz, P., Merandez, J., Hodgson, A., Hogues, M.,
Relly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Ilchtarge, O., Llu, J., Llu, W., Logan, O., Lu, J., Lucier, R.,
Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S.,
Nalys, N., Nalson, A., Nguyen, R., Nguyen, S., Oswal, G.,
Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E.,
Shen, H., Simon, M., Sparks, A., Stamps, A., Scherer, S., Shah, E.,
Bristor, D., Weinstock, I.R., Williamson, A., Worley, K., Wren, J.,
Wensford, G., Welnstock, I.R., Williamson, A., Worley, K., Wren, J.,
R., Chases, I to 117732)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 117732)

Submitted (11-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 16, 1999 this sequence version replaced gi:5881454.

* NOTE: This is a "working draft' sequence. It currently consists of 23 contigs. The true order of the pieces are in not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                               r chromosome 3L/71F1 clone RPC198-21K15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     le.
In leng
Jo in length
11822 bp in length
11832 bp in length
11385 bp in length
1885 bp in length
1893 bp in len'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           838: contig of 838 bp in length
1645: contig of 807 bp in length
3485: contig of 847 bp in length
3485: contig of 847 bp in length
4351: contig of 866 bp in length
6048: contig of 1697 bp in length
7829: contig of 1697 bp in length
17320: contig of 1923 bp in length
17331: contig of 2568 bp in length
17531: contig of 2403 bp in length
17531: contig of 2403 bp in length
17531: contig of 2403 bp in length
24775: contig of 2403 bp in length
24775: contig of 3821 bp in length
24775: contig of 4685 bp in length
38082: contig of 4685 bp in length
46290: contig of 8208 bp in length
54186: contig of 8208 bp in length
79413: contig of 18405 bp in length
79618: contig of 18405 bp in length
79619: contig of 18405 bp in length
79619: contig of 18405 bp in length
7732: contig of 16041 bp in length
                                                                    AC010050 117732 bp
Drosophila melanogaster
SEQUENCING IN PROGRESS *
                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                  ACO10050.3 GI:6056153
HTG: HTGS_PHASE1.
fruit fly.
     seg_name: gb_htg4:AC010050
                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       839
1646
32493
32493
4352
6049
7830
12321
114724
114724
1232
20055
224776
22476
238083
38083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54187
66009
79414
90799
101692
                                                                                                DEFINITION
                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                ACCESSION
                                                                                                                                                                VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (24 FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Mo 63108, USA
Mo 108. USA
Mo 11099 this sequence version replaced gi:4263446.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 11 contigs. The true order of the pleces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                    Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis:
Materston, R.H.
AC006902 96468 bp DNA HTG 26-FEB-1999
Caenorhabditis elegans clone Y74AllY, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown length
contig of 10846 bp in length
gap of unknown length
contig of 8928 bp in length
gap of unknown length
contig of 6721 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           150 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68439: gap of unknown remyc...
79778: contig of 11339 bp in length
79793: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of unknown length contig of 10056 bp in length gap of unknown length contig of 11154 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2040: contig of 2040 bp in length 2055: gap of unknown length 0960: contig of 8905 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93036: contig of 13243 bp in length 93051: gap of unknown length 96468: contig of 3417 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown length
of 9675 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to: 96468
                                                                                                                                                                                                                                                                                The sequence of Caehorhabditis elegans clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:6239"
/clone="Y74A111"
30222 a 17588 c 18100 g 30408 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to reverse of: AC006902
                                           ***, 11 unordered pieces.
                                                                                              AC006902.2 GI:4309900
                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 96468)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21836:
30764:
30779:
37500:
47190:
47205:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68424:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-08-653-294-15 x AC006902/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                    HTG; HTGS_PHASE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2056
10961
10976
21822
21837
30765
30765
37516
47191
47206
57256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68440
79779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79794
93037
93052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1
```

source

FEATURES

BASE COUNT

ORIGIN

```
Align seg 1/1
BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (03-A0G-1999) Production Sequencing Facility, DOE Joint Common Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Oct 31, 1999 this sequence version replaced gi:5686571.

* NOTE: This is a "working draft sequence. It currently consists of 6 contigs. Gaps between the contigs. As are represented as runs of N. The order of the pieces.

* is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homomogapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135436)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * This sequence will be replaced
* This sequence will be replaced
* by the finished sequence as it is available and
* the accession number will be preserved
* 1 32143: contig of 32143 bp in length
* 32144 42505: contig of 10362 bp in length
* 42506 76913: contig of 34408 bp in length
* 76914 94682: contig of 17769 bp in length
                                                                                                                 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of unknown length
122423: contig of 27741 bp in length
gap of unknown length
135436: contig of 13013 bp in length.
                                                                                                                                                                                                                                                                                                                                             to: 117732
                 1. .117732
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/chtomsome="3L/71F1"
/clone="RPCI98-21K15"
22525 c 23405 g 35555 t 26
                                                                                                                                                                                                          Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AC010050 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                       99919 TATCGACTTTTAATGCAATTAGATAAGAGA 99890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .135436
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
/clone="CIT-HSPC_431G16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing of Human Chromosome
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                   10
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .135436
                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeuIleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 135436)
DOE Joint Genome Institute.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC008496.2 GI:6165177
                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-15 x AC010050/rev
                                                                                                                                                                                                          Ouality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_htg4:AC008496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122424
                                                                                                                   Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
```

```
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Erra D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (06-NOV-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone RG011J21 is from the first release of the human BAC library CITB-978SK-B. The library contains cloned DNA from the male fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 170136)
Graves.T. Becker,M and Hawkins,M.
The sequence of H. sapiens BAC clone RG011J21
Upublished (1997)
Q-bases 1 to 170136)
Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AC003082 170136 bp DNA PRI 06-N
DEFINITION HUMBED CLONE RG011J21 from 7q31, complete sequence.
ACCESSION AC003082. GI:2588625
318 others
                                                                                                                                              Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                               from: 1
36803 t
                                                                                                                                                                                                                                                                                                                                                                                                                        mailto:saplens@watson.wustl.edu
28075 g
                                                                                                                                                                                                                                                                                                                                                            to reverse of: AC008496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-15 x AC008496/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAPPING INFORMATION:
29385 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE INFORMATION:
                                                                                                                                              Ouality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pr3:AC003082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo saptens
40855 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                           alignment_scores:
```

```
/rpt_family="L"
51668. .56075
7.rpt_family="L"
complement(52387. .52447)
Anote="similar to EST AA489840 (NID:g2220715) ab04f12.s1"
52387. .5246
Anote="similar to EST AA366493 (NID:g2218599) aa54c11.s1"
Complement(52387. .52480)
Anote="similar to EST AA488997 (NID:g2218599) aa54c11.s1"
56076 .56419
                                                                                                                                                                                                                                                                          note="similar to EST AA425675 (NID:g2106395) zw47b05.sl"
omplement(38607. .39020)
                                                                                                                                        33572, 33506
/rpt_family="L1"
34091, 34382
/rpt_family="ALU"
complement(34850, 35137)
/rpt_family="ALU"
35955, 3607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48999)
                                                                                                                                                                                                                                                                                                                                                              .41959)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cmplement(44490. .44609)
rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .65939)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44565. 46946
/rpt_family="L1"
complement(48709.
/rpt_family="ALU"
/9881. 4990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_tam...
,9193. .59213
/rpt_family="L1"
complement(60100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="MER"
56420. .56942
/rpt_family="L1"
complement(57178.
                                                                                                                                                                                                                                                                                                                                           /rpt_family="L1"
complement(41821.
/rpt_family="L1"
41957. .43047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64113. ..64253

./rpt_family="ALU"

complement(65648.

/rpt_family="ALU"

66049. .66338

./rpt_family="L1"

66424. .66798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66819. .66995
/rpt_family="L1"
67032. .67335
/rpt_family="ALU"
67336. .68129
/rpt_family="L1"
                                    /rpt_family="L1"
30980, 31186
/rpt_family="L1"
31384, 31422
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y="ALU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rpt_family="ALU"
9193. .59213
                                                                                                                                                                                                                                                                                                   rpt_family="L1"
9165. 2010-
                                                                                                                                                                                                                                                                                                                                                                                                                                      0/2. .43358
pt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3682. .44482
rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="L1"
3072. .43358
          'rpt_fam11y="L1
10183. .30377
                                                                                                                        31441. .31480
'rpt_family="L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family
4565. 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7pt_famil
3986. .64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                famil
                          repeat_region
                                                           repeat_region
                                                                                            repeat_region
                                                                                                                              repeat_region
                                                                                                                                                             repeat_region
                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). This clone is available from Research Genetics, Inc. (http://www.resgen.com). VECTOR: Beblobaclin Selection: chloramphenicol
                                                                                                                                                                                                                                                                                                                                       complement(1. .93)
/rpt_family="L1"
/rpt_family="L1"
/rpt_family="L1"
complement(1164. .1582)
/rpt_family="L1"
/rpt_family="L1"
/rpt_family="L1"
/rpt_family="L1"
/rote="similar to EST AA489840 (NID:92220715) ab04f12.s1"
/rote="similar to EST AA489997 (NID:92218599) aa54c11.s1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="L1"

complement(33173. .23302)

/rote="similar to EST AA488997 (NID:q2218599) aa54c11.s1"

complement(23173. .23244)

/rote="similar to EST AA489840 (NID:q2220715) ab04f12.s1"
                                                                                                                       The clone sequenced to the left is RG067E13, 200 bp overlap. Actual start of this clone is at base position 196 of RG011J21; actual end is at 170136 of RG011J21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2451. .2528

//note="similar to EST AA366493 (NID:g2018832)"

//note="lamily="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23184. .23261
/note="similar to EST AA366493 (NID:g2018832)"
complement(27159. .27188)
                                                                                                                                                                                         This clone contains STS sWSS2102 (NID:9940333).
Location/Qualifiers
1. .170136
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(15996. .16123)
rpt_family="L1"
.6125. .21465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpt_family="L1"
complement(21024, .21439)
rpt_family="L1"
2327, .23337
                                                                                                                                                                                                                                                                                        /clone="RG011J21"
/clone_lib="CITB-978SK-B"
/map="7q31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="L1"
28018. .28045
/rpt_family="L1"
complement(28082. .28155)
                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(5525. .5543)
/rpt_family="L1"
3635. .8923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4719. .4845)
rpt_family="L1"
complement(4929. .5336)
rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="ALU"
complement(29362,
/rpt_family="L1"
29513, 29694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="ALU"
8924. .8948
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family="L1"
3200. .28284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pt_family="L1"
1086. .28175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="L1"
29943. 30142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpt_family
                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                              repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                           FEATURES
```

to: 299719

from: 1

```
to reverse of: AC006780
                                    1 TyrArgLeuLeulleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         matio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.00
                                                                                                             seq_name: gb_htg2:AC006858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_pl2:AF026087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AF026087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3048
3062
6817
6831
35766
35780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95763 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
 Align seg 1/1
                                                                                                                                                                                                                                           VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                         REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston, R.H.

Direct Submission

AL Submission

Oniversity School of Medicine, 4444 Forest Park Mashington

University School of Medicine, 4444 Forest Park Parkway, St. Louis,

MO 63108, USA

On Mar 1, 1999 this sequence version replaced gi:4263158.

* NOTE: This is a "working draft' sequence. It currently

* consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* truns of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina: Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. 1 (asses 1 to 299719)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                       3047: contig of 3047 bp in length

3062 6816: contig of 3755 bp in length

8817 6830: gap of unknown length

8818 555: contig of 28935 bp in length

881 35765: contig of 28935 bp in length

881 35779: gap of unknown length

786 299719: contig of 263940 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of Caehorhabditis elegans clone Unpublished
                                                                       Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
                                                                                                                                                                                                        from: 1 to: 170136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="Y47D9A"
55063 c 53844 g 95007 t
                                                                                                                                                                                                                                                                  1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:6239
69165. .69708
/rpt_family="MER'
                                                                                                                                                                                                                                                                                                                                                                                                                                              AC006780.2 GI:4309792
HTG; HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-15 x AC006780/rev
                                                                                                                                                                                                        Align seg 1/1 to: AC003082
                                                                       Quality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouality: 38.00
Ratio: 3.800
Percent Similarity: 100.000
                                                                                                                                                  alignment_block:
US-08-653-294-15 x AC003082
                                                                                                                                                                                                                                                                                                                      seq_name: gb_htg2:AC006780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3048
3062
6817
6831
35766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95763
   repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
```

```
AC006858.1 GI:4263490
HTG: RTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota: Metazoa: Nematoda: Secernentea: Rhabditia; Rhabditida;
Rhabditing: Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis:
Waterston.R.H.
                                                                                                             seq_documentation_block:

LOCUS AC006858 299719 bp DNA HTG 25-FEB-1999
DEFINITION Caenorhabditis elegans clone Y47D9X, *** SEQUENCING IN PROGRESS
ACCESSION AC006858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (24-FEB-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. 10 Mo 63108, USA

**NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - 13-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3047: contig of 3047 bp in length 3061: gap of unknown length 6816: contig of 3755 bp in length 6830: gap of unknown length 35765: contig of 28935 bp in length 35779: gap of unknown length 299719: contig of 263940 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION Schizosaccharomyces pombe Satl gene, partial cds. ACCESSION AF026087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 299719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Caehorhabditis elegans clone Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 10
Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: AC006858 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55063 c 53844 g 95007 t
163290 TACAGGTTATTGATTCGTATGGAGCACAGA 163261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163290 TACAGGITATIGATICGIATGGAGCACAGA 163261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuLeuIleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 299719)
Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299719:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-15 x AC006858/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2253 bp
```

Louis,

```
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                       JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                    FEATURES
  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="Aab84238.1"
/db_xref="G1:2612955"
/translation="ILTDKEQKQENAIPVLLTRPDILGVDITLSPGEEKCFRLKRRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KOKVLCRLELSKSRYRTGEMMITELEGELDAMVRQVHMOLESVERIVPDIRIRNSVGTE
RATRKVWCRITRGVFELENMSASMVVPEECPETFETQOFGVEHFLRVELLRAVNKKRE
MOGPAHPRYSEEVOSPSRSRYSEEVORVSEGRLSEEVSKEEEKKGGRESGQHKRMASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKLLDGESNEEGGGEFQDHGMRSEINEEVLEEEDEEKIALLKKLESKQPMATRFEITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /innction="restores Gl arrest under starvation conditions to sat1- mutant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRTAPTYKGLAFRFQHALVIGVQSATNNACVEHEFEITIVPNVQQQPELPLGKNSGN)
QSSKLFADLSKPIIETDAAEIEEVSAEKARRQFGKNGIRLSQDAQEEEKQKKKYEQH
                                                                                                                           1 (bases 1 to 2253)
Seth-Smith, H., Kominami, K. and Toda, T.
Direct Submission
Submitted (19-SEP-1997) Cell Regulation, Imperial Cancer Research Fund, 44 Lincoln's Inn Fields, London WC2A 3PX, UK
Location/Qualifiers
1 0 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMM6PR 2428 bp mRNA PRI 07-JAN-1995
Human cation-dependent mannose 6-phosphate-specific receptor mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2428) Pohlmann, R., Nagel, G., Schmidt, B., Stein, M., Lorkowski, G., Krentler, C., Cully, J., Meyer, H.E., Grzeschik, K.-H., Mersmann, G., Hasilik, A. and von Figura, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INSREMQIQHAPTTFAAETIQCVLPIRIEKRVVWMEDGMEGGMEGMQPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complete cds. M19258 M19259 M1959 M16985 J G13:187282 M16985.1 G13:187282 Mannose 6-phosphate-specific receptor. Mannan placenta, cDNA to mRNA (library of Clontech), clones P[4a.29]. Homo sapiens
                                                                                 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
Schizosaccharomycetaceae; Schizosaccharomyces.
                                                                                                                                                                                                                                                               /organism="Schizosaccharomyces pombe"
/strain="972h-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 2253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 9 Gaps: 0 Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                               Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota;
                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:4896"
<898. .>2223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   976 TATCGACTCCTAATATATCTGGACGAG 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AF026087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeuIleArgLeuAspGlu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Sat1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                             /note="8-111"
  GI:2612954
                                                                                                                                                                                                                                                                                                                                                                                                     /gene="sat1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-15 x AF026087/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                 <898. .2223
/gene="sat1
                                                                                                                                                                                                                                                                                                                                                               /gene="sat1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.00
4.625
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_pr1:HUMM6PR
  AF026087.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                  TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                     gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDS
                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
```

```
/db_xref-"GDB:G00-120-162"
/profeel_id="AAA59542.1"
/db_xref-"G1-30A593747."
/tb_xref-"G1-"MPPFYSCWRTGLLLLLAVAVRESWQTEEKTCDLVGEKGKESEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELALVRRLKPLFNKSFESTVGGSDTYIYIFRVCREAGNHTSGAGLVQINKSNGKETV
VRALRETHIFRGSNWIMLIYIYRGGEDTOPHGGKEORRAVVNIS CSNRHTLADNFNYSEE
RGKVQDCFYLFEMDSSLACSPEISHLSVGSILLLYTFASLVAVYVGGFLVVVGAR
GMEQFPHLAFWQDLGNLVADGCDFVCRSKPRNVPAAYRGVGDDQLGEESEERDDHLLP
                                                                                                       though the cleavage
Cloning of a cDNA encoding the human cation-dependent mannose 6-phosphate-specific receptor broc. Natl. Acad. Sci. U.S.A. 84 (16), 5575-5579 (1987) 87289647

The protein is a presumptive prepropeptide, though the cleavag site for the mature peptide was not determined. Draft entry and computer readable copy of sequence [1] kindly provided by K.von Figura, 01-OCT-1987.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="M6PR"
/note="mannose 6-phosphate-specific receptor protein"
618 a 534 c 576 g 700 t
319 bp upstream of HindIII site; chromosome 12.
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="mannose 6-phosphate-specific receptor protein signal peptide"
146, .979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146. .979
/gene="M6PR"
/note="mannose 6-phosphate-specific receptor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 2428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                     <1.2428
/note="mps receptor mRNA"
146.223
/gene="M6PR"</pre>
                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TyrArgLeuLeulleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to reverse of: HUMM6PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="M6PR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-08-653-294-15 x HUMM6PR/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                            sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
```

THIS PAGE BLANK (USPTO)

```
Chlamydomonas reinhardtii R
Sequence of the tapetum-spe
Scytalidium catalase gene.
Human secreted protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide(s) and proteins derived from Staphylococcus aureus rotored on computer readable medium and used in the production of anti-S.aureus vaccines

Protorio on computer readable medium and used in the production of anti-S.aureus vaccines

Protorio on computer readable medium and used in the production of anti-S.aureus vaccines

Colim 1; Page 1230-1231; 3271pp; English.

Colim 1; Page 1230-1231; 3271pp; English.

Colim 2; Page 1230-1231; 3271pp; English.

Colim 4; Pred-only memory (RoM) or CD-ROM, Homology searches using medium, preferably selected from a floppy or hard disk, random access of the invention. The DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The collypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences of computer readable medium.

Computer readable medium.

Sequence 1816 BP; 539 A; 307 C; 240 G; 657 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers

Location/Qualifiers

1. 300

/*tag= a

/note= "these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
                                                                                                                                                                                                                                                                                     Staphylococcus aureus contig SEQ ID #351.
Computer readable medium: vaccine; S.aureus infection; immunodetection cellulitis; eyelld infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-0UL-1997;
05-7AN-1997; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Chol GH, Dillon PJ, Fannon MR, Kunsch CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 9
Gaps: 0
Percent Identity: 88.889
2413
2569
2794
3791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
to
  1.6e+03
1.7e+03
1.9e+03
2.7e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1387 TATCGTTTACTAATAACATTAGACGAA 1361
  91.88
91.33
90.59
87.92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeuIleArgLeuAspGlu 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: V74662
                                                                                                                                                                                                             standard; DNA; 1816 BP
                                                                                                                                                                                                                                                                 16-MAR-1999 (first entry)
31.00
31.00
31.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-15 x V74662/rev
                                                                                                                                   seq_name: N_Geneseq_36:V74662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seg_name: N_Geneseg_36:X06749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38.00
                                                                                                                                                                                                                                                                                                                                                                                                                           Staphylococcus aureus.
                                                                                                                                                                                     seq_documentation_block:
  N_Geneseq_36:V41261
N_Geneseq_36:Q36520
N_Geneseq_36:T42791
N_Geneseq_36:V59714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP-786519-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosen CA;
                                                                                                                                                                                                                                      V74662;
                                                                                                                                                                                                                   A PART OF THE PROPERTY OF THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1816 | Staphylococcus aureus contig S
14024 | E. coli O157 antigen gene clu
2485 | Rabbit GnT I CDNA clone. Human
2485 | Floral organ-specific chitinas
110000 | Continuation (11 of 17) of
603 | Human anti-angiogenic l6K hPRL
1498 | Rice anthranilate synthase fir
1734 | Rice anthranilate synthase genomic
174 | Staphylococcus aureus contig SE
174 | Staphylococcus aureus contig SE
174 | Bacillus thuringiensis ssp is
175 | Staphylococcus sequence of f
1756 | Contiguous sequence determined
1756 | Total contiguous sequence from t
1757 | Rybrid synthase gene clu
1758 | Rybrid synthase gene clu
1759 | Rybrid synthase gene clu
1751 | Rybrid synthase gene clu
1751 | Rybrid synthase gene clu
1752 | Rybrid synthase gene clu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i Polynucleotide sequence from the polynucleotide sequence from the sequence from the sequence from the sequence from the sequence of the sequence of the specification chicken growth differentiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BRCA2 cancer susceptibility ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse G3BP cDNA. New ubiquitin
Granulocytic Ehrlichia protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA encoding a hexosaminidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T. harzianum exochitinase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human GAP-SH3 domain binding
                                                                                                                                                                                                  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 !
579 !
1128
1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.09
646.49
149.75
160.02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129.68
129.68
425.14
425.14
3.00+03
3.00+03
3.20+03
3.20+03
86.58
86.58
86.58
86.58
86.58
86.58
86.58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2e+03
9e+03
9e+03
0e+03
1e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4e+03
1.5e+03
1.5e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .2e+03
.8e+03
.6e+04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.1e+03
1.4e+03
  N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102.30
86.73
86.73
86.73
102.30
103.00
103.00
103.00
103.00
103.00
103.00
103.00
103.00
104.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.00
105.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZSCOTE
120.71
99.03
110.44
109.92
0 73.44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Orig 2
38.00 1
37.00 36.00 1.
36.00 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
OM of: US-08-653-294-15 to:
                                                 Date: Feb 8, 2000 1:28 PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search information block:
Query: US-08-653-294-15
Query length: 10
                                                                                                                                                                                  Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Database: N_Geneseq_36:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N_Geneseq_36:Q25594 -
N_Geneseq_36:V49983 -
N_Geneseq_36:V21209_10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_36:T84095
N_Geneseq_36:Q29262
N_Geneseq_36:T29774
N_Geneseq_36:N90712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
N_Geneseq_36:V74662
N_Geneseq_36:X06749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N_Geneseq_36:X20560
N_Geneseq_36:T80415
N_Geneseq_36:N50107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:X01698
N_Geneseq_36:X01701
N_Geneseq_36:X23749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:T80414
N_Geneseq_36:V15570
N_Geneseq_36:V36099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N_Geneseq_36:T31725
N_Geneseq_36:V84064
N_Geneseq_36:T58392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_36:x20258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36:014809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N_Geneseq_36:Q14810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36:V83003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6:X26856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genesed_36:T78508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N_Geneseq_36:T79695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Geneseq_36:X23754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16:V36211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N_Geneseq_36:X13352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_Geneseq_36:V45819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _Geneseq_36:V73474
_Geneseq_36:V81791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genesed_36:V75507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N_Geneseq_36:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N_Geneseq_36
N_Geneseq_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N_Genesed_36
N_Genesed_36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Geneseq_3(
N_Geneseq_3(
N_Geneseq_3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N_Genesed_3
N_Geneseq_3
```

```
6717 TITAGAATTCTAGIGAGGITAGAIGAA 6691
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers 50. .1393
                                                                                                                                                                                                                                                                                                                    σ
                                                                                                                                                                                                                                                                                                to reverse of: X06749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a /product= GnT_I 2435. .2440 /*tag= b
                                                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeulleArgLeuAspGlu
                                                                                                                                                                                                                                                                                                                                                                          Q25594 standard; cDNA; 2485 BP. Q25594;
                                                                                                                                                                                                                                                                                                                                                                                                    03-DEC-1992 (first entry)
                                                                                                                                                                                                                                                                     alignment_block:
US-08-653-294-15 x X06749/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-1990; US-620098.
(HSCR-) HSC RES & DEV LP.
                                                                                                                                                                                                                                  Quality: 37.00
Ratio: 4.111
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:025594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sarkar M, Schachter H; WPI; 92-217073/26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctolagus cuniculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-JUN-1992.
29-NOV-1991; CA0417
                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; R24779
                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9209694-A
                                                                                                                                                                                                                                                                                                  Align seg 1/1
/*tag= a
/product= sugar_transferase
/note= "wbdN gene (ORF1), this region is
specifically claimed in Claim 6; encodes W88312"
858. .2042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               it= N-acetyl_transferase
"wbdR gene (ORF12), this region is
specifically claimed in Claim 6; encodes W88323"
                                                                                                                                                                            encodes W88313"
                                                                                                                                                                                                                         encodes W88314"
                                                                                                                                                                                                                                                                       encodes W88315"
                                                                                                                                                                                                                                                                                                                                                        encodes W88317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W88312, W88313, W88314, W88315, W88316, W88317, W88318, W88319, W88321, W88322, W88323.
                                 E. coli 0157 antigen gene cluster.
O antigen: 0157 antigen; diagnosis; wbdN gene; wzx gene; wzy gene; wbdP gene; wbdO gene; wbdR gene; transferase; polymerase; flippase; diarrhoea; haemorrhagic colitis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "H-repeat, may play a role in gene cluster
assembly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene (ORF10); encodes W88321"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene (ORF11); encodes W88322
                                                                                                                                                                                                       /product= sugar_transferase
/note= "wbdo gene (ORF3), this region is
specifically claimed in Claim 6;
                                                                                                                                                                                                                                                   /product- O_antigen_flippase
/note- "wzx gene (ORF4), this region is
specifically claimed in Claim 6;
                                                                                                                                                                                                                                                                                                                                      - sugar_transferase
wbdP gene (ORF6), this region is
specifically claimed in Claim 6;
                                                                                                                                                                    /note= "wzy gene (ORF2), this region is specifically claimed in Claim 6;
                                                                                                                                                                                                                                                                                                 per gene (ORF5); encodes W88316"
                                                                                                                                                  /*tag= b
/product= 0_antigen-polymerase
                                                                                                                                                                                                                                                                                                                                                                                /noté= "ÓRF7; encodes W88318"
7606. .8578
                                                                                                                                                                                                                                                                                                                                                                                                                "ORF8; encodes W88319"
                                                                                                                                                                                                                                                                                                                                                                                                                                          "ORF9; encodes W88320"
                                                                                  Location/Qualifiers
       X06749 standard; DNA; 14024 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .11893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .13123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .13821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "manD
                                                                                                                                                                                                                                                                                                                                               /note= "wbdP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .10519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note- "manc
                                                                                                                                                                                                                                                                                .5232
                                                                                                                                                                                                                                                                                                                     .6471
                                                                                                                                                                                                                                                                                                                                                                                                                        .9089
                          26-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product=
/note= "wb
                                                                                                                                                                                                                                                                                                   'product-
                                                                                                                                                                                                                                                                                                                                       /product=
                                                                                           .861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= '
                                                                                                                                                                                                                                                                                          /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                         'note-
                                                                                                                                                                                                                                                                                                            note=
                                                                                                                                                                                                                                                                                                                               /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                       *tad=
                                                                                                                                                                                                                                                                                                                                                                                                                                  *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                              *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10523.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1998; AU0315.
22-JUL-1997; AU-008162.
01-MAY-1997; AU-006545.
(UNSY ) UNIV SYDNEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tag=
                                                                                                                                                                                                                                   2744.
                                                                                                                                                                                                                                                                                4132.
                                                                                                                                                                                                                                                                                                                                                                  6491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reeves PR, Wang L;
WPI; 99-059669/05.
P-PSDB; W88312, W883
W88320, W88321, W883
seq_documentation_block
                                                                         Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09850531-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-NOV-1998.
                                                                                                                                        CDS
                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                SDS
                                                                                                                                                                                                                                                                                                                     SOS
                                                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                        CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
```

```
Nucleic acid molecules specific for bacterial polysaccharide antigens - useful for detecting specific strains in, e.g. food, faces or pattent samples
Claim 6; Fig 8; 165pp; English.
This is the nucleotide sequence of a gene cluster involved in the biosynthesis of the Escherichia coli o157 O antigen. The class of the Escherichia coli o157 O antigen. The class of the Escherichia coli o157 O antigen. The class of the Escherichia coli o157 O antigen gene sequences. 12 Open reading frames within the gene cluster were identified on the basis of homology to known sequences. The genes encode proteins (see W88312-23) involved the gene cluster were identified on the basis of homology to known sequences. The genes encode proteins (see W88312-23) involved the cluster were identified on the polysaccharide antigen and in the transport or processing of polysaccharide antigen and in the transport genes, particularly wbd (transferase), wax assembly and transport genes, particularly wbd (transferase), wax clisters improves the specificity of methods for the detection and identification of o antigen gene clusters improves the specificity of methods for the detection and identification of on antigens, e.g. in tests of food or faecal derived samples, or samples from patients. The O antigen is a major virulence factor of enteropathogenic E. coli strains that cause diarrhoea and haemorrhadic collitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Figure and rabbit DNA sequences encoding GNT I enzymes - for converting mannose to hybrid and complex N-glycan(s) Claim 3; Fig 4; 57pp; English.

Rabbit liver GNT I was purified and digested with pepsin, then trypsin. The peptide fragments were sequenced and used to design degenerate PCR primers (see Q30220-5). cDNA was prepared from total RNA from rabbit liver. PCR was carried out on the cDNA preparation. One of the two PCR products was cloned into the Smal site of pGEM7z for sequencing and then used as a riboprobe. The riboprobe was used to screen a rabbit liver cDNA library in lambda gtl0. The largest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rabbit GnT I CON clone...
High mannose glycoprotein; UDP-N-acetyl-glucosamine; alpha-3-D-mannoside; beta-1,2-N-acetyl-glucosaminyl transferase I; N-glycans; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 14024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 9
Gaps: 0
Percent Identity: 66.667
```

ξ<sup>1</sup>

```
claim 1; Pages 40 41; 67pp; Japanese.

This represents a floral organ-specific chitinase encoding gene sequence along with a floral organ-specific promoter sequence. The promoter derived from rice associated with chitinase is specific to floral organs and allows expression of genes in the flower parts of monocotyledonous plants. The expression of desired genes specifically in the floral parts
                                                                                                                                                                                                                                                                                                                                                                                                    V49983;
10-NOV-1998 (first entry)
Floral organ-specific chitinase gene with promoter sequence.
Floral-organ specific gene: chitinase; promoter; Orga sativa; rice;
flower part; monocotyledonous plant; bacterial resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .1234
/*tag= a
//otce= floral-organ specific promoter sequence"
//tag= b
insert in a positive clone was 1.6kb. An 80bp riboprobe was prepared from the 5'-terminal of the 1.6kb insert and used to rescreen the library. The largest cDNA insert was cloned into pGEM-7z to obtain pGEM-7z-rcgntl. The full-length rabbit GNT coding sequence was eventually obtained from overlapping clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Promoter sequence associated with chitinase, specific to floral organs - allows expression of genes in the flower parts of monocotyledonous plants
                                                                                         669 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "floral-organ-specific chitinase"
/note= "contains introns"
                                                                                                                                                Percent Identity: 66.667
                                                                                                                                                                                                                                                        to: 2485
                                                                                           644
                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: Q25594 from: 1
                                                                                         623 C;
                                                                                                                                                                                                                                                                                                    1072 TACAAACTGCTGGTTCAGCTTGATGAA 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NISB ) JAPAN TOBACCO INC.
Inoue T, Ito T, Saito H, Takakura Y;
WPI; 98-388123/33.
P-PSDB; W64776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                   1 TyrArgLeuLeuIleArgLeuAspGlu 9
                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID V49983 standard; DNA; 2636 BP.
                                                                                         549 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "conta
1235. 1691
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /number= 1
1777. .1909
/*tag= e
/number= 2
1910. .2108
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number= 2
2109. 2502
/*tag= g
/number= 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1692. .1776
/*tag= d
                                                                                                                                                                                                          alignment_block:
US-08-653-294-15 x Q25594/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number=
                                                                                                                                                  Quality: 36.00
Ratio: 4.000
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                             seq_name: N_Geneseq_36:V49983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-JUL-1998.
26-DEC-1997; J04892.
27-DEC-1996; JP-349505.
                                                                                         2485 BP;
                                                                             See also Q25595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9829542-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa
                                                                                                                                       alignment_scores:
                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exon
                                                                                                                                                                                                                                                                                                                                                                                           88888888
```

```
nm base 1000001 (Methanococcus jannaschii circula
LOCUS V21209 Accession V21209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           V01698 standard; DNA; 603 BP.

X01698 standard; DNA; 603 BP.

X01698; Standard; DNA; 603 BP.

X01698; Standard; DNA; Entry)

Runan anti-angiogenic hPRL Met-1Cys199 antisense DNA.

Human anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis; growth hormone; hGH; hGH-V; capillary endothelial cell proliferation; placental vascularisation; pregnancy; treatment; angiogenic disease; tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation; arthritis; atherosclerotic plaques; corneal graft neovascularisation; wound healing; proliferative retinopathy; macular degeneration; trachoma; granulation; glaucoma; ocular; uveitis; fracture; Osler-Weber syndrome;
of monocotyledonous plants, allows modifications to be made in the structure or function of these parts allowing the introduction of desired characteristics such as increased resistance to bacterial attack. Sequence 2636 BP; 722 C; 696 G; 561 T;
                                                                                                                                                                                                                                                                                     to: 2636
                                                                                                                                        Length: 9
Gaps: 0
Percent Identity: 77.778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to reverse of: V21209_10 from: 1
                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97039 TACAGGAGATTGCTGAAGTTAGACCAGAGG 97010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              510000
610000
710000
810000
1010000
1110000
1310000
1410000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110000
210000
310000
410000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1510000
1610000
1664976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                213 TACAGGGCATTAATTAAACTAGATGAA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg_documentation_block:
Continuation (11 of 17) of v21209 from
WP Sequence split into 17 fragments LOW
WP V21209_01 100001 210
WP V21209_02 200001 310
WP V21209_03 300001 410
WP V21209_04 400001 510
WP V21209_05 500001 710
WP V21209_06 600001 710
WP V21209_06 600001 710
WP V21209_08 1000001 1010
WP V21209_18 1000001 1010
WP V21209_19 1000001 1010
WP V21209_11 1100001 1310
WP V21209_12 1200001 1310
WP V21209_14 1400001 1510
WP V21209_14 1400001 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V21209 from
                                                                                                                                                                                                                                                                                                                             Φ
                                                                                                                                                                                                                                                                                     to reverse of: V49983
                                                                                                                                                                                                                                                                                                                             1 TyrArgLeuLeuIleArgLeuAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-15 x V21209_10/rev
                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: N_Geneseq_36:V21209_10
                                                                                                                                          36.00
4.500
88.889
                                                                                                                                                                                                                        alignment_block:
US-08-653-294-15 x V49983/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.00
3.889
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: N_Geneseq_36:X01698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                   alignment_scores:
Quality:
                                                                                                                                                             Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                       Align seg 1/1
                                                            Sequence
    ខ្លួខ្លួន
```

arthritis; atherosclerotic plaques; corneal graft neovascularisation;

```
PF 19-MAY-1999; U00691.

PR 13-MAY-1999; U00691.

PR WIF: 99-045132/04.

PR WHI: 99-04513/04.

CC files in chick chorioallattoic membrane and (iii) inhibit consists a probable abnormality of placental vascularisation disease in modificating tumour formation or growth in a patient or for modulating vascularisation of aptient's placental in patient or for modulating vascularisation of aptient's placental in patient or for application and poperior of application, arthritic such as rheumatoid carborathy such as diabetic carborathy such as diabetic carborathy proliferative rethopathy such as diabetic carboraty vascularisation in wound healing such as hypertrophic scars or keloid scars, neovascular adhesion, chronic variose union fractures, osler weber syndrome, popularion of such as hypertrophic scars or keloid scars, such as chord or encoderma, retrolemal insoppication and social scars or heloid social scars or heloid social such as contraceptive agents. Or enco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-JUN-1999 (first entry)
Human anti-angiogenic 16K hPRL Met-1Prol42 antisense DNA.
Human; anti-angiogenic 16K hPRL Met-1Prol42 antisense hPL; angiogenesis;
Human; anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis;
growth hormone; hGH; hGH-V; capillary endothelial cell proliferation;
placental vascularisation; pregnancy; treatment; angiogenic disease;
tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation;
psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             with pre-eclampsia, intrauterine growth retardation, and placental
                    ulcer; leukaemia; reproductive disorder; contraceptive agent; gene therapy; pre-eclampsia; intrauterine growth retardation; placental dysfunction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.667 Length: 10
9.000 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: X01698 from: 1 to: 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID x01701 standard; DNA; 603 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: N_Geneseq_36:X01701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-15 x X01698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                       W09851323-A1.
                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dysfunction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X01701;
K K K K E E E E E
```

```
PR 12-MAX-1998; US-046394.

REGGC ) UNIV CALIFORNIA.

PR (REGC ) UNIV CALIFORNIA.

PR MATIL 309-045192/04.

PR New antl-analydenic peptides - comprise N-terminal fragments of human piacental lactogen, human growth hormone, growth hormone variant of borsonscutive amino acids selected from the N-terminal end of human piacental lactogen (hEL), human growth hormone (hGH), growth commone variant (hGH V), or human prolactin such peptides (1) inhibit compliants on expectific receptor which does not bind an intact full length hormone variant (hGH V), or human prolactin such peptides (1) inhibit and glogenesis in chick chorloallantoic membrane and (iii) binds to at least one specific receptor which does not bind an intact full length of HGH, hbt., prolactin or hGH-V. The invention also describes a method for congenial to probable abnormality of placental vascularisation diring propable abnormality of placental vascularisation diring propable abnormality of placental vascularisation diring congenes.

CC diagnosing a probable abnormality of placental vascularisation disease in a subject, for inhibiting tumour formation or growth in a patient or for a subject, for inhibiting tumour formation or growth in a patient of peptides can be used for preventing or treating e.g. malignant tumours, and cascularisation of growth and signature peptides can be used for preventing or rethingations such as rheumatod and placents of architecture, voelar would healing proliferative rethingations such as rheumatode contributions. The propagent of and choricoartonma, retrolental fibroplasia, scleroderma, solid tumours, uveitis, and reproductive disorders such as follicular and luteal cycle and choricoartonma, they can also be used as contraceptive agents. DNA encoding the peptides can be used in agene therapy. The measurement of abnormal levels of N-terminal fragments of the proper parameter of and choricoartonma. They can also 
              wound healing; proliferative retinopathy; macular degeneration; trachoma; granulation; glaucoma; ocular; uveitis; fracture; Osler-Weber syndrome; psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion; ulcer; leukaemia; reproductive disorder; contraceptive agent; gene therapy; pre-eclampsia; intrauterine growth retardation; placental dysfunction; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-JUN-1999 (first entry)
Rice anthranilate synthase first isozyme alpha-subunit DNA fragment.
Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: X01701 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID X23749 standard; DNA; 1498 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      135 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.667
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: N_Geneseq_36:X23749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-15 x X01701
                                                                                                                                                                                                                             12-MAY-1998; U09691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                           Homo sapiens.
WO9851323-A1.
                                                                                                                                                                                                         19-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
ME BY B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ?
```

```
W93815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
  Rice anthranilate synthase first isozyme alpha-subunit DNA variant.
Anthranilate synthase; alpha-subunit; ASA; rice; isozyme; plant; seed;
maize; wheat; tryptophan content; nutritional value; ss.
                                         /product= "ASA synthase"
/note= "Partial coding sequence. Incomplete exon 2"
1102. .1233
                                                                                                                                                                                                                                                                                      DNA ancodes "a-subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops, e.g. rice, maize or wheat Example 5; Page 131-133; 152pp; Japanese.
This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops. Sequence 1498 BP; 343 A; 362 C; 404 G; 389 T;
maize; wheat; tryptophan content; nutritional value; ss. Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                            1318. .1498
/*tag= d
/number= 2
/note= "partial exon 2 sequence"
                                                                                                                                                                                                                       29-AUG-1997; JP-235049.
(HOKK ) HOKKO CHEM IND CO LTD.
(NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
HASSEGAWA H, TETAKAWA T, TOZAWA Y, WAKASA K;
WPI; 99-228882/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-1998; J03883.
29-AUG-1997; JP-235049.
(HOKK ) HOKKO CHEM IND CO LID.
(NORQ ) JAPAN MIN AGRIC FORESTRY & FISHERIES.
HORQ ) TAPAN MIN AGRIC FORESTRY WAKASA K;
WPI; 99-228982/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: X23749 from: 1 to: 1498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/product= "ASA synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10
                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualiflers
1. .1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TyrArgLeuLeuIleArgLeuAspGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:

ID X23754 standard; DNA; 1734 BP.

AC X23754;

DT 25-JUN-1999 (first entry)
                                                                                                /number= 1
1234. .1318
/*tag= c
/number= 1
                                  1102. .1498
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                           33.00
4.125
80.000
                                                                                         /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: N_Geneseq_36:X23754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-08-653-294-15 x X23749
                                                                                                                                                                                                   11-MAR-1999.
31-AUG-1998; JO3883.
                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
Percent Similarity:
                                                                                                                                                                                         WO9911800-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9911800-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-MAR-1999.
                                                                                                               intron
                                                                                                                                              exon
                                                                               exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
```

```
II-MAR-1999.
II-MAR-1999.
II-MAR-1999.
II-MAG-1997, JP-235049.
II-MAG-1997, JP-235049.
II-MAG-1997, JP-235049.
II-MAG-1997, JP-235049.
II-MAG-1997, JP-235049.
III-MAG-1997, JP-235049.
III-MAG-1997, JP-235049.
III-MAG-1998, JP-238982/19.
III-MAG-199882/19.
III-MAG-19982/19.
III-MAG-19982/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JUN-1999 (first entry)
Rice anthranilate synthase first isozyme alpha-subunit DNA.
Anthranilate synthase; alpha-subunit; ASA: rice; isozyme; plant; seed;
maize; wheat; tryptophan content; nutritional value; ss.
DNA encodes "a-subunit of first isozyme of rice anthranilate synthase - used for improving tryptophan production and nutritional value of crops. e.g. rice, maize or wheat claim 8; Page 142-145; 152pp; Japanese.

This invention describes a novel rice anthranilate synthase first isozyme alpha-subunit. The encoding DNA can be used to produce transformant plants and seeds, of e.g. rice, maize or wheat, with enhanced tryptophan content and nutritional value of the crops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.00 Length: 10
4.125 Gaps: 0
80.000 Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: X23754 from: 1 to: 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= "ASA synthase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: X23748 from: 1 to: 1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TACCGCTGCCTCGTCAGGGAGGACGACCGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TACCGCTGCTCGTCAGGGAGGACGACGC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .1734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
ID X23748 standard; DNA; 1734 BP.
AC X23748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.00
4.125
80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: N_Geneseq_36:X23748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-15 x X23754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-08-653-294-15 x X23748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9911800-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
```

intron

exon

exon

intron

intron

exon

exon

```
6716. .6940
/*tag= e
/note= "encodes residues 177 to 251 of OCIF, see R99925"
6941. .8960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8961. .9349
/*tag= 9
/note= "encodes residues 252 to 380 of OCIF, see R99925"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding detectlastogenesis inhibitory factor protein - useful for bone resorption control, esp. treatment of osteoporosis for bone resorption control, apanese fragment of osteoporosis the sequences given in 1318pp; Japanese fragment of the genomic DNA encoding the full length osteoclastogenesis inhibitory factor (OCIF) of the invention has a molecular weight by SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-reducing conditions. The protein is adsorbed onto cation-exchangers or heparin and its activity is lowered after 10 mins at 70 deg.C. ocif is useful in the control of bone resorption and therefore
                                                                                                                                                                                           23-APR-1997 (first entry)
Fragment of human OCIF genomic DNA-2.
Osteoolastogenesis inhibitory factor; OCIF; heparin; bone resorption; osteoporosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deg.C. OCIF is useful in the control of bone resorption and therefor in the treatment and prevention of disorders of bone resorption, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-AUG-1996.
20-FEB-1995; J00374.
20-FEB-1995; JP-054977.
21-UUL-1995; JP-207508.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
GOLO M, Higashlo K, Kobayashl F, Mochizuki S, Morinaga T; Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H; 96-4(03320/40.
                                                                                                                                                                                                                                                                                                                                   130. 499
/*tag= a
/note= "encodes residues -11 to 112 of OCIF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1920 C;
Align seg 1/1 to: V20767 from: 1 to: 9898
                                                         1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3184 A;
                                                                                                                                                    seq_documentation_block:
ID T33183 standard; DNA; 10190 BP.
AC T33183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T33183 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -ncc
/*tag= f
8961.
                                                                                                                   seq_name: N_Geneseq_36:T33183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 3.300
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-08-653-294-15 x T33183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10190 BP;
                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                 intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exon
                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          exon
                                                                                                                                                                               Claim 1; Page 16-26; J6pp; English.

Claim 1; Page 16-26; J6pp; English.

The present sequence represents human OCIF genome DNA which is specifically claimed in the present invention. The present sequence represent human OCIF genome DNA which is specifically claimed in the present invention. The present invention describes: (1) a method of inhibiting the formation of osteoclasts and/or antipyretic proteins, which have the following characteristics: (1) MW determined by SDS-PAGE of approximately 60 kDa under reducing conditions, and 60 kDa and 120 kDa under non-reducing conditions; (1) a sequence (III) (see W53239); (iii) affinity to cation exchangers and heparin; (iv) its osteoclast formation inhibiting activity reduced by heating at 70 degrees Celsius for 10 minutes or 56 degrees Celsius for 10 minutes, and (v) its antipyrestic activity reduced by heating at 90 degrees Celsius for 10 minutes, and (z) a method for preparing the above proteins. The proteins are useful for, e.g. treatment and consequence of osteoporosis, rheumatism or multiple sclerosis, and also as antigens for immunological diagnosis of these diseases and disorders. Osteonce 9898 BP; 3110 A; 1835 C; 1871 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inhibition of osteoclast formation and/or antipyretic activity useful for, e.g. treating osteoporosis, rheumatism and multiple
                                                                                                             15-UUL-1998 (first entry)
Human OCIF genome DNA-2.
Human; OCIF; genome; osteoclast; antipyretic; osteoporosis; rheumatism; multiple sclerosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                            Location/Qualifiers
130. .9057
/*tsg* a
/notes "contains introns"
130. .499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-AUG-1997; J02859.
19-AUG-1996; JP-235928.
(SNOW ) SNOW BRAND MILK PROD CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Morinaga T, Nakagawa N, Yasuda H;
WPI; 98-169150/15.
                                                         seq_documentation_block:
ID V20767 standard; DNA; 9898 BP.
                                                                                                                                                                                                                                                                                                                                                      500. .4503
/*tag= c
/number= 1
4504. .4695
/*tag= d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= e
/number= 2
6716 .6940
/*tag= f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /number= 3
6941. .8668
/*tag= 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /number= 2
4696. .6715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /number= 3
8669. .9057
/*tag= h
/number= 4
                                                                                                                                                                                                                                                                                                                   /*tag= b
/number= 1
                  seq_name: N_Geneseq_36:V20767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouality: 33.00
Ratio: 3.300
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-08-653-294-15 x V20767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; W53238
                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores
```

3187 T;

ΰ

2648 TATGAACTICTCATTAGGATGCAGGAGAAG 2677

ä

```
PER WOSSOLISTANDERS.

PR 05-NOV-1997; UZ0313.

PR (WHED ) WHITEREAD INST BIOMEDICAL RES.

Hudson T. Lander Es, Wang D;

PR Hudson T. Lander Es, Wang D;

RPI: 98-286974/25.

PR Hudson T. Lander Es, Wang D;

RPI: 98-286974/25.

PR 40-286974/25.

A10269-X12937 are human DNA fragments which contain biallelic polymorphic CC markers which have been isolated using the primers represented in CX 09121-X10268. The base occupying the primers respecanted in CX 09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in CX 09121-X10268. The base occupying the polymorphic typing for use in entity didual for use in CC e. g. forensics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, CC muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial chypercholesterolemia, polycystic kidney disease, hereditary cycloshis, von Willebrand's disease, tuberous scierosis, hereditary cycloshis, von Willebrand's disease, tuberous scierosis, hereditary haemorrhagic telanglectasia, familial colonic polyposis, Ehlers-Danlos
                                                                                   WPI: 95-131177/17.

WPI: 95-131177/17.

WPI: 95-131177/17.

PFDB: R71384.

WP class of semaphorin peptide(s) and polypeptide(s) - are potent modulators of nerve cell growth and regeneration are potent modulators of nerve cell growth and regeneration.

Example 2: page 85-88; 104pp; English.

Example 3: page 85-88; 104pp; English.

Example 4: page 85-88; 104pp; English.

Example 5: page 85-88; 104pp; English.

Example 5: page 85-88; 104pp; English.

Example 6: page 85-88; 104pp; English.

Example 6: page 85-88; 104pp; English.

Example 7: page 85-88; 104pp; English.

Example 7: page 85-88; 104pp; English.

Example 6: page 85-88; 104pp; English.

Example 7: page 85-88; 104pp; Engl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human biallelic polymorphic DNA fragment EST91495b.
Polymorphism: biallelic; human: forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament; treatment; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 13
Gaps: 1
Percent Identity: 69.231
                                                                Matthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   544 TACCGCCTACTAATATCGAAGTTTCGTCTTGATTCAAGA 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeulle.....ArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: Q87446 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577 C;
                                                                Kolodkin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  681 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X12081 standard; DNA; 150 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.50
3.250
76.923
13-SEP-1993; US-121713.
(REGC ) UNIV CALIFORNIA.
Bentley DR, Goodman CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-653-294-15 x Q87446/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seg_name: N_Geneseg_36:x12081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2504 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sed_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9820165-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
   11-NOV-1995 (first entry)
Tribolium semaphorin I cDNA.
Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium; variola major virus; smallpox; semaphorin receptor binding activity; modulation; nerve cell growth; immune response; viral pathogenesis; neurological disease; neuro-regeneration; oncological infection; ds.
Tribolium sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Borrella burgdorferi nucleic acids - used to develop products for the detection, diagnosis, characterisation, prevention and therapy of infections, particularly Lyme disease claim 1; Page 908-914; 1128pp; English.

X20248 to X20402 represent polynucleotide sequences isolated from Borrella burgdorfer! (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of blosynthetic products, e.g. enzymes. Borrella belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrella causes epidemic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                                                                             Borrelia burgdorferi polynucleotide sequence #11.

Borrelia burgdorferi; spirochete; bacterium; pathogen; Lyme disease; epidemic relapsing fever; endemic relapsing fever; Lyme borreliosis; infection; diagnosis; characterisation; detection; ds.

Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3760 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clayton R, Dougherty BA, Fraser C, Lathigra R, Smith HO,
White OR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1401 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from: 1 to: 10502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 8
Gaps: 0
Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1402 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product- semaphorin I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: X20258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3939 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q87446 standard; cDNA; 2504 BP.
                                                                                                                          X20258 standard; DNA; 10502 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355. .2493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-653-294-15 x X20258/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUN-1998; U12764.
03-SEP-1997; US-057483.
20-JUN-1997; US-050359.
22-JUL-1997; US-053374.
                                seq_name: N_Geneseq_36:x20258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: N_Geneseq_36:Q87446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 4.125
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10502 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-1995.
13-SEP-1994; UI0151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 99-081217/07.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                    WO9858943-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lyme disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09507706-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                       30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aliqnment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            087446;
```

to: 2504

632 T;

614 G;

```
syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.

Sequence 150 BP; 38 A; 38 C; 32 G; 41 T;
      8888888888
```

Length: 8
Gaps: 0
Percent Identity: 62.500 alignment\_block: US-08-653-294-15 x X12081/rev alignment\_scores:
Quality: 32.00
Ratio: 4.000
Percent Similarity: 100.000

to: 150 from: 1 Align seg 1/1 to reverse of: X12081

```
D73590 CELK060G3F Yuji Kohar
D74728 CELK084F3F Yuji Kohar
D75423 CELK104C7F Yuji Kohar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Location="trypanosoma bruce;"
/db_xref="taxon:5691"
/clone="sheared DNA-2ZR17"
/clone="sheared DNA-2ZR17"
/clone=lb="sheared DNA-ZZR17"
/clone=lb="sheared DNA-ZZR17"
/clone=lb="sheared DNA-ZZR17"
/clone=lb="sheared DNA-ZZR17"
/note="vector: pUcl8; Site_1: Smal; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma bruce! (TREU927/4 GUTAt 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb): The v + 1 method used for the library construction is described in detail in Smith, H.O. and Venter, JC. (Making small insert libraries for whole genome shotgun sequencing projects: In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barelli, Oxford University Press, 1999): "...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma.

1 (bases 1 to 491)
El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujil,C., Gerard,C., Leech,V., de Jong,P., Ullu,E., Melville,S.,
Donelson,J., Fraser,C. and Adams,M.
Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library
                                                                                                                                                                                                                                                 AQ652500 491 bp DNA GSS 22-JUN-1999
Sheared DNA-22K17.TF Sheared DNA Trypanosoma brucei genomic clone
Sheared DNA-22K17, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
Clones are derived from the TrgR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: M13-Forward
Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trypanosoma brucei.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
Other GSSs: Sheared DNA-22K17.TR
Contact: Najib M. El-Sayed
Contact: Najib M. El-Sayed
Contact: Najib M. El-Sayed
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 9
Gaps: 0
Percent Identity: 77.778
360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from: 1
160.90
160.90
160.90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to reverse of: AQ652500
130.80
130.80
130.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQ652500
AQ652500.1 GI:5145686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-15 x AQ652500/rev
36.00
36.00
36.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 4.333
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.00
                                                                                                                                               seq_name: gb_gss15:AQ652500
                                                                                                                                                                                                               seq_documentation_block:
LOCUS AQ652500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores
gb_est5:D73590
gb_est5:D74728
gb_est5:D75423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                      ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Documentation .. | A0652500 Sheared DNA-22KI7.TF S | AA10573 m184g04.rl Stratagene | AA10573 m184g04.rl Stratagene | AA37241 UI-M-AKO-ade-f-09-0-UI | AA40214 zf03b05.rl Soares_feta | AA040214 zf03b05.rl Soares_feta | AA040214 zf03b05.rl Soares_feta | AA106940 m192h06.rl Stratagene | A1413784 me91h02.xl Soares mous | AA465578 aa24f06.rl NCI_CGAP_G7 | AM048963 UI-M-BHI-amo-q-04-0-UI | AA45776 yx69909.rl Soares_melancy | AA137143 zl02f08.rl Soares_preg | AA137144 zl02f08.rl Soar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A40169324 yy38f03.rl Soares meland
A4016922 zk32f05.rl Soares_preg
W8810 zb72g01.rl Soares_preg
A443708 ve81b03.rl Soares_preg
A443708 ve81b03.rl Soares_preg
A443970 ab05h01.rl Soares_preg
A4489970 ab05h01.rl Soares_preg
N3340 yz03f12.rl Soares_meland
A489970 ab05h01.rl Soares_meland
A489970 ab05h01.rl Soares_meland
A489970 ab05h01.rl Soares_preg
W2057 898009.rl Knowles Sol
A4632641 np87b04.sl Knowles Sol
A463267 cv17b09.xl NCL_CGAP_PR
A105578 vy86009.rl NCL_CGAP_PR
A105578 wy86009.rl NCL_CGAP_PR
A105518 wy86000.xl NCL_CGAP_PR
A105518 wy85000.xl NCL_CGAP_PR
A8897536 aj62e11.sl Soares_test
A8897536 wy85000.xl NCL_CGAP_PR
A105518 wy85000.xl NCL_CGAP_PR
A105519 uo60510.xl NCL_CGAP_PR
A105519 uo60510.xl NCL_CGAP_PR
A105519 uo60510.xl NCL_CGAP_PR
A105528 dy85200.xl NCL_CGAP_PR
                                                                                                                                                                                                                                             Command line parameters:

MODEL=frame+_p2n.model_DEV=x1p

-q-/cgnl_l/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.1

-q-/cgnl_l/USPTO_spool/US08653294/runat_04022000_160700_15770/app_query.fasta.1

-DB=EST -0PMT=fastap -SUFFTX=rst -GAPOP=12.000 -GAPDXT=4.000

-MINNATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GGAPOP=4.500

-GGAPEXT=0.050 -KGAPOP=10.000 -KGAPEXT=0.500 -FGAPOP=6.000

-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000

-DELEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000

-DELEXT=7.000 -YGAPOP=10.000 -YGAPOP=0.000

-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE-LOCAL

-OUTPWT=pfs -NORM=ext -MINLEN=0 -MALLEN=1000000 -USER=US08653294

-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                               About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESCOTE L ESC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  250076
11399.00
1399.00
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.40
1399.4
       to: EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search information block:
Query: US-08-653-294-15
Query length: 10
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31 700
31
                                                                               Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strd
   OM Of: US-08-653-294-15
                                                                           4:03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9b_est8 AA040214

9b_est9:AA085256

9b_est9:AA106940

9b_est27:A1413784

9b_est15:AA465578

9b_est18:AA048963

9b_est18:AA048963

9b_est18:AA048963

9b_est18:AA048963

9b_est18:AA048963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est5:H87502
gb_est9:AA114917
gb_est15:AA489970
gb_est6:N53340
gb_est5:N34201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est22:AI005191
gb_gss8:AQ036625
gb_est25:AI310218
gb_gss3:B29703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_est6:N46203
gb_est8:AA036922
gb_est7:W88510
gb_est14:AA423708
                                                                           Date: Feb 8, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gb_est37:A1956148
gb_est20:AA897536
gb_est36:A1888684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_est18:AA674758
gb_est17:AA632641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est38:AW027634
gb_est30:AI635238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est9:AA105773
gb_est6:N92217
gb_est35:AI837241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est22:AI066787
gb_est44:AW192536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_gss15:AQ652500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est9:AA122242
gb_est7:W22057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est39:AW130547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_est17:AA648974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est5:D75467
gb_est5:D73508
```

sed\_name:

ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS

TITLE JOURNAL COMMENT

```
N92217 22 bp mRNA EST 04-APR-1996 y290d07.r1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:290317 5' similar to gb:X56253_rnal CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);contains element THR repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia) digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from 4 multiple sclerosis G. Becker (NIDS/NIH).

G. Becker (NIDS/NIH).

a 48 c 47 g 75 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="male"
/tissue_type="multiple sclerosis lesions"
/dev_stage="multiple sclerosis l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: estewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ETPFIME.
High quality sequence stop: 47.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata; Vertebrata, Mammalia, Butheria, Primetes; Catarrhin; Hominidae; Homo.

1 (Dases I to 223)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-Merck EST Project
Unpublished (1995)
On Sep 21, 1992 this sequence version replaced gi:276322.
Contact: Wisson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .222
/organism="Homo sapiens"
/db_xref="cDB :3906157"
/db_xref="taxon:9606"
/clone="IMAGE:290317"
/clone_llb="Soares_multiple_sclerosis_2NbHMSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: N92217
                                                                                                                                                                                                                                                        N92217.1 GI:1264526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-08-653-294-15 x N92217/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .700
seq_documentation_block:
LOCUS N92217
DEFINITION y290407.r1 So
                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                   uman.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                           SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Eutheria; Marra M., Hiller,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B., The ising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
The Mashu-HHMI Mouse EST Project
Unpublished (1996)
On Apr 14, 1993 this sequence version replaced gi:693450.
Contact: Marra M./Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HMI Mouse EST Project
Fax: 314 286 1800
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                        seq_documentation_block:
Locus AAL05773 189 bp mRNA EST 04-FEB-1997
DEFINITION m184g04.rl Stratagene mouse kidney (#937315) Mus musculus CDNA clone IMAGE:518742 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:312>yu
Putative full length read
vector to vector length is 372
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 140.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to reverse of: AA105773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="females"
                                                                                                                                                                                                                                                                                  AA105773.1 GI:1654862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
us-08-653-294-15 x AA105773/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ၁
09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.00
4.625
88.889
                                 gb_est9:AA105773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
```

FEATURES

seq\_name: gb\_est6:N92217

Align seg 1/1

BASE COUNT ORIGIN

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

MEDLINE JOURNAL

```
/db_xref="taxon:9506"
/db_xref="taxon:9606"
/clone="IMAGE:375825"
/clone="IMAGE:375825"
/clone="IMAGE:375825"
/clone="IMAGE:375825"
/clone="the="search" | fetal="theart_NDHH19W"
/sex="unknown"
/dev_stage="l9 weeks"
/dev_stage="l9 weeks"
/dev_stage="l9 weeks"
/dev_stage="l9 weeks"
/dev_stage="l9 weeks"
/dev_stage="lb weeks"
/dev_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butharyota; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 285)
11 (bases 1 to 285)
12 (bases 2 to 285)
13 (bases 3 to 285)
14 (bases 4 to 285)
15 (bases 5 to 285)
16 (bases 6 to 285)
17 (bases 7 (bases 11, B.)
18 (bases 7 (bases 11, B.)
18 (bases 1, Bases 11, B.)
18 (bases 1, Bases 1, Base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                      Length: 10
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
t
to: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
                                                                                                              111 THIFFILL THEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ρ
                                                                          σ
   from: 1
                                                                          1 TyrArgLeuLeuIleArgLeuAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA040214.1 GI:1516490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        O 09
to: AI837241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 37.00
Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NDHL19W
                                                                                                                                                                                                                        seq_name: gb_est8:AA040214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence contained an oligo-dr track that was present in the oligonuclectide that was used to prime the synthesis of first strand cDNB and therefore this may represent a bonafide poly A tail. The sequence tag present in the CDNA between the NotI site and the oligo-dr track served to verify it as a clone from the non-normalized hypothalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP CDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP CDNA clones, this record will be updated accordingly when that means is determined. Seq primer: MI3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodenita; Sciurognathi; Muridae; Murinae; Mus.
I (bases 1 to 275)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                         AI837241 275 bp mRNA EST 14-JUL-1999 UI-M-AKO-ade-f-09-0-UI.S1 NIH_BMAP_MHY Mus musculus cDNA clone UI-M-AKO-ade-f-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Jun 5, 1998 this sequence version replaced gi:3188055. Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .275
/organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Rés. 6 (9), 791-806 (1996)
97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_LIB=NIH_BMAP_MHY
TAG_TISSUE=hypothalamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                              AI837241.1 GI:5471494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.00
4.625
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-653-294-15 x AI837241
                               seq_name: gb_est35:AI837241
                                                                                                              seq_documentation_block:
LOCUS AI837241
                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                               AI837241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
```

source

FEATURES

BASE COUNT

alignment\_block:

DEFINITION

ORGANISM

SOURCE

REFERENCE AUTHORS

TITLE JOURNAL MEDLINE COMMENT

ACCESSION VERSION KEYWORDS

```
H87592 344 bp mRNA EST 21-NOV-1995 W1790B.rl Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:252442 5' similar to 9b:X56253 rnal CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stops: 330
Source: INAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (life@inage.llnl.gov) for further information.
Insert Length: 658 Std Error: 0.00
Seq primer: MI3RPI
High quality sequence stop: 330.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases, 1 to 344)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le.M., Lenono,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Materston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-Merck EST Project
Unpublished (1995)
On Apr 14, 1993 this sequence version replaced gi:635818
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                    to reverse of: AA085256 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .344
/organism="Homo sapiens"
/db_xref="GDB:3885608"
                                                                                                                                                                                                                                                                                            1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                 128 TACCAGCTTTTACTACAAATGGATGAAAGA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.Fatima Bonaldo.
                                                                                                                                                US-08-653-294-15 x AA085256/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H87592.1 GI:1069171
Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est5:H87592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              numan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores
                                                                                                                                                                                                                    Align seg 1/1
                                                                                                              alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zn12q08.rl Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
IMAGE:547262 5' similar to gb:X56253_rnal CATION-DEPENDENT
MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9666"
/clone="IMAGE:547262"
/clone="IMAGE:547262"
/dcove_stage="tayone hwr neuron (#937233)"
/dab_host="SOLR (kanamycin resistant)"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dr.
Differentiated, post mitotic hwr neurons. Average insert size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCACGAG 3' a. 3' adaptor sequence: 5'
GAATTCGCCACGAG 3' a. 3' adaptor sequence: 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 328)
11 (bases 1 to 328)
11 (bases 1 to 328)
11 (bases 2 to 328)
11 (bases 3 to 328)
11 (bases 4 to 328)
11 (bases 5 to 328)
11 (bases 6 to 328)
11 (bases 7 to 10 to 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: estewarson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should likept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807\text{-}828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 670 Std Error: 0.00 Seq primer: -28M13 reof from Amersham High quality sequence stop: 198.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 5, 1995 this sequence version replaced gi:797884 Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                to: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                            Align seg 1/1 to reverse of: AA040214 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .328
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTCGAGTTTTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                              216 TACCAGCTTTTACTACAAATGGATGAAAGA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GDB:3925452"
                                                                                                                                                                                                                    1 TyrArgLeuLeulleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA085256
AA085256.1 GI:1627314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 bp
                                                                    US-08-653-294-15 x AA040214/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37.00
                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est9:AA085256
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AA085256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores
```

10

BASE COUNT

ORIGIN

FEATURES

to: 351

```
1 (bases 1 to 398)

Marra, M., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylle, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,
Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Haterston, R. and Wilson, R.
Unpublished (1999)

On Apr 21, 1998 this sequence version replaced gi:3071892.
Contact: Marra M/Mashu-NCI Mouse EST Project 1999
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4444 Forest Park Parkway. Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Tel: 314 286 1800
Email: Moseest@atson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. 
High quality sequence stop: 375.
                                                                                                                                                                                                                                                                                            AI413784 398 bp mRNA EST 09-FEB-1999 me91h02.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:402963 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:402963"
/clone_llb="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 9
Gaps: 0
Percent Identity: 88.889
                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .398 // /Organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                             162 TACCTCCTCCTCATCAGACTGGATGAG 136
                                                              to reverse of: AA106940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 g
                                                                                                                     σ
                                                                                                                     1 TyrArgLeuLeuIleArgLeuAspGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI413784.1 GI:4257288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="unknown
   US-08-653-294-15 x AA106940/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37.00
4.625
88.889
                                                                                                                                                                                                                                              seq_name: gb_est27:AI413784
                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS A1413784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Manmalia, Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Manmalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus. 1 (bases 1 to 351).

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The Washu-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marsa M/Mouse EST Project
Washington University School of Medicinep
Washington University School of Medicinep
H444 Forest Park Parkway, Box 8501, St. Louis, Mo 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="InAGE:519515"
/clone_11b="Stratagene mouse kidney (#937315)"
/sex="females"
/tissue_Lype="kidney"
/tissue_Lype="kidney"
/dev_stage="4 weeks"
/lab_host="$colk (kanamycin resistant)"
/note="Organ: kidney; Vector: pBluescript SK-; Site_1:
/note: kidney; Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AA106940 351 bp mRNA EST 04-FEB-1997
DEFINITION m192h06.r1 Stratagene mouse kidney (#937315) Mus musculus cDNA clone IMAGE:519515 5' similar to 9b:M22810 Mouse androgen-regulated protein mRNA, complete cds (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps: 0
Gaps: 0
Percent Identity: 88.889
Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                          to: 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 448.
Location/Qualifiers
1. 351
/organism="Mus musculus"
/strain="c57/B16"
/db_xref="taxon:10090"
                                                                                                                                                                                       from: 1
                                                                                                                                                                                                                                                                                      1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                    Align seg 1/1 to reverse of: H87592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA106940.1 GI:1660749
EST.
                                                                                        alignment_block:
US-08-653-294-15 x H87592/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.625
Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.00
                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est9:AA106940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:313363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
```

ORIGIN

LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

sed\_name:

ORGANISM

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

```
Email: mESTemail.iih.gov

The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized pineal glands library cDNA Library Preperation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined. POLYA-YES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polylinker; Site_1: Not I; Site_2: Eco RI; The WILBARD M.S. library is a subtracted library derived from NIH_BMAP_M.S.1 which in turn is a subtracted library derived from a mixture of normalized libraries from ten regions of the mouse brain (cerebellum, brain stems, olfactory bulbs, hypothalamus, cortex, amydala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M.S.1 library and a pool of 5,000 clones obtained from non-normalized and normalized mouse brain
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 407)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                        AW048963 407 bp mRNA EST 18-SEP-1999 UI-M-BHI-amo-g-04-0-UI.sl NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BHI-amo-g-04-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UT-M-BH1-amo-g-04-0-UI"
/clone=lb="NHE BMAP_M-S2"
/dev_stage="127-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Mar 16, 1998 this sequence version replaced gi:2961735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 .407
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAG_LIB=NIH_BMAP_M_S2
TAG_TISSUE=pineal-glands
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 6 (9), 791-806 (1996)
97044477
205 TACCAGCTTTTACTACAAATGGATGAAAGA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAG_SEQ=AAGAC'
91 c
                                                                                                                                                                                                                                           AW048963.1 GI:5909492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     spinal cord
                                                                      gb_est38:AW048963
                                                                                                                                                                                                                                                                                         house mouse.
Mus musculus
                                                                                                                    seq_documentation_block:
LOCUS AW048963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                    AW048963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BASE COUNT
                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                         VERSION
KEYWORDS
                                                                           sed_name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                         SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA465578 402 bp mRNA EST 15-AUG-1997 and 402 bp mRNA saddf06.r1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:814211 5' similar to gb:X56253_rna1 CATION-DEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This clone is available royalty-free through LLNL; contact the IMMGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28ml3 rev2 Er from Amersham High quality sequence stop: 313.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Eutheria: Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 402)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           constructed by Bento Soares and M. Fatima Bonaldo." 87 c 106~g 119~t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumor Gene Index
Unpublished (1997)
On May 9, 1995 this sequence version replaced gi:802540.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:814211"
/clone_lib="NCI_CGAP_GCB1"
/tissue_type="germinal center B cell"
//lab.host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                to: 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1
                                                                      to: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="GDB:6032206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrArgLeuLeulleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
                                                                                                                 Align seg 1/1 to reverse of: AA465578
                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                             AA465578.1 GI:2191745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-08-653-294-15 x AA465578/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 37.00
Ratio: 3.700
Percent Similarity: 100.000
                                                                    to: AI413784
alignment_block:
US-08-653-294-15 x AI413784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .402
                                                                                                                                                                                                                  gb_est15:AA465578
                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AA465578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                    Align seg 1/1
```

00

BASE COUNT

₽

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 433)

Hillier,L. Lennon,G. Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rikin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thlerry-Med,J., Prayaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
97044478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1810
Fax: 315 180 180
Fax: 315 180 180
Fax: 315 180
Fax: 
                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AA.137143 433 bp mRNA EST 14-MAY-1997
LOCUS 2.102f08.r1 Socials_pregnant_uterus_NbHPU Homo sapiens CDNA clone
DEFINITION IMAGE:491175 5' similar to 9b.x56253_rnal CATION-DEPENDENT
MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Sep 12, 1996 this sequence version replaced gi:1393248.
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Homo sapiens"
/db_xref="GDB:3805762"
/db_xref=xxon:9606"
/clone="ImAcE:491175"
/clone_lib-"Soares_pregnant_uterus_NDHPU"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                       to: 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Gaps:
                                                                                                                       to reverse of: N28776 from: 1
                                                                                                                                                                                                                     129 TACCAGCTTTTACTACAAATGGATGAAAGA 100
                                                                                                                                                                                     1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA137143
AA137143.1 GI:1698378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
                                                          US-08-653-294-15 x N28776/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .433
                                                                                                                                                                                                                                                                                                             seq_name: gb_est10:AA137143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                alignment_block
                                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L Unpublished (1995)
Conteat: Wilson RX
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: esfewatson.wustl.edu
High quality sequence stops: 323
Source: IMAGE Consortium, Lint, This clone is available royalty free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 323.
High quality sequence stop: 323.
                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:

132 bp mRNA

LOCUS

128776

EST

04-JAN-1996

LOCUS

128776

DEFINITION yx69909.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone

IMAGE:267040 5' similar to 9b:X55253_rnal CATION-DEPENDENT

MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 432)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hollman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rikkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 10
Gaps: 0
Percent Identity: 60.000
Percent Identity: 88.889
                                                                                                                                                        407
                                                                                                                                                        <u>ب</u>
                                                                                                                                                                                                                                                   The WashU-Merck EST Project
                                                                                                                                                                                                                  1 TyrArgLeuLeulleArgLeuAspGlu 9
                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N28776.1 GI:1147012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouality: 37.00
Ratio: 3.700
Percent Similarity: 100.000
                                                                                                                                                     Align seg 1/1 to: AW048963
88.88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .432
                                                          alignment_block:
US-08-653-294-15 x AW048963
                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est5:N28776
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
```

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE TITLE JOURNAL COMMENT

source

FEATURES

BASE COUNT

ORIGIN

```
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 342.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N46203 14-FEB-1996
yy38f03.r1 Scares melanocyte 2NbHM Homo sapiens CDNA clone
IMAGE:273533 5' similar to 95:X56253_rnal CATION-DEPENDENT
MANNOSE-6-PHOSPHATE RECEPTOR PRECURSOR (HUMAN); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutherfa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 434; L. (bark,N.; Dubuque,T., Elliston,K., Hawkins,M.; Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Raikfu,L., Rohlfing,T., Soares,M., Tan,F., Treyaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1995)
On May 18, 1995 this sequence version replaced gi:811021.
Contact: Wilson University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares melanocyte 2NbHM"
                                                                                                                       Length: 9
Gaps: 0
Percent Identity: 88.889
                                                                                                                                                                                                                                                                                                                                                                                                                     to: 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .434
/organ1sm="Homo sapiens"
/db_xref="GDB:3883175"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:273533"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242 TACCTCCTCTCATCAGACTGGATGAG 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, R.
The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TyrArgLeuLeuIleArgLeuAspGlu 9
                                                                                                                                                                                                                                                                                                                                                                                                                     from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N46203.1 GI:1187369
                                                                                                                           37.00
4.625
88.889
                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AI849304
                                                                                                                                                                                                                                                                                         alignment_block:
US-08-653-294-15 x AI849304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
Locus N46203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_est6:N46203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human.
                                                                                         alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="CSTRELGG"
/strain="CSTRELGG"
/db_xref="taxon:1000"
/clone="UI-M-AJI-aha-b-09-0-UI"
/clone="UI-M-AJI-aha-b-09-0-UI"
/clone="UI-M-AJI-aha-b-09-0-UI"
/clone="UI-M-AJI-aha-b-09-0-UI"
/clone="UI-M-AJI-aha-b-09-0-UI"
/db_host="DHIOB (Life Technologies)"
/db_host="DHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 301 443 1706
Fax: 301 443 1706
Fax: 301 443 1706
Fax: 301 43 1706
Fax: 301 443 1706
Fax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AI849304 433 bp mRNA EST 15-JUL-1999 UI-M-AJ1-aha-b-09-0-UI.sl NIH_BMAP_MOB_N Mus musculus cDNA clone UI-M-AJ1-aha-b-09-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 433) Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              On Jun 22, 1998 this sequence version replaced g1:3247013. Contact: Chin, H Mational Institute of Mental Health 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD 20892-9643, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 others
    Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ų
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                         1 TyrArgLeuLeuIleArgLeuAspGluArg 10
                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 g
                                                                                                                                                                                                        from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AI849304.1 GI:5493210
                                                                            alignment_block:
US-08-653-294-15 x AA137143
                                                                                                                                                                                                        Align seg 1/1 to: AA137143
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est35:AI849304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   house mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POLYA-Yes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97044477
```

BASE COUNT ORIGIN

SOURCE

AUTHORS TITLE

REFERENCE

JOURNAL MEDLINE COMMENT

FEATURES

DEFINITION

ACCESSION VERSION KEYWORDS

を からいい

alignment\_scores:

Quality: 37.00 Length: 10
Ratio: 3.700 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 60.000

alignment\_block: US-08-653-294-15 x N46203/rev

Align seg 1/1 to reverse of: N46203 from: 1 to: 434

THIS PAGE BLANK (USPTO)

.

OM protein - protein search, using sw model

Run on:

8, 2000, 01:29:38 February

Search time 122.56 Seconds (without alignments)
2.319 Million cell updates/sec

US-08-653-294-16 Title: Perfect score: Sequence:

1 YRLLIRRILLRY 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 seqs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	-B2702 84-79-8	B2702	pg	Į,	HLA-B2702 84-75-84	nomodula	recepto	PGE2 receptor codi	aglandi	aglandi	Prostaglandin-EP3-	Human prostaglandi	Human EP3-V recept	a	Polyprotein of DEN	U	Yeast transcriptio	H-Delta-1 polypept	CREB binding prote	Cellular transcrip	Actinobacillus ple	nct	Human proteasome c	~	din end	Human DNAX toll-11	)epti	Peptide contg. alt	tant pept	Curvularia verrucu	atfis	in with	thermally	ORF10 glycosylase.
SUMMARIES		ΠD	~	3379	379	290	542	377	228	228	951	951	951	741	741	559	59	346	382	N	905	005	173	151	296	2	S)	35	9	55	13	3	618	R52029	1170	73
		BB	7	-	7	-	٦	Н	-	-	٦	Н	Н	٦	-	Н	٦	٦	П	П	П	-	Н	Н	Н	1	Н	Н	Н	Н	П	М	Н	Н	Н	П
		Length	12	12	12	20	20	20	9	9	9	æ	9	σ	0	39	3391	9	4	9	4	44	m	ø	9	0	σ	0	15	21	21	40	ω	216	2	N
	ery	Match		•	٠			•			•		•	٠			6.9					٠	•		•		•							1.7		
•	* ă	Ma	œ	œ	œ	ŝ	õ	ភ	Ñ	ŝ	ñ	ຮັ	ŝ	ñ	ñ	Ñ	ഗ്	ហ	Š	ŝ	īΩ	ī	ŝ	Ŋ	ìΫ́	က်	'n	က်	က်	'n	ίς	ķ	'n	į,	ίς	5
		Score	48	48	48	34	34	34	34	34	34	34	34	34	34	33	33	32	32	32	32	32	31	31	31	31	31	31	30	30	30	30	30	30	30	30
	Result	No.	Н	7	m	7	'n	9	7	∞	σ'n	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

Thymine DNA glycos Neuronal nicotinic Curvularia verrucu Chloroperoxidase. Rat VRRP-1 (VRZ) c Human transient re Virulence gene clu Immunomodulatory p Immunomodulatory p Peptide #3 used in Peptide #4 used in	ALIGNMENTS			<pre>HLA: p74; alpha1-helix; human-leucocyte-associated antigen; inhibitor; T-cell lysate; membrane protein; mammal; heat shock protein; Hsof); APC; B. cell caldim 4.4 http://doi.org/10.1006</pre>						Compsns. comprising lymphoid surface membrane proteins - which may		alindromes and iragments o This sequence represents	se sequences can be used to isolate e. p74 is a T-cell surface membrane	protein associated with T-cell activation in mammalian T-cells, and is	also immunologically cross reactive with the heat shock protein Hsc70. p74 is found in a limited number of cell types, but is particularly	expressed on B and T cells. p74 can be isolated by lysis of a suitable	cell with an amphoteric detergent, and then passed through an arinnity column containing a covalently bound HLA-B2702 palindromic peptide.	Compositions comprising the extracellular fragment of p74 combined with	
W81465 W09022 W12042 W99790 W55961 W47264 W47264 W33783	ALIG	AA.	<u>e</u>	in-leuco lein; ma	g cell.			93. STANFORD JUNIOR		surfac	lish.	present intigens	ne. The Ll lysat	ell acti	reactive umber of	p74 ca	ergent, :ly boun	extrace	differ
нанананана		; 12	y)	humi prot	it i			FORI	Ξ̈́	hoid	Eng.	l re	drog -ce]	Ď-E	ຣຣິມ	13.	dete	the	1 I I
222 5020 6000 7000 7000 7000 7000 7000 7000 7		standard; peptide;	st entr	helix; ambrane	n prese		U12985.	20	Krensky AM; /25.	ng lymp	29pp;	5-R9543 ssociat	14 palin	d with	illy cro	d T cel	oteric   a cova	rising	ocyte (
51.7 51.7 51.7 51.7 51.7 50.0 50.0 50.0		ģ	f11	lal.	196		1129	S-1	X 2	131	12;	1541 16-8	20 44 20 44	ate	110	a a	idu.	JIIO.	i E d
	•	ıdar	34-7	ate;	ant	ij.			C,	Z D	ge	ocyt Str	34 - 7 70 c	2001	2 2 2 2 2 3	E .	an a Cain	20.00	יין היי אור היי
00000000000000000000000000000000000000		1 95429	95429; 2-NOV-1996 LA-B2702	LA; p74; c-cell lyse	cytolysis; antigen presenting	WO9513288-A1	10-NOV-1994;	10-NOV-1993; US-1504 (STRD ) UNIV LELAND	Clayberger C, Kre WPI; 95-194027/25.	ns.	xample; Pa	Uman-leuc	HLA-B2702 84-79-84 palindrome. These the protein p74 from a T-cell lysate.	rotein ass	lso immund 74 is four	xpressed	ell with a olumn cont	omposition	cytotoxic 1
W W W W W 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4		54.3	AC DI DE 1							-		8 8 8 8						-	

compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracelular portion of p74 and determining the amount of binding between the candidate compound and p74. Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.

888888888

; 0 Score 48; DB 1; Length 12; Pred. No. 0.0038; 0; Mismatches 2; Indels 82.8%; 83.3%; Query Match 82.8 Best Local Similarity 83.3 Matches 10; Conservative

ö

Gaps

||| |||| |||| | YRLAIRRIALRY 12 1 YRLLIRRILLRY 12 ò g

7 RESULT W33798 ID W33 AC W33

W33798 standard; peptide; 12 AA. W33798;

~

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
R92907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             đ
   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                         The immunomodulating dimer peptide(s) - based on a Class I HiA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimune diseases.

Trample 1: Page 198 and W33778-9 were assayed for their immunomodulating cativity. A peptide-type compound or variant is claimed which has a citivity. A peptide-type compound or variant is claimed which has cativity. A peptide-type compound or variant is claimed which has compound activity, including the N-terminal acylated and/or creminal amidated or estavitied forms of up to 60 anino acids, where the peptide-type compound comprises the formula: A-B, where A, B = CC (R aa76-71) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CC Small amino acid; aa82 = R or L; aa83 = G or R; and as represents amino acid sequences in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HiA-B alphal domain (positions of a tany peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HiA-B alphal domain (positions of 19-84). They can be used to inhibit the proliferation of interest to cativate CTLS. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proliferation of reliance of transplants or for treating autoimmune diseases, e.g. diabetes, and also he was a starthritis and lupus erythematosis. The products can also be used for preventing relection and also he was a condition and also he was a c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 17; Page 35; 41pp; English.
This sequence represents a specifically claimed immunomodulating
dimer peptide of the invention. A peptide-type compound or variant is
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autodimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-JUN-1998 (first entry)
Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunomodulating dimer peptide(s) - based on a Class I HLA-1 alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 48; DB 1; Length 12;
Pred. No. 0.0038;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                             24-MAY-1996, US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                           Beulow R, Clayberger C, Krensky AM; WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W33799 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 83.3'
Watches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                    22-MAY-1997; U08689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
WO9744351-A1.
                                                                                                                                                                             Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rejection.
                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    m
NEW TOOLS OF COLOR OF THE PROPERTY OF THE PROP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
```

```
claimed which has immunomodulating activity, including the N-terminal actypated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B -(R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a pydrophobic or small amino acid; aa80 = I or N; aa81 = G or R; and are represents amino acid; aa82 = R or L; aa83 = G or R; and are represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (7TL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proliferation of I cells in response to anti-CD3. The peptide can be proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus errythematosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to abuther administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clayberger C, Krensky AM, Parham P;
WPI; 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched
donor hosts - using Class I B75-84 MHC antigen of the recipient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82.8%; Score 48; DB 1; Length 12; 83.3%; Pred. No. 0.0038; 1ive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58.6%; Score 34; DB 1
50.0%; Pred. No. 2.4;
11ve 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO93-2-OCT-1995.
05-APR-1995; U04349.
05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R92907 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLLIR-----RILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Similarity 83.3%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLAIRLNERRENLRIALRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ||| |||| |||
| YRLAIRRIALRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 10; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
WO9526979-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The products
Sequence 12
```

```
N-PSDB; Q46125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
                                                                                                                                                                                                                                                                                                   The products
Sequence 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP-557966-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
R42281
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   While of 191940.7. The compensation of cris.

Tomposes. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of Cris.

Example 12, 20pp; English.

RS413, and RS5415.R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the than 18702 84-75-84 palindrome. These sequences can be used to isolate the protein associated with T-cell activation in mammalian T-cells, and is a liam uncologically cross reactive with the heat shock protein Hsc70. Protein associated with T-cell activation in mammalian T-cells, and is a liam to all mitted number of cell types, but is particularly cypressed on B and T cells. Pl4 can be isolated by lysis of a suitable expressed on B and T cells. Pl4 can be isolated by lysis of a suitable column containing a covalently bound HiA-B2702 palindromic peptide.

Column containing a covalently bound HiA-B2702 palindromic peptide.

Compositions comprising the extracellular fragment of p74 combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis. Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the mount of binding between the candidate composation containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete with p74 for the binding of the p74 ligand.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ï
                                                     12-NOV-1996 (first entry)
12-NOV-1996 (first entry)
14.A B2702 84-75-84 palindrome.
15.ALA 1702 84-75-84 palindrome.
16.ALA 1702 84-75-84 palindrome.
17.Cell 19sate; membrane protein; mammal; heat shock protein; Hsc70; APC;
18.Cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation;
17.Cytolysis; antigen presenting cell.
17.Cytolysis; antigen presenting cell.
18.Cytolysis; antigen presenting cell.
18.Cytolysis; antigen presenting cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1998 (first entry)
Immunomodulating dimer peptide #1.
Immunomodulating dimer; Immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.6%; Score 34; DB 1; Length 20; 50.0%; Pred. No. 2.4; 2; Indels live 0; Mismatches 2; Indels
                                                                                                                                                                             18-MAY-1995.
10-NOY-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W33778 standard; peptide; 20 AA.
                            R95428 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 YRLLIR-----RILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 58.6
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
WO9744351-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W33778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
            R95428
                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
treating autoimmune diseases

Claim 16; Page 35; 41pp; English.

Claim 16; Page 35; 41pp; English.

Claimed which has immunomodulating activity including the N-terminal acylated and/or c-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V, aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa80 = I or N; aa31 = G or R; and as represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B compounds comprise amino acid sequences related to a class I HLA-B compounds (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antiqenic peptides or proteins of Interest to activate CTLs. They can also inhibit the cused for preventing rejection of transplants or for treating autoimmune cused for preventing rejection of transplants or for treating autoimmune cused for preventing rejection of transplants or for treating autoimmune cused for preventing rejection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New prostaglandin E receptor protein and DNA encoding it - used to study prostaglandin binding, agonists and antagonists etc. Claim 5, 10; Figure 4; 22pp; English.
The prostaglandin E receptor can be used to clone other PGE receptor genes, to clarify the structure of PGE receptors, to elucidate the function of PGE and to identify PGE agonists/ antagonists. The receptor is produced by recombinant methods,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGE2 receptor coding sequence (Clone MP653).
Prostaglandin E receptor; prostaglandin; binding; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%; Score 34; DB 1; Length 20; 50.0%; Pred. No. 2.4; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109. .130
/label- Transmembrane domain 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           260. .283
/label= Transmembrane domain 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59. .89
/label= Transmembrane domain 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- Transmembrane domain 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .55
|abel= Transmembrane domain 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label- Transmembrane domain 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R42281 standard; Protein; 361 AA. R42281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-1993,
24-FEB-1993, 102873.
24-FEB-1992, JP-036580.
23-MAR-1992, JP-064889.
(TAKE ) TAKEDA CHEM IND LTD.
ICHİKAWA A, NARUMIYA S;
WPI; 93-274435/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLLIR-----RILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 YRLAIRLNERRENLRIALRY 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-FEB-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 58.6
Best Local Similarity 50.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label-
```

ä

```
Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
                                                                                                                                                                           SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SE
                                                                                                       g
                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               셤
                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                      Gaps
transforming a host cell, culturing the cell and retrieving the recombinant protein from the culture medium. This PGE2 receptor is a derivative of the clone MP660 (046124) having 89 base pairs deleted from the coding sequence resulting in replacement of 30 C-terminal amino acids with a different sequence of 26 amino acids. Sequence 361 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label- Phosphorylation site.
/note- Phosphorylation is by cAMP protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New prostagiandin E receptor protein and DNA encoding it - used to study prostaglandin binding, agonists and antagonists etc. Claim 10; Figure 1; 22pp; English.

The prostaglandin E receptor can be used to clone other FGE receptor genes, to clarify the structure of FGE receptors, to elucidate the function of FGE and to identify FGE agonists/ antagonists. The receptor is produced by recombinant methods, transforming a host cell, culturing the cell and retrieving the recombinant protein from the culture medium.
                                                                                                                                                                                                                      ö
                                                                                                                                                                           58.6%; Score 34; DB 1; Length 361;
llarity 77.8%; Pred. No. 46;
Conservative 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-1994 (first entry)
PGE2 receptor coding sequence (Clone MP660).
Prostaglandin E receptor; prostaglandin; binding; agonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Phosphorylation site.
/note= Phosphorylation is by cAMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tabel- N-glycosylation site.
11. .55
| Transmembrane domain 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     260. .283
/label= Transmembrane domain 6.
304. .325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label = Transmembrane domain 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      109. .130
/label- Transmembrane domain 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- Transmembrane domain 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               152. 173
/label- Transmembrane domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label- N-glycosylation site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label- Transmembrane domain 260. .283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                R42280 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Narumiya S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-SEP-1993,
24-FEB-1993, 102873.
24-FEB-1992, JP-036580.
23-MAR-1992, JP-064889.
                                                                                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ichikawa A, Narum
WPI; 93-274435/35.
                                                                                                                                                                                                                                                                                                     323 LLLRKILLR 331
                                                                                                                                                                                                                                                             3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; 046124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP-557966-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antaqonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                         RESULT
  888888
                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

DB 1; Length 365;

58.6%; Score 34;

Query Match

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New prostaglandin EP3 receptors and DNA - used partic. to identify medulators of prostaglandin receptor activity for transment of diseases.

Claim 2; Page 43-45; 64pp; English.

Claim 2; Page 43-45; 64pp; English.

The sequence represents a human uterus prostaglandin-EP3-9

Transment of mil. wt. 40,507). The sequence contains 4 conserved

N-glycosylation sites in putative extracellular regions, and a conserved region (R69515) in transmembrane region-VII common to other EP3 receptors. Conserved Aps residues are found in exofacial loops I and 2, and a conserved Aps found in all elocation in any be used to identify receptor-agonists and receptor-antagonists, for use in therapy of e.g. glaucoma, side-effects of non-steroidal antilniammatories, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338. .345 /
/note= "conserved sequence in EP3 receptors"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-1994; CA0320.
25-JUN-1993; US-083746.
(M-RI) ) MERCK FROSST CANADA INC.
Abramovitz M, Adam M, Boie Y, Metters K, Rushmore TH; WPI; 95-052012/07.
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 1;
Pred. No. 46;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note- "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note- "N-glycosylation site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-SEP-1995 (first entry)
Prostaglandin-EP3-21 receptor.
Human uterus prostaglandin-EP3-21 receptor;
prostaglandin-EP3 receptor-agonist;
prostaglandin-EP3 receptor-agonist;
                Pred. No. 46;
                                                                                                                                                                                                                                                              R69518;
02-SEP-1995 (first entry)
Prostaglandin-EP3-9 receptor.
Human uterus prostaglandin-EP3-9 receptor;
prostaglandin-EP3 receptor-agonist;
prostaglandin-EP3 receptor-agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note- "N-glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metastasis, renal vasoconstriction, etc
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
77.8%; FL.
                                                                                                                                                                                                                                         R69518 standard; Protein; 365 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R69517 standard; Protein; 388
R69517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.6%;
77.8%;
                Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 7; Conserv
                                                                                                        ||:|:||||
323 LLLRKILLR 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:|:||||
347 LLLRKILLR 355
                                                                                 3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 95-052012
N-PSDB; Q81951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified_site
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9500552-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R69517
ID RC
DT OC
DT OC
C DE PO
KW HU
```

```
New human prostaglandin EP3 receptor(s) - useful for treatment and prevention of, e.g. inflammation

Drevention of, e.g. inflammation

Drevention of, e.g. inflammation

Everyther and a sequences.

This represents a human EP3-VI receptor. A replication or expression vector comprising cDNA sequences encoding EP-3V or EP3-3VI can be used to transform a host cell. The host cell is cultured and the polypeptides can be recovered from the culture medium. The polypeptides combine specifically with a prostaglandin PGEZ receptor and can be used as a preventive and treating agent for inflammation.
                                                                             New prostaglandin EP3 receptors and DNA - used partic. to identify modulators of prostaglandin receptor activity for treatment of diseases.

Treatment of diseases.

Claim 2: Page 40-41: 64pp: English.

Claim 2: Page 40-41: 64pp: English.

The sequence represents a human kidney prostaglandin-EP3-alpha receptor (mol. Wt. 43.315). The sequence contains 4 conserved normalizes in putative extracellular regions, and a conserved region (R69515) in transmembrane region-VII which has been used to generate a probe for isolation of other EP3 receptor genes. Conserved Arg found in all eicosanoid receptors is found in transmembrane region-VII. The receptor molecular and receptor-agonists and receptor-antagonists, for use in therapy of e.g. glaucoma, side-effects of non-steroidal antiinflammatories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-AUG-1998 (first entry)

Human prostaglandin EP3-VI receptor.

Prostaglandin E2 receptor; EP3-V receptor; human; treatment; inflammation; EP3-VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58.6%; Score 34; DB 1; Length 393; 77.8%; Pred. No. 50; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 1; Length 390;
Pred. No. 49;
2; Mismatches 0; Indels
                      Adam M, Boie Y, Metters K, Rushmore TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W57410 standard; Protein; 402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W57411 standard; Protein; 393 AA.
(MERI ) MERCK FROSST CANADA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.6%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-MAY-1998.
14-OCT-1996; 291150.
14-OCT-1996; JP-291150.
(ONOY) ONO PHARM CO LTD.
WPI: 98-313474/28.
N-PSDB; V29611.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W57410;
19-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 77.8'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 58.6
Best Local Similarity 77.8
Matches 7; Conservative
                        Abramovitz M, Adam
WPI; 95-052012/07.
N-PSDB; Q81949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|:||||
347 LLLRKILLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|:||||
347 LLLRKILLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
J10113185-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W57411;
19-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
W57410
      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DA P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        New prostaglandin EP3 receptors and DNA - used partic. to identify modulators of prostaglandin receptor activity for treatment of diseases.

Claim 2: Page 42-43; 64pp; English.

Claim 2: Page 42-43; 64pp; English.

The sequence represents a human uterus prostaglandin-EP3-21

The sequence contains 4 conserved

C N-glycosylation sites in putative extracellular regions, and a conserved region (R69515) in transmembrane region-VII common to other EP3 receptors. Conserved Cys residues are found in other EP3 receptors. Conserved Cys residues are found in exceptoral loops 1 and 2, and a conserved Arg found in all elocation receptor any be used to identify receptor agonits and creceptor any be used to identify receptor agonits and creceptor any be used to identify receptor agonits and conserved Cys receptor any be used to identify receptor agonits and conserved cys receptor and conserved cys glaucoma, side-effects of non-steroidal antiinflammatories, cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.6%; Score 34; DB 1; Length 388; 77.8%; Pred. No. 49; 1.1ve 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338. .345
/note= "conserved sequence (R69515) used
construct probe (Q81948)"
                                                                                                                                                                                                                                                                                                                                                                 Adam M, Boie Y, Metters K, Rushmore TH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prostaglandin-Ep3-alpha receptor.
Human Kidney prostaglandin-Ep3-alpha receptor;
prostaglandin-Ep3 receptor-agonist;
prostaglandin-Ep3 receptor-antagonist.
                                                                                        /note= "N-glycosylation site"
217
                                                                /note= "N-glycosylation site"
                                                                                                                                                'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "N-glycosylation site"
                                                                                                                                                                           /note= "N-glycosylation
338. .345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  metastasis, renal vasoconstriction, etc.
Sequence 388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
338. .345
                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    25-JUN-1993; US-083746.
(MERI ) MERCK FROSST CANADA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R69516 standard; Protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 58.6
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JAN-1995.
09-JUN-1994; CA0320.
25-JUN-1993; US-083746.
                                                                                                                                                                                                                                                                            05-JAN-1995.
09-JUN-1994; CA0320
                                                                                                                                                                                                                                                                                                                                                                                  WPI; 95-052012/07.
N-PSDB; Q81950.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 LLLRKILLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                   Abramovitz M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_site
                                          modified_site
                                                                                    modified_site
                                                                                                                              nodified_site
                                                                                                                                                                      modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified_site
      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      region
                                                                                                                                                                                                                   region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
```

R69516

ò g

ö

Gaps

ö

Gaps

```
modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nodified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHF; DSS
 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 15
W06590
 ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                 New human prostaglandin EP3 receptor(s) - useful for treatment and prevention of, e.g. inflammation (claim 2) Pages 16-17; 27pp; Japanese.

This represents a human EP3-V receptor. A replication or expression vector comprising cDNA sequences encoding EP-3V or EP3-3VI can be used to transform a host cell. The host cell is cultured and the polypeptides can be recovered from the culture medium. The polypeptides specifically with a prostaglandin PGE2 receptor and can be used as a preventive and treating agent for inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W06591;
12-SEP-1997 (first entry)
Polyprotein of attenuated DEN-2 virus, strain 16681, PDK-53.
Bengue 2 virus; polyprotein; capsid; prM; M; E; NSI, NS2A; NS2B; NS3; NS4A; NS4B; NS5; PDK-53; quadravalent vaccine; immunity; serotype; chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; bufferque fever; fatal dengue haemorrhagic fever; dengue shock syndrome; DHF; DSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "N-linked glycosylation site, encoded by NAC"
982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note- "N-linked glycosylation site, encoded by NAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "N-linked glycosylation site, encoded by NAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note- "N-linked glycosylation site, encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
Human EP3-V receptor.
Prostaglandin E2 receptor; EP3-V receptor; human; treatment; inflammation; EP3-VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 1; Length 402;
Pred. No. 51;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note= "N-linked glycosylation site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2. .114
/label=_Capsid_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W06591 standard; Protein; 3391 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1128. .1345
/label= NS2A
1346. .1475
/label= NS2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //6. .1127
/label= NS1
905
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              strain 16681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    115. .205
/label- prM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1476. .2093
/label= NS3
2094. .2242
/label= NS4A
                                                                                       06-MAY-1998.
14-OCT-1996; 291150.
14-OCT-1996; JP-291150.
(ONOX) ONO PHARM CO LTD.
WPI: 98-315474/28.
N-PSDB: V29610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            206. .280
/label= M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 281. .775
/label= E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             347 LLLRKILLR 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dengue 2 virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified_site
                                                      Homo sapiens.
J10113185-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             පු
ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PARTHER THE FELT THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE FOR THE SERVICE F
```

```
N-FSDB; 149304.

N-FSDB; 149304.

PW-53, a clone of infectious attenuated Dengue 2 virus strain 16681

- also chimeric DEN-2/1, DEN-2/3 and DEN-1/4 viruses, used as a quadravalent vaccine for protecting against Dengue virus infection class claim 27; Page 122-136; 261pp; English.

This sequence represents the polyprotein from attenuated Dengue 2 virus, strain 16681. The attenuated virus is designated PDK-53. The polyprotein comprises the capsid, prM, M, E, NS1, NS2A, NS2B, NS3A, NS4A, contain comprises the capsid, prM, M, E, NS1, NS2A, NS3A, NS4A, contains and not be used in the production of quadravalent vaccine which provides immunity against all four serotypes of dengue virus. The vaccine also comprises a chimeric DEN-2/4 virus, and/or a chimeric DEN-2/4 virus. The new quadravalent vaccines are used to protect against infection by all four serotypes of dengue virus, DEN-1, DEN-3 and DEN-4, which can lead to dengue fever or fatal dengue hemorrhagic fever/dengue shock syndrome (DHF/DSS). Host cells are used to produce the recombinant protein products of the DNA constructs of common and the component of the component of the constructs of common and the component of the component of the constructs of the component of commonent of the component of commonent of the component of commonent 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-1997 (first entry)
Polyprotein of DEN-2 virus, strain 16681.
Polyprotein of DEN-2 virus, strain 16681.
Dengue 2 virus; polyprotein; capsid; prm; M; E; NS1; NS2A; NS2B; NS3; NS4A; NS4B; NS5; PDR-53; quadravalent vaccine; immunity; serotype; chimeric DEN-2/1 virus; chimeric DEN-2/3 virus; chimeric DEN-2/4 virus; dengue fever; fatal dengue haemorrhagic fever; dengue shock syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56.9%; Score 33; DB 1; Length 3395
54.5%; Pred. No. 6.8e+02;
.ive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note- "N-linked glycosylation site"
206. .280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gubler DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                     06-JUN-1996; U09209...
06-JUN-1996; US-481329...
(UYMA-) UNIV MAHIDOL AT SALAYA...
(USSH ) US DEPT HEALTH & HUMAN SERVICES...
BHARRARAPIENATH N. BULTAPET S., Chang J.,
Halstead SB. Kinney R., Trent DW;
WPI; 97-052330/05.
                                                                                                                                                                                                                                              /note- "Encoded by KKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2. .114
/label= Capsid_protein
115. .205
/label= prM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dengue 2 virus, strain 16681.
Key Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W06590 standard; Protein; 3391 AA.
2243. .2491
/label= NS4B
2492. .3391
/label= NS5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label- M
281. .775
/label- E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2728 RMLINRFIMRY 2738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 RLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                misc_difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; T49304
```

/note= "N-linked glycosylation
776. .1127

ö

```
PEC-1996.

PP (0-50-1996.)

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PI (10SH) US DEPT HEALTH & HUMAN SERVICES.

PI (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH & HUMAN SERVICES.

PP (10SH) US DEPT HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH HEALTH
                                               note= "N-linked glycosylation site"
                                                                                            note- "N-linked glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Encoded by KKA"
                                                                                                              /1128. 1345
/1abel= NS2A
/1abel= NS2B
1476. 1475
/1abel= NS3
/1abel= NS3
2044. 2242
/1abel= NS4A
2243. 2491
/1abel= NS4B
2492. 3391
/1abel= NS4B
/label= NS1
905
                                                                                                                                                                                                                                                                                                                                                                                                            misc_difference
                      modified_site
                                                                      modified_site
                                                                                                                     protein
                                                                                                                                                                   protein
                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                               protein
```

ó Query Match 56.9%; Score 33; DB 1; Length 3391; Best Local Similarity 54.5%; Pred. No. 6.8e+02; Matches 6; Conservative 2; Mismatches 3; Indels

Gaps

2 RLLIRRILLRY 12 ò

|:|| | :|| 2728 RMLINRFTMRY 2738

Search completed: February 8, 2000, 01:29:39 Job time: 1751 sec

THIS PAGE BLANK (USPTO)

Н

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

 protein search, using sw model OM protein February 7, 2000, 11:54:26; Search time 117.7 Seconds (without alignments) 4.809 Million cell updates/sec Run on:

US-08-653-294-16 58 Perfect score:

1 YRLLIRRILLRY 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 1000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Listing first 45 summaries

PIR\_62:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	mbrial a	histocompatibility	probable efflux pr	type I site-specif	hypothetical prote	ribosomal protein	hypothetical prote	hypothetical prote	prostaglandin E2 r	prostaglandin E2 r	prostaglandin E2 r	DNA-directed RNA p	prostaglandin E2 r	DNA-directed RNA p	DNA-directed RNA p	TB2/DP1 protein ho	adenylate kinase (	prostaglandin E2 r	Na+/H+ antiporter	hypothetical prote	prostaglandin E re	prostaglandin E2 r	prostaglandin E(2)	prostaglandin E re	prostaglandin E re	protaglandin recep	prostaglandin E re	prostaglandin E2 r	prostaglandin E re	alpha recepto-	
SUMMARIES	Ω	36	99	6	Ξ	7	34	95	C71618	99	9	9	12	2	2	34	99	56	2	34	14	7	7	38	2	디	74	급	6	37	8	
	DB		7	~	N	(7)	7	N	~	7	7	7	~	7	٦	N	~	~	7	7	7	7	7	7	~	~	7	7	(4	7	7	
	Length	40	348	559	1055	278	298	814	1712	39	48	62	78	78	185	185	185	213	217	313	352	361	361	362	364	364	365	365	365	365	366	
ď	×٩	. w	ď	ς.	ς.	÷.	0	o.	60.3	ω.	ω.	œ,	œ.	œ.	œ.	8	ω.	œ.	œ.	ω.	ω.	ω.	æ	œ.	œ.	œ	ω.	œ.	œ.	œ,	œ.	
	Score	. "	36	36	36	35.5	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	
	Result No.	-	7	m	4	Ŋ	ø	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53	30	

prostaglandin E2 r	procagnandin Eecep prostaalandin E re	protaglandin recep	prostaglandin E re	prostaglandin E re	prostaglandin E re	prostaglandin E re	prostaglandin E2 r	prostaglandin E re	hypothetical prote	hypothetical prote	hypothetical prote	genome polyprotein	hypothetical prote
JC2056	S51317	138750	S51316	S43375	S51313	S51318	B53216	S51319	B64174	T13646	S50578	GNWVMV	D72110
010	4 (1	7	~	~	N	~	~	~	~	~	~	-	~
367	374	388	388	390	390	393	411	425	575	735	928	3434	133
58.6	28.0	58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6	58.6	56.9
34	3.4	34	34	34	34	34	34	34	34	34	34	34	33
31	4 m	34	32	36	37	38	39	40	41	42	43	44	42

## ALIGNMENTS

```
fimbrial assembly protein PilC - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Species: Date: (OS-May-1998 #sequence_revision 08-May-1998 #text_change 20-Aug-1999
C;Accession: D70365
R;Deckert, G; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Recession: D70365
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Rocession: 1408 cAQP>
A;Cross-references: GB:AE000705; NID:92983310; PIDN:AAC06902.1; PID:92983312; GB:AE00
C;Genedics:
A;Genee: pilC:
C;Superfamily: secretion protein xcpS
```

ö Gaps ö Length 408; 2; Indels Score 37; DB 2; Pred. No. 14; 1; Mismatches Query Match 63.8%; Best Local Similarity 72.7%; Matches 8; Conservative

. 1 YRLLIRRILLR 11 δ

g

RESULT 2
329990
histocompatibility antigen, HLA-F-like - rhesus macaque
C;Species: Macaca mulatta (rhesus macaque)
C;Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999
C;Accession: 529990
R;Bontrop, R.R.
submitted to the EMBL Data Library, February 1993
A;Reference number: \$29990
A;Accession: \$2990
A;Accession: \$29990
A;Accession: \$29900
A;Accession: \$29000
A;A

Gaps ö 62.1%; Score 36; DB 2; Length 348; llarity 54.5%; Pred. No. 19; Conservative 4; Mismatches 1; Indels Best Local Similarity Matches 6; Conserva Query Match

ö

86

ò ద

```
A; Reference number: $49823
A; Reference number: $49823
A; Residues: 1-278 cRIC>
A; Molecule type: DNA
A; Residues: 1-278 cRIC>
A; Cross-references: EMBL: 246796; NID: 9577794; PID: 9577814
A; Residues: 1-278 cRIC>
A; Cross-references: EMBL: 246796; NID: 9577794; PID: 9577814
A; Residues: 1-278 cRIC>
A; Cross-references: EMBL: 246796; NID: 94038890
A; Title: The yeast SS3 gene is essential for secretory protein translocation and enc
A; Reference number: $39583; MUD: 94038890
A; Residues: 16-278 cREN>
A; Molecule type: DNA
A; Residues: 146-278 cREN>
A; Residues: 146-278 cREN>
A; Cross-references: EMBL: X74499; NID: 9414690; PID: 9414691
B; Coster, F.; Jonniaux, J.L.; Goffeau, A.
Yeast II, 673-679, 1995
A; Title: Analysis of a 32.8 kb segment of yeast chromosome IV reveals 21 open reading
A; Accession: S55836
A; Accession: S55836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Burger, G.; Plante, I.; Lonergan, K.M.; Gray, M.W.
J. Mol. Biol. 245, 522-537, 1995
A; Title: The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba castellanii: c
A; Reference number: $53845; MUID:95147275
A; Reference number: $53849
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-298 <BUR>
A; Residues: 1-298 <BUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residudes: 1-278 <FOUD
A;Cross-references: EMBL:274383; NID:91431562; PID:e253404; PID:91431563; MIPS:YDR087
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; References: Embl: X82086; NID:9558241; PID:9558260
A; Cross-references: Embl: X82086; NID:9558241; PID:9558260
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1994
B; Foury, F.; Jonniaux, J.L.; Purnelle, B.; Coster, F.; Goffeau, A.
A; Reference number: S67889
A; Accession: S67904
hypothetical protein YDR087c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein D4478; hypothetical protein YD8554.20c
C;Species: Saccharomyces cerevisiae
C;Date: 13-Jan-1995 #sequence_revisian
C;Accession: S48776; S49842; S395836; S67904
R;Coster, F.; Jonniaux, J.L.; Goffeau, A.
Submitted to the EMBL Data Library, October 1994
A;Reference number: S48758
A;Accession: S48776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S53849
ribosomal protein S3 - Acanthamoeba castellanii mitochondrion (SGC6)
C;Species: mitochondrion Acanthamoeba castellanii
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Feb-1999
C;Accession: S53849
R;Burger, G.; Plante, I.; Lonergan, K.M.; Gray, M.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-278 <COS>
A; Residues: 1-278 <COS>
A; Cross-references: Testences: ABL:X82086; NID:q558241; PID:g558260
R; Richards, C.; Harris, D.E.
submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 35.5; DI
Pred. No. 19;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 YLLLIRRVLFSQLKY 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YRLLIRRIL---LRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trac
A;Reference number: A71570; MUID:99000809
A;Accession: E71490
                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: E71490
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 3.1.21.3) chain hsdR - Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A.Accession: F64114
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: nucleic acid sequence not shown; translation not shown
A.Status: 1-1055 crigR>
A.Status: 1-1055 crigR>
A.Status: references: GB:U32808; GB:L42023; NID:g1574739; PID:g1574743; TIGR:HI1285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: hsdR
C;Superfamily: unassigned DEAD/H box helicases; DEAD/H box helicase homology
C;Superfamily: DNA binding; hydrolase; P-loop; restriction modification system
C;Reywords: ATP; DNA binding; hydrolase; P-loop; restriction modification system
F;300-665/Domain: DEAD/H box helicase homology CDEAD>
F;404-409/Region: nucleotide-binding motif B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                     probable efflux protein - Chlamydia trachomatis (serotype D, strain UW3/Cx) C;Species: Chlamydia trachomatis
C;Species: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 21-Nov-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        type I site-specific deoxyribonuclease (EC 3.1.21.3) chain hsdR - Haemophilu
C;Species: Haemophilus influenzae
C;Date: 18-4ug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
C;Accession: F64114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Cross-references: GB:AE001334; GB:AE001273; NID:g3329078; PID:g3329089
A:Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: ygeD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 2; Length 1055;
Pred. No. 56;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB 2
Pred. No. 30;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62.1%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 62.1%;
Best Local Similarity 63.6%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 63.0
Perhac 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1017 RLLVRRALOKY 1027
                                                                                            |: :|::||||
| RVALRKLLLRY 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 YRLLLTRVLKR 419
                                                     2 RLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 RLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-559 <ARN>
```

ò q Gaps

RESULT S48776

ò

```
Cydrocesion: D55995
R;An, S; Yang, J; So, S;W; Zeng, L.; Goetzl, E.J.
Biochemistry 33, 14496-14502, 1994
A;Title: Isoforms of the Ep91 subtype of human prostaglandin E-2 receptor transduce bo A;Reference number: A55995; MUID:95072021
A;Reterence number: A55995; MUID:95072021
A;Rete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: C55995
R;An, S:; Yang, J:; So, S.W.; Zeng, L.; Goetzl, E.J.
Biochemistry 33, 14496-14502, 1994
A;Tille: Isoforms of the EP3 subtype of human prostaglandin E-2 receptor transduce bo A;Reference number: A55995; MUID:95072021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;An, S.; Yang, J.; So, S.W.; Zeng, L.; Goetzl, E.J.
Blochemistry 33, 14496-14502, 1994
A;Title: Isoforms of the EP3 subtype of human prostaglandin E-2 receptor transduce bo A;Reference number: A55995; MUID:95072021
                                                                                                                                                                                                                                                                                                                                                                    prostaglandin E2 receptor, subtype EP3 splice form III - human (fragment) C:Species: Homo sapiens (man) C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostaglandin E2 receptor, subtype EP3 splice form II - human (fragment) C; Species: Homo sapiens (man) C; Species: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostaglandin E2 receptor, subtype EP3 splice form IV - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2
Pred. No. 5.2;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB;
Pred. No. 6.4;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A Accession: C55995
A Status: preliminary
A Status: preliminary
A Residues: 1-39 CANA
A Residues: 1-39 CANA
A Cross-references: GB:L32661
C; Superfamily: prostaglandin E receptor
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.6%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 58.6
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                           Query Match
Best Local Similarity
Matches 7; Conserv
                                                        1 YRLLIRRILLRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ||:|:||||
22 LLLRKILLR 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: B55995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
B55995
                                                                                                                                            g
                                                            å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T00953
R; Vysotskaia, V.S.: Osborne, B.I.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji, C
K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.;
submitted to the EMBL Data Library, May 1998
A; Description: Arabidopsis thaliana chromosome 1 BAC F20D22 complete sequence.
A; Reference number: Z14214
A; Accession: T00953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.; .; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.; Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; CITOSS - Treferences: EMBL: AC002411; NID: 92570223; PID: 93142290; GSPDB: GN0059; ATSP: F20D2; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GB:AE001362; NID:93845148; PID:93845151; TIGR:PFB0315w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Geme: Arsp:F20D22.3
A:Map position: 1
A:Introns: 64/1: 144/1; 239/3; 304/1; 386/1; 415/2; 473/3; 516/3; 554/3; 594/2; 624/3;
A;Cross-references: GB:U12386; NID:9562028; PID:9562053 A;Experimental source: strain Neff; ATCC 30010 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: C71618
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1712 <GAR>
A; Cross-references: GB: AEO01386; GB: AEO01362; NID: 93845148; PID: 93845151; TIGR
C; Genetics: A; Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F20D22.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PFB0315w - malaria parasite (Plasmodium falciparum) C;Species: Plasmodium falciparum C:Species: Plasmodium falciparum C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 07-May-1999 C;Accession: C71618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.3%; Score 35; DB 2; Length 1712; 50.0%; Pred. No. 1.4e+02; ive 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; DB 2; Length 298;
Pred. No. 25;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-814 <VYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60.3%; Score 35; DB 2;
60.0%; Pred. No. 67;
iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   60.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 60.0 Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.3
Best Local Similarity 50.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : || :|::|||
126 FMLLKKRVILRY 137
                                                                                                                                                                                  A;Genome: mitochondrion
A;Genetic code: SGC6
C;Keywords: mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |::||:|| |
263 LVVRRLLLNY 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 LLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                            C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
```

ö

ö

```
NAVadirected RNA polymerase (EC 2.7.7.6) 22K chain - vaccinia virus (strains WR and C C) Species vaccinia virus

Nilternate names: J4R protein
C) Species: vaccinia virus
A) Note: host Homo sapiens (man)
C: Date: 28 - Dec - 1987 # sequence_revision 28 - Dec - 1987 # text_change 11-Jun-1999
C; Accession: A25734; I23092; G42513
R; Broyles, S.S.; Moss, B.
Proc. Natl. Acad. Sci. U. SA. B3, 3141-3145, 1986
A; Title: Homology between RNA polymerases of poxviruses, prokaryotes; and eukaryotes: A; Reference number: A25734; MUID: 86205852
A; Residues: 1-185 CBNA
A; Residues: 1-185 CBNA
A; Molecule type: DNA
A; Residues: 1-185 CBNA
A; Molecule type: DNA
A; Residues: 1-185 CAND
A; Schroeder, E.; Zettlmeissl, G.; Streeck, R.E.
Nucleic Acids Res. 13, 985-998, 1985
A; Title: Nucleotide sequence of a cluster of early and late genes in a conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved segment of the conserved seg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-185 <GOB>
A; Cross-references: GB: M35027; NID:9335317; PIDN:AAA48084.1; PID:9335432
A; Experimental source: strain Copenhagen
B; Goebel, S.J.; Johnson, G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, Virology 179, 247-266, 1990
A; Title: The complete DNA sequence of vaccinia virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: L4R protein
C;Species: variola virus
C;Decies: variola virus
C;Decies: 0-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 18-Jun-1999
C;Accession: F36845; S33095
R;Blinov, V.M.
submitted to GenBank, November 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A42531; MUID:91021027
A; Contents: annotation; possible protein coding frames
A; Note: neither amino acid nor nucleotide sequence is given
C; Superfamily: vaccinia virus DNA-directed RNA polymerase 22K polypeptide
C; Keywords: early protein; nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-directed RNA polymerase (EC 2.7.7.6) chain J4R - variola virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 185;
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Description: not shown.
A; Reference number: A36859
A; Accession: F36845
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24 YAVINRNVLLRY 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                 LLLRKILLR 52
                                  3 LLIRRILLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                      õ
                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-directed RNA polymerase (EC 2.7.7.6) subunit H - Methanococcus jannaschii
C; Species: Methanococcus jannaschii
C; Species: Methanococcus jannaschii
C; Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999
C; Accession: F64429
R: Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
F. Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
Fron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klank, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.M.; Arithe: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; WUID:96337999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prostaglandin E2 receptor, subtype EP3 (clone 74A) - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 23-Jul-1999
C;Accession: C53216
R;Breyer, R.M.; Emeson, R.B.; Tarng, J.L.; Breyer, M.D.; Davis, L.S.; Abromson, R.M.; Fe
A;Title: Alternative splicing generates multiple isoforms of a rabbit prostaglandin E-2
A;Reference number: A53216; MUID:94164982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB:U67546; GB:L77117; NID:q1591687; PIDN:AAB99042.1; PID:q1591692;
                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-78 <BUL>
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:U04275; NID:9467982; PIDN:AAA17414.1; PID:9467983
C;Superfamily: prostaglandin E receptor EP1
C;Keywords: alternative splicing; transmembrane protein
                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                    Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 78;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Start codon: TTG
C;Superfamily: DNA-directed RNA polymerase chain E
C;Keywords: nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB 2
Pred. No. 10;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB
Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                       ω,
                                                                                                                                                                                                                                                                    Score 34;
Pred. No.
                                                                                          A.Cross-references: GB.L32660
C.Superfamily: prostaglandin E receptor EP1
C.Keywords: alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative 5
                                                                                                                                                                                                                                                                    58.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: FOR970764-971000
                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity
Matches 6; Conserv
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62 <ANA>
                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:|:|!||
||LLERKILLR 30
                                                                                                                                                                                                                                                                                                                                                                                                        3 LLIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |||:|:||:
70 YRLVIKRII 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A: Accession: C53216
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-78 <BRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLLIRRIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22
                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

ω.

ö

```
A; Molecule type: DNA
A; Residues: 1-185 < PLDA
A; Residues: 1-185 < PLDA
A; Residues: 1-185 < PLDA
A; Cross-references: GB: X69198; NID: 9456758; PIDN: CAA49022.1; PID: 9297261
A; Experimental Source: strain India-1967, ssp. major, isolate Ind3
A; Experimental Source: strain India-1967, ssp. major, isolate Ind3
B; Shchelkunov, S.N.; Blinov, V.M.; Totmenin, A.V.; Marennikova, S.S.; Kolykhalov, A.A.;
A; Shchelkunov, S.N.; Blinov, V.M.; Totmenin, A.V.; Marennikova, S.S.; Kolykhalov, A.A.;
A; Strain S. S. 1953
A; Title: Nucleotide sequence analysis of variola virus HindIII M, L, I genome fragments.
A; Recreace number: S33069; MUID: 93190624
A; Accession: S33069; MUID: 93190624
A; Accession: S33069; MUID: 93190624
A; Molecule type: DNA
A; Residues: 1-185 < SHC>
A; Residues: 1-185 < SHC>
A; Residues: 1-185 < SHC>
A; Cross-references: EMBL: X67119; NID: 962330; PIDN: CAA47580.1; PID: 962357
A; Experimental source: strain India-1967, isolate Ind3
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992
C; Superfamily: vaccinia virus DNA-directed RNA polymerase 22x polypeptide
C; Keywords: nucleotidyltransferase; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 58.6%; Score 34; DB 2; Length 185; Best Local Similarity 50.0%; Pred. No. 24; Matches 6; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQ
```

Search completed: February 7, 2000, 11:54:27 Job time: 24337 sec

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 8, 2000, 00:59:54 ; Search time 63.71 Seconds
(without alignments)
5.625 Million cell updates/sec Run on:

US-08-653-294-16 58 1 YRLLIRRILLRY 12 Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Perfect score: Sequence: Scoring table:

82229 segs, 29864866 residues Searched:

82229 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	018304 caeno	P33617 macaca mula				_							P43115 homo sapien	P46069 oryctolagus	P45299 haemophilus	P40048 saccharomyc		Q05598 salmonella	_					T		methanc	herpes	herpes	_		Ø	P53121 saccharomyc	zea may	P12091 oryza sativ
SUMMARIES	ID	YHS5_CAEEL	HLAF_MACMU	YD87_YEAST	RT03_ACACA	RPOH_METJA	DP1_MOUSE	RPO6_VACCV	S	KAD_RICPR	YK50_YEAST	PE23_MOUSE	PE23_RAT	PE23_HUMAN	PE23_RABIT	YRAM_HAEIN	PTP3_YEAST	POLG_MVEV	CBIQ_SALTY	LICA_MYCCA	OPPB_LACLA	OPPB_LACIC	VMD2_HUMAN	CRTI_CERNC	POLG_DEN26	POLG_DEN27	Y290_METJA	VGLM_HSV6U	VGLM_HSV6Z	SYD_MYCGE	- 1	SRB4_YEAST	YGN9_YEAST	RPOB_MAIZE	RPOB_ORYSA
	Length DB	411	æ	78	86	78 1	85	85	82	13	22	65	65	90	디	'n	928	80	25	38	19	13	85	621	91	391	11	44	44	20	53	87	802	75	075
æ	Ouery Match Le	3.8	ć,	٦.	ö	58.6	œ.	ω.	ω.	ω.	ъ.	ω.	ω.	ω.	8.	œ.	œ.	œ.	e.	9	9.	é.	ė.	ė.	ė.	٠.	ς.	ς.	5.	'n.	Š.	ъ.	'n.	ď.	δ.
	Score	37	36	35.5	35	34	34	34	34	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32
	Result No.	1	7	m	4	Ŋ	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34

P38717 saccharomyc P23174 cricetulus P34741 saccharomyc P45481 mus musculu P47760 chlamydla t P06796 mus musculu P25789 homo sapten P21670 rattus norv P19390 haemophilus P22235 haemophilus			) MOSOME I.	habditia; Rhabditida; erinae; Caenorhabditis.	J databases. MILY.	oduced through a collaboration cs and the EMBL outstation e are no restrictions on its	s its content is in no way Usage by and for commercial ttp://www.isb-sib.ch/announce/	2;	; Length 411; 1; Indels 0; Gaps 0;			) A CHAIN F PRECURSOR (HLA F	Vertebrata; Mammalia; checidae; Cercopithecinae;
35 32 55.2 1229 1 SIP3 YEAST 37 32 55.2 1281 1 MDR3_CRIGR 38 32 55.2 2441 1 CRP_MOUSE 39 31 53.4 122 1 RLI7_CHLTR 40 31 53.4 120 1 RCSK_MOUSE 41 31 53.4 261 1 PRC9_HOWAN 42 31 53.4 261 1 PRC9_HOWAN 43 31 53.4 265 1 BEX1_HAEIN 44 31 53.4 265 1 BEX1_HAEIN 45 31 53.4 265 1 BEX1_HAEIN 45 31 53.4 265 1 BEX1_HAEIN	ALIGNMENTS RESULT 1	YHSS_CAEEL ID YHSS_CAEEL STANDARD; PRT; 411 AA. AC 018304;	DT 15-JUL-1999 (Rel. 38, Created) DT 15-JUL-1999 (Rel. 38, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DE HYPOTHETICAL 48.2 KD PROTEIN ZR849.5 IN CHROMOSOME I.	ON ZARAZYON SECENTIAL SECONDO ON BUKARYOTA; Metazoa; Nematoda; Secernentea; Ri OC Rhabditina; Rhabditoidea; Rhabditidae; Pelod			CC use by non-profit institutions as long as its content is in no way CC modified and this statement is not removed. Usage by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/	WORMPEP; ZK849.5; CE16750 PFAM: PF01062: Worm_famil Hypothetical protein. SEQUENCE 411 AA; 48236	Query Match 63.8%; Score 37; DB 1 Best Local Similarity 70.0%; Pred. No. 5.8; Matches 7; Conservative 2; Mismatches	Qy 3 LLIRRILLRY 12       ::   Db 128 LLIRRTIRY 137	S E	AC P3361/; DT 01-FEB-1994 (Rel. 28, Created) DT 01-FEB-1994 (Rel. 28, Last sequence update) DT 15-JUL-1999 (Rel. 38, Last annotation update) DE HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA DE ANTIGEN) (LEUKOCYTE ANTIGEN F).	nta-r Contarta (Rhesus macaque). Macaca mulatta (Rhesus macaque). Eukaryota; Metazoa; Chordata; Craniata; Eutheria; Primates; Catarrhini; Cercopii Macaca.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 94038890.
ESNAULT Y., BLONDEL M.-O., DESHAIES R.J., SCHEKMAN R., KEPES F.;
"The yeast SSS1 gene is essential for secretory protein translocation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                               BY SIMILARITY.

BY SIMILARITY.

HIA CLASS I HISTOCOMPATIBILITY ANTIGEN,
ALPHA CHAIN F.

EXTRACELULAR ALPHA-1.

EXTRACELLULAR ALPHA-2.

EXTRACELLULAR ALPHA-3.

CONNECTING PEPTIDE.
                                             OTTING N., BONTROP R.E.; "Characterization of the rhesus macague (Macaca mulatta) equivalent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
                                                                                                 -!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL 33.2 KD PROTEIN IN SSS1-SLU7 INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 1; Length 348;
Pred. No. 7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C / FY1679;
COSTER F., JONNIAUX J.-L., GOFFEAU A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
3A375142 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                       [mmunogenetics 38:141-145(1993]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1994 (Rel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 146-278 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.1%;
54.5%;
                                                                                                                                                                                                                                                                                                             PIR; S29990; S29990.
HSSP; P03989; 1HSA.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                               EMBL; 221819; CAA79885.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 62.1
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                    PFAM: PF00047; 19; 1.
PFAM: PF00129; MHC_I; 1.
MHC I; Transmembrane; Gl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |: :|::||||
98 RVALRKLLLRY 108
[1]
SEQUENCE FROM N.A.
MEDIJNE; 93246295.
                                                                                                                                                  MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226
109
348 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YDR087C OR D4478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YD87_YEAST
P35178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
YD87_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Castellation.";
organization.";
J. Mol. Baiol. 245:522-537(1995).
-: SUBCELLULAR LOCATION: MITOCHONDRIAL.
-: SUBCELLULAR ELONGS TO THE S3P FAMILY OF RIBOSOMAL PROTEINS.
encodes a conserved protein of the endoplasmic reticulum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ښ</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acanthamoeba
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BURGERY, PARTE I., LONERGAN K.M., GRAY M.W.;
BURGERICAL BOOK OF the amoeboid protozoon, Acant.
"The mitochondrial DNA of the amoeboid protozoon, Acant.
castellanii: complete sequence, gene content and genome
                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
              EMBO J. 12:4083-4093(1993).
-!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE NNP-1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                            278 AA; 33202 MW; FAD7CAC9 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7BA48AD7 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ATTOCHONDRAL RIBOSOMAL PROTEIN 83.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ed. No. 7.5;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                Score 35.5;
Pred. No. 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U12386; AAD11841.1; -.
PROSITE; PS00548; RIBOSOMAL_S3; FALSE_NEG.
PFAM; PF00189; Ribosomal_S3_C; 1.
PFAM; PF00417; Ribosomal_S3_N; 1.
Ribosomal protein; Mitochonditon.
SEQUENCE 298 AA; 36060 MW; 7BA48AD7 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Acanthamoebidae; Acanthamoeba
                                                                                                                                                                                                                                                                                                  PIR; S48776; S48776.
Hypothetical protein; Nuclear protein.
DOMAIN 266 274 POLY-GLU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acanthamoeba castellanii (Amoeba).
                                                                                                                                                                                                                                                                                                                                                                                                              61.2%;
60.0%;
                                                                                                                                                                                                                                EMBL; Z46796; CAA86809.1; -.
EMBL; Z74383; CAA98907.1; -.
EMBL; X82086; CAA57616.1; -.
EMBL; X74499; CAA52607.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 30010 / NEFF;
MEDLINE; 95147275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 YRLLIRRIL---LRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RT03_ACACA
P46754;
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         셤
```

Length 298;

DB 1;

60.3%; Score 35;

Query Match

us-08-653-294-16.rsp

```
1||:|:||:
70 YRLVIKRII 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPO6_VACCV
P07391;
                                                                                                                                                          DP1_MOUSE
Q60870;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
TRANSMEM
SEQUENCE
                                                                                                       RESULT 6
DP1_MOUSE
DP1_MOUSE
DP1_MOUSE
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.
DP1_NOV.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPO6_VACCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                            ద
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED custation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "RNA polymerase subunit H features a beta-ribbon motif within a novel fold that is present in archaea and eukaryotes.";
J. Mol. biol. 287:753-760(1999).
-: FUNCTION: DNA-DEPENDEN RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAINE-JAL-1 / DSM 2661 / ATCC 43067;

STRAINE-JAL-1 / DSM 2661 / ATCC 43067;

STRAINE-JAL-1 / DSM 2661 / ATCC 43067;

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCANNE J.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GCOANNE J.D.,

SUTTON G.G., MERRICK J.M., RIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.F., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORDOWSKY M.,

KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.;

"COMPLETE GENOME SEQUENCE Of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01110; RNA_POL_H_23KD; 1.
PFAM: PF01191; RNA_POL_H; 1.
Transferase: Transcription: DNA-directed RNA polymerase; 3D-structure.
SEQUENCE 78 AA: 9001 MW; 9F10C0F3 CRC32;
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO OTHER ARCHAEBACTERIAL RPOH AND TO THE C-TERMINAL OF EUKARYOTIC SUBUNIT ABC27 (RPB5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE; 99208760.
THIRU A., HODACH M., ELORANTA J.J., KOSTOUROU V., WEINZIERL R.O.,
MATTHEWS S.;
                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                              Indels
                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT H (EC 2.7.7.6).
                            .;
3
                                                                                                                                                                                                                                                                          78 AA
Pred. No. 10;
4; Mismatches
                                                                                                                                                                                                                                                                          PRT;
50.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U67546; AAB99042.1; -.
PDB; 1HMJ; 05-APR-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 273:1058-1073(1996)
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methanococcus jannaschii.
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                             : || :|::|||
126 FMLLKKRVILRY 137
                                                                              1 YRLLIRRILLRY 12
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                 RPOH OR MJ1039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Methanococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; MJ1039;
                                                                                                                                                                                                                                        RPOH_METJA
ID RPOH_METJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jannaschii
                                                                                                                                                                                                                                                                                                058443
                                                                                                                                q
                                                                                 ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP022 OR J4R OR FIO.
Vaccinia virus (strain WR), and Vaccinia virus (strain Copenhagen).
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIJNE; 96194804.
PRIESCHL E.E., PENDL G.G., HARRER N.E., BAUMRUKER T.;
"The murine homolog of TB2/DP1, a gene of the familial adenomatous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=WR;
MEDLINE; 8620582.
BROXLES S.S., MOSS B.;
HOMOLOGY between RNA polymerases of poxviruses, prokaryotes, an eukaryotes: nucleotide sequence and transcriptional analysis of vaccinia virus genes encoding 147-RDa and 22-KDa subunits.";
Proc. Natl. Acad. Sci. U.S.A. 83:3141-3145(1986).
                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-APR-1988 (Rel. 07, Created)
1-APR-1988 (Rel. 07) Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE 22 KD POLYPEPTIDE (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1;
Pred. No. 9.5;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 106 POTENTIAL.
185 AA; 21050 MW; FC5BA4A2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 185 AA
185 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.68;
58.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U28168; AAB07994.1; -. MGD; MGI:1270152; DP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyposis (FAP) locus."
Gene 169:215-218(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        || :|| | ||:
133 YRKIIRPIFLRH 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE; 96194804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ransmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orthopoxvirus
                                                                              01-NOV-1997
01-NOV-1997
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ID DATA DOLLAR RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF THE RESERVATION OF TH
```

ö

6; Conservative

Query Match Best Local Similarity Matches 6; Conserv

ö

Gaps

ö

58.6%; Score 34; DB 1; Length 78; 66.7%; Pred. No. 3.8; 1ive 3; Mismatches 0; Indels

us-08-653-294-16.rsp

```
'Nucleotide sequence analysis of variola virus HindIII M, L, I genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S33095; S33095
                                                                                                  COMPLETE GENOME.
STRAIN-INDIA-1967 /
MEDLINE; 93202281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=MADRID E;
MEDLINE; 99039499.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADK OR RP638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KAD_RICPR
ID KAD_RICPR
AC Q92CS6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VICOLOGY 179:517-563(1990).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-COPENHAGEN;
GOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
                                                                                                                                                                                                                                                                       SOEBEL S.J., JOHNSON G.P., PERKUS M.E., DAVIS S.W., WINSLOW J.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SHCHELKUNOV S.N., BLINOV V.M., TOTMENIN A.V., MARENNIKOVA S.S., KOLYKHALOV A.A., FROLOV I.V., GHIZHIKOV V.E., GYTOROV V.V., GASHIKOV P.V., BELANOY E.E., BELAVIN P.A., RESENCHUK S.M., ANDZHAPARIDZE O.G., SANDAKHCHIEV L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                      MEDLINE: 85215527.
PLUCIENNICZAK A., SCHROEDER E., ZETTLMEISSL G., STREECK R.E.;
"Nucleotide sequence of a cluster of early and late genes in a conserved segment of the vaccinia virus genome.";
Nucleic Acids Res. 13:985-998(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: THIS ENZYME CONSISTS OF AT LEAST EIGHT SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1993 (Rel. 27, Created)
1-0CT-1993 (Rel. 27, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE 22 KD POLYPEPTIDE (EC 2.7.7.6).
RPO22 OR J4R OR L4R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 185;
Pred. No. 9.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M35027; AAA48084.1; -.
PIR; 123092; RNYZ22.
Transferase; DNA-directed RNA polymerase; Transcription.
SEQUENCE 185 Aa; 21342 MW; 2947E2C5 CRC32;
                                                                                                                                                                                                                                                                                                                           "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-INDIA-1967 / ISOLATE IND3;
MEDLINE; 93190624.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M13209; AAB59833.1; -. EMBL; X01978; CAA26018.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 50.00
المالية والمالية المالية الما
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 :: | :||||
24 YAVINRNVLLRY 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 YRLLIRRILLRY 12
SEQUENCE FROM N.A.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                           STRAIN COPENHAGEN
                                                                                                                                                                                                                                                MEDLINE; 91021027
                                                                                                                                                                                                                                                                                                                                                                                                      COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBSTRATES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Variola virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA(N)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RPO6_VARV
P33054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPO6_VARV
ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                   SHCHELKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;
"Genes of variola and vaccinia viruses necessary to overcome the host protective mechanisms.";
FEBS Lett. 319:80-83(1993).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                              -!- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O., SICHERITZ-PONTEN T., ALSMARK U.C.M., PODOWSKI R.M., NAESLUND A.K., ERIKSSON A.-P.WINKLER H.H., KURLAND C.G.; "The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                  -1- SUBUNIT: THIS ENZYME CONSISTS OF AT LEAST EIGHT SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 396:133-140(1998).

-!- FUNCTION: THIS SMALL UBIQUITOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.

-!- CATALYTIC ACTIVITY: ATP + AMP - ADP + ADP.

-!- SUBGNIT: MONOMER (BY SIMILARITY).

-!- SUBCELLIAR LOCATION: CYTOPLASMIC.

-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          subdivision; Rickettsiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11arity 50.0%; Pred. No. 9.5; Conservative 3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-DEC-1999 (Rel. 39, Created)
15-DEC-1999 (Rel. 39, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA-directed RNA polymerase; Transcription.
35 AA; 21354 MW; 547A4AC2 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rickettsia prowazekii.
Bacteria; Proteobacteria; alpha subdivis;
Rickettsiaceae; Rickettsieae; Rickettsia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                       / ISOLATE IND3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, X67119; CAA47580.1; -. EMBL, S55844; AAB24677.1; -. EMBL, X69198; CAA49022.1; -. PIR; F36645; F56845.
Virus Res. 27:25-35(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 :: | :|||||
24 YAVINRNVLLRY 35
```

ö

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P30137;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1999 (Rel. 39, Last annotation update)
PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-NOV-1997 (Rel. 25, Last sequence update)
HYPOTHETICAL 39, 4 KD PROTEIN IN METI-SIS2 INTERGENIC REGION.
                                                                                                                                                                Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 352;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
POHL T.M., POHL F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                Score 34; DB 1;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 1;
Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39406 MW; F5B1BB2A CRC32;
                                                                                                                               3CFD3026 CRC32
                                                                                                                                                                                                                                                                                        352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 AA
                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                    EMBL; AJ235272; CAA15078.1; -. PROSITE; PS00113; ADENYLATE_KINASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                       Saccharomycetaceae; Saccharomyces.
                                                                                               PROSITE; PSUOLLS, Transferase; Kinase; ATP-binding.
                                                                                                                                 213 AA; 24503 MW;
                                                                                                                                                                58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z28295; CAA82149.1; -.
                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l protein.
352 AA; 3
                                                                                                                                                                                                                        ||||:|:| ||
|116 LLIKRVLGRY 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S38147; S38147
Hypothetical protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||:||: |
223 FRLLVRRLYL 232
                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                          3 LLIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 YRLLIRRILL 10
                                                                                                                                                                                                                                                                                     YK50_YEAST
P36151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PE23_MOUSE
P30557;
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PE23_MOUSE
                                                                                                                                                                                    Matches
 δ
                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QΩ
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HASEGAMA H., NEGISHI M., ICHIKAWA A.;

MALLINE; SUBJAYIS.

"Two isoforms of the prostaglandin E receptor EP3 subtype different
in agonist-independent constitutive activity.";

"Two isoforms of the prostaglandin E receptor EP3 subtype different
in agonist-independent constitutive activity.";

"I Biol. Chem. 271:1867-1860(1996).

"I Biol. Chem. 271:1877-1860(1996).

"I BIOL. Chem. 271:1877-1860(1996).

"I BIOL. Chem. 271:1877-180 ROBER PROSTRIC ACID SCREPTOR

MAY BE INVOLVED IN INHIBITION OF SODIUM AND WATER REABSORPTION IN KIDNEY

"TUBULUA AND CONTRACTION IN UTERINE SMOOTH MUSCLE. THE ACTIVITY OF

THIS RECEPTOR CAN COUPLE TO BOTH THE INHIBITION OF ADENYLATE

CYCLASE MEDIATED BY G-1 PROTEINS, AND TO AN ELEVATION OF

INTRACELLULAR CALCIUM. THE VARIOUS FORMS CAN INTERACT WITH

DIFFERENT SECOND MESSENGER SYSTEMS.

"INTRACELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN."

"INTRACELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN."

"INTRACELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN."

"INTRACELLULAR LOCATION: INTEGRAL MEMBRANE SPLICING. THEY HAVE

"INTRACELLULAR LOCATION: INTEGRAL MEMBRANE SPLICING."

"INTRACELLULAR LOCATION: INTEGRAL MEMBRANE COUPLE TO G-I PROTEINS."

"MERREAS GAMMA: COUPLES TO MULTIPLE G-PROTEINS."

"MERREAS GAMMA COUPLES TO MULTIPLE G-PROTEINS."

"MERREAS GAMMA COUPLES TO MULTIPLE G-PROTEINS."

"MERREAS GAMMA COUPLES TO MULTIPLE G-PROTEINS."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRIE A., SUGIMOTO Y., NAMBA T., HARAZONO A., HONDA A., WATABE A., NEGISHI M., NARUMIYA S., ICHIKAWA A.;
"Third isoform of the prostaglandin-E-receptor EP3 subtype with different C-ferminal tail coupling to both stimulation and inhibition of adenylate cyclase.";
Eur. J. Blochem. 217:313-318(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: LIGAND BINDING IS AFFECTED BY CAMP-DEPENDENT PHOSPHORYLATION
                                                                                                                                                                                                                                                                                            MEDLINE; 92202182.
SUGIMOTO Y., NAMBA T., HONDA A., HAYASHI Y., NEGISHI M.,
ICHIKAWA A., NAKUMIYA S.;
"Cloning and expression of a cDNA for mouse prostaglandin E receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HIRATA M., NARUMIYA S., ICHIKAWA A.; "Two isoforms of the EP3 receptor with different carboxyl-terminal domains. Identical ligand binding properties and different coupling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 93155085.
SUGIMOTO Y., NEGISHI M., HAYASHI Y., NAMBA T., HONDA A., WATABE A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: KIDNEY, UTERUS, AND MASTOCYNOMA CELLS, IN A LESSER AMOUNT IN BRAIN, THYMUS, LUNG, HEART, STOMACH,
                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHOWS HIGH AGONIST-INDEPENDENT CONSTITUTIVE INHIBITION OF ADENYLATE CYCLASE, WHILE BETA HAS NO AGONIST INDEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION (ALPHA AND BETA FORMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EP3 subtype.";
J. Biol. Chem. 267:6463-6466(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            properties with Gi proteins.";
J. Biol. Chem. 268:2712-2718(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (GAMMA FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A. (BETA FORM). 93155085.
                                                                                                                                                                                                      FROM N.A. (ALPHA FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D10204; BAA01051.1; -. EMBL; D13321; BAA02578.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRAIN MEMBRANES
musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 94039052.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INHIBITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
```

```
GCRDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCRDB;
ö
                                                                                                                                                                                                                                                             IRDHINYASSISIELPCPGSSALMWSDQLER -> MMNNLKW
TFIAVPVSLGLRISSPREG (IN ISOFORM BETA).
IRDHINYASSSTSLPCPGSSALMWSDQLER -> VANAVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                             P34980; Q63194; Q64376;

01-FEB-1994 (Rel. 28, Created)

01-FEB-1994 (Rel. 28, Last sequence update)

15-DEC-1999 (Rel. 39, Last annotation update)

PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY;
MEDLINE; 93343951.
TAKEUCHI K., ABE T., TAKAHASHI N., ABE K.;
"Molecular cloning and intrarenal localization of rat prostaglandin E2 receptor EP3 subtype.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ALPHA AND GAMMA FORMS).
STRAIN-SPRAGUE-DAWLEY; TISSUE-KIDNEY;
MEDILINE; 94183262
TAKENCHI K., TAKAHASHI N., ABE T., ABE K.;
"Two isoforms of the rat kidney EP3 receptor derived by alternative
                                                                                                                                                                                                                                                                                 IRDHTNYASSSTSLPCPGSSÄLMWSDQLER -> V
CSSDGQKGQAISLSNEVVQPGP (IN ISOFORM
                                                                                                                                                                                                                                                                                                                                                       ö
                                                                            G-protein coupled receptor; Transmembrane; Glycoprotein;
Lipoprotein; Palmitate; Phosphorylation; Alternative splicing.
DOMAIN 130 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                     Score 34; DB 1; Length 365; Pred. No. 19;
                                                                                                                                                                             5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                          2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                            4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                        1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem. Biophys. Res. Commun. 194:885-891(1993).
                      GCRDB: GCR_0367; --
GCRDB: GCR_0549; --
GCRDB: GCR_0944; --
MGD: WGI: 97795; PTGEREP3.
PROSITE; PS00237; G_PROTEIN_RECEPTOR; FALSE_NEG.
PFAM; PF00001; 7tm_1; 1.
                                                                                                                                                                                                                                                                                                            91CB103C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                       365 AA.
                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                            365 AA; 40077 MW;
                                                                                                                                                                                                                                                                                                                                     58.68;
77.88;
EMBL; D17406; BAA04229.1;
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 77.8-
                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                   323 LLLRKILLR 331
                                                                                                                                                                                                                                                                                                                                                                        3 LLIRRILLR 11
                                                                                                 DOMAIN
TRANSMEM
                                                                                                                 DOMAIN
TRANSMEM
                                                                                                                                                            TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                            RANSMEM
                                                                                                                                                                               FRANSMEM
                                                                                                                                                                                                PRANSMEM
                                                                                                                                                                                                                   RANSMEM
                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                 /ARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                       PE23 RAT
                                                                                                                                   DOMAIN
                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
8
                                                                                                                                                                                                                                                                                                                                                                          ò
```

```
THE RAW SPILELING INTERCENDENT SERVESSION OF OCCORDINGLY.

BIOCHER BOOK N.A. (ALPHA AND BETA FORMS).

RESIDENCE FOOK N.A. (ALPHA AND BETA FORMS).

RESIDENCE FOOK N.A. (ALPHA AND BETA FORMS).

RESIDENCE FOOK N.A. (BETA DEVELORE C. JUNGERHANN K., FERDINGLE GARLES STATES ```

```
ö
  IRDHTNYASSSTSLPCPGSSVLMWSDQLER -> MMNNLKR
SFIALPASLSMRISSPREG (IN ISOFORM BETA).
IRDHTNYASSSTSLPCPGSSVLMWSDQLER -> VANAVSS
CSSDQQKGQAISLSNEVVHPGP (IN ISOFORM
GAMMA).
   PE23_HUMAN STANDARD; PRT; 390 AA.
P43115; Q12943; Q12944; Q12945; Q16546;
O1-NOV-1995 (Rel. 32, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROSTACLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE
   SEQUENCE FROM N.A.
MEDLINE; 94139918.
ADAM M., BOTE Y., RUSHWORE T.H., MULLER G., BASTIEN L., MCKEE K.T.,
METTERS K.M., ABRAMOVITZ M.;
"Cloning and expression of three isoforms of the human EP3 prostanoid
receptor.";
  Gaps
   SCHWID A., THIERRAUCH K.H., SCHLEUNING W.D., DINTER H.; "Splice variants of the human EP3 receptor for prostaglandin E2."; Eur. J. Biochem. 228:23-30(1995).
   YANG J., XIA M., GOETZL E.J., AN S.;
Tcloning and expression of the EP3-subtype of human receptors for
prostaglandin E2.";
Biochem. Biophys. Res. Commun. 198:999-1006(1994).
  ö
  MEDLINE; 94183149.
KUNAPULI S.P., FEN MAO G., BASTEPE M., LIU-CHEN L.-Y., LI S.,
CHEUNG P.P., DERIEL J.K., ASHBY B.;
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   1; Length 365;
   Indels
                EXTRACELLULAR (POTENTIAL).
   6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
  P -> RA.
V -> S (IN REF. 3 AND 4).
S -> F (IN REF. 3).
F302B36A CRC32;
CYTOPLASMIC (POTENTIAL).
                                 CYTOPLASMIC (POTENTIAL).
  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
   ö
  BY SIMILARITY.
  Score 34; DB
Pred. No. 19;
                          5 (POTENTIAL)
  2; Mismatches
   POTENTIAL. POTENTIAL.
  152 P
51 V
354 S
39942 MW;
  FEBS Lett. 338:170-174(1994).
   h 58.6%;
Similarity 77.8%;
7; Conservative
  RECEPTOR, EP3 SUBIYPE).
1151
1273
2229
2229
3229
3323
365
365
365
365
  365
  Homo sapiens (Human).
  152 1
51
354 3
365 AA;
   Query Match
Best Local Similarity
Matches 7; Conserv
   ||:|:||||
323 LLERKILLR 331
   SEQUENCE FROM N.A.
   TISSUE-UTERUS;
MEDLINE; 95188908.
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A. MEDLINE; 94183149.
  TISSUE-KIDNEY;
MEDLINE; 94161771
  3 LLIRRILLR 11
131
152
174
204
204
204
304
304
103
310
336
336
  336
DOMAIN
TRANSMEM
DOMAIN
TRANSMEM
                                 DOMAIN
TRANSMEM
DOMAIN
   DISULFID
  VARIANT
CONFLICT
CONFLICT
SEQUENCE
  TRANSMEM
   CARBOHYD
   CARBOHYD
  VARSPLIC
  DOMAIN
  PTGER3
  RESULT 13
PE23_HUMAN
   q
  ó
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  "Molecular cloning and expression of human EP3 receptors: evidence of three variants with differing carboxyl termini."; Br. J. Pharmacol. 112:377-385(1994).
   SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. CAUTION: IN REF. 7 EP3B IS KNOWN AS EP3E, EP3C AS EP3D AND EP3D AS
   AS EP3-I, EP3A, OR EP3A1.
-!- TISSUE SPECIFICITY: EXPRESSED AT LEAST IN SMALL INTESTINE, HEART,
  REGAN J.W., BAILEY T.J., DONELLO J.E., PIERCE K.L., PEPPERL D.J., ZHANG D., KEDZIE K.M., FAIRBAIRN C.E., BOGARDUS A.M., WOODWARD D.F., GIL D.W.,
Cloning and expression of a prostaglandin E receptor EP3 subtype irom human erythroleukaemia cells.";
   MEDLINE; 96074809.

KOTANI M., TANKA I., OGAWA Y., USUI T., MORI K., ICHIKAWA A., NARMONI M., TANKA I., NARAO K.;

MARUMIYA S., YOSHIMI T., NARAO K.;

"Molecular cloning and expression of multiple isoforms of human prostaglandin E receptor EP3 subtype generated by alternative messenger RNA splicing: multiple second messenger systems and tissue-specific distributions.";

Mol. Pharmacol, 48:869-879(1995).
   AN S., YANG J., SO S.W., ZENG L., GOETZL E.J.; Isoforms of the EP3 subtype of human prostaglandin E2 receptor transduce both intracellular calcium and cAMP signals."; Biochemistry 33:14496-14502(1994).
  lochem. J. 298:263-267(1994).
   EMBL; S69200; AAB29854.1; -.
EMBL; L27490; AAC13374.1; -.
EMBL; L27488; AAC13372.1; -.
EMBL; L27489; AAC13373.1; -.
  SEQUENCE FROM N.A.
TISSUE-SMALL INTESTINE;
MEDLINE; 94356288.
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A. MEDLINE; 97230456.
   SEQUENCE FROM N.A.
   95072021
  AND PANCREAS.
                                 from human ery
   TISSUE-UTERUS;
MEDLINE: 9507;
   TISSUE-KIDNEY
```

ö

Gaps ö

Length 390, Indels

DB 1;

411 AA.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETAIN-NEW ZEALAND WHITE; TISSUE-KIDNEY CORTEX;

MEDLINE; 94164982.

ABROMSON R.M., EMESON R.B., TARNG J.L., BREYER M.D., DAVIS L.S.,

ABROMSON R.M., FERRENBACH S.M.;

ABROMSON R.M., FERRENBACH S.M.;

That ternative splicating energies multiple isoforms of a rabbit prostaglandin E2 receptor.";

J. Biol. Chem. 269:6163-6169(1994).

THIS RECEPTOR ROR PROSTAGLANDIN E2 (PGE2). THE ACTIVITY OF THIS RECEPTOR CAN COUPLE TO BOTH THE INHIBITION OF ADENYLATE CYCLASE MEDIATED BY G-I PROTEINS, AND TO AN ELEVATION OF INTRACELLULAR CALCIUM. THE VARIOUS FORMS CAN INTERACT WITH DIFFERENT SECOND MESSENGER SYSTEMS (BY SIMILARITY).

CHORDING RECEPTOR THE SECOND MESSENGER SYSTEMS (BY SIMILARITY).

TERMINUS ARE PRODUCTS: AT LEAST FOUR FORMS THAT DIFFERS AT THE C-ITERNATIVE PRODUCTS: A LIGAND BINDING PROPERTIES BUT DIFFERENT.

CHENTING ARE PRODUCTS: AT LEAST FOUR FORMS THAT DIFFERENT.

CROUPLING PROPERTIES WITH G PROTEINS. THE SEQUENCE OF CLONE 77A IS
  EP3C/EP3-II).
IRYHTNNYASSTSLPCQCSSTLMMSDHLER -> EEFWGN
IN ISOFORM EP3B/EP3-II).
IRYHTNNYASSSTSLPCQCSSTLMMSDHLER -> MRKRRL
REQEEFWGN (IN ISOFORM EP3D).
  IRYHTNNYASSSTSLPCQCSSTLMWSDHLER -> VANAVS
SCSNDGQKGQPISLSNEIIQTEA (IN ISOFORM
  01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PROSTAGLANDIN E2 RECEPTOR, EP3 SUBIYPE (PROSTANOID EP3 RECEPTOR) (PGE
  TISSUE SPECIFICITY: IN THE KIDNEY, HIGH LEVELS OF EXPRESSION ARE SEEN IN MEDULLARY THICK ASCENDING LIMB, AND LOWER LEVELS IN THE CORTICAL AND MEDULLARY COLLECTING DUCTS.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
   Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL)
   Score 34; DB 1
Pred. No. 21;
2; Mismatches
  POTENTIAL. POTENTIAL.
  EMBL; U04274; AAA17413.1; -. EMBL; U04273; AAA17412.1; -.
   58.6%;
   Query Match
Best Local Similarity 77.8
7; Conservative
   STANDARD;
   390
  390
 253
283
307
327
349
390
390
390
390
  347 LLLRKILLR 355
  3 LLIRRILLR 11
 228
2284
284
328
328
350
360
360
360
  360
  PE23_RABIT
P46069;
 TRANSMEM
DOMAIN
TRANSMEM
                                    DOMAIN
TRANSMEM
   CARBOHYD
VARSPLIC
  VARSPLIC
  CARBOHYD
  VARSPLIC
   DOMAIN
  PTGER3
   RESULT 14
PE23_RABIT
  g
G
  ò
   PROJECTION (1) 1. 1. G-protein; Glycoprotein; G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein; Palmitate; Phosphorylation; Alternative splicing. Lipoprotein; Palmitate; EXTRACELLULAR (POTENTIAL).
   CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
3 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
  G_PROTEIN_RECEPTOR; FALSE_NEG.
   6; BAA19951.1;
7; BAA19951.1;
3; BAA19951.1;
                                    CAA58740.1;
CAA58741.1;
CAA58742.1;
CAA58743.1;
   AAA21132.1;
AAA21133.1;
AAA21134.1;
   AAA68193.1;
   AAA60076.1;
  BAA07419.1
BAA07420.1
   AAA68191.1
  AAA68192.1
   AAA21131.1
  BAA07417.1
   AAA21130.1
   BAA07418.
  PS00237;
   GCR_2667;
GCR_2668;
   EMBL: U13217; PEMBL: U13218; PEMBL: D86095; EMBL: D86087; PEMBL: D86088; EMBL: D86088; EMBL: D86088; GCRDB; GCR_088; GCRDB; GCR_088; GCRDB; GCR_088
   X83862;
X83863;
  Lipoprotein; E
DOMAIN
TRANSMEM 5
DOMAIN 7
  013214;
  x83861;
  D38298;
  MIM; 176806
   DOMAIN
TRANSMEM
  DOMAIN
TRANSMEM
DOMAIN
  PROSITE;
  GCRDB;
GCRDB;
GCRDB;
GCRDB;
  GCRDB;
GCRDB;
GCRDB;
   GCRDB;
GCRDB;
GCRDB;
  GCRDB;
GCRDB;
GCRDB;
GCRDB;
GCRDB;
GCRDB;
  GCRDB;
GCRDB;
  GCRDB;
GCRDB;
GCRDB;
   GCRDB;
GCRDB;
   GCRDB;
GCRDB;
   GCRDB;
GCRDB;
  GCRDB;
  GCRDB;
   GCRDB;
  GCRDB;
  EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
   EMBL;
EMBL;
   EMBL;
EMBL;
  EMBL;
EMBL;
  EMBL;
EMBL;
EMBL;
```

```
VENTER J.C.; "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.";
  Science 269:496-512(1995).
-!- SIMILARITY: STRONG, TO E.COLI YRAM
   셤
    SYNTHEST
  ò
   ö
   BY SIMILARITY.

T -> A (IN CLONE 72A).
VIHENN -> EEFWEK (IN CLONE 72A).
MISSING (IN CLONE 72A).
VIHENNEQKDEIQRENRNYSHS -> IRYHINNYASSSTSL
MISCHG (IN CLONE 74A).
MISCHG (IN CLONE 74A).
VIHENNEQKDEIQRENRNYSHSGQHEEARDSEKS -> HSP
   AIGDLQISTHISKTNKYFEGLMKTFHSLAYL (IN CLONE 80A).
   Gaps
   STRAINED / KW20:
MEDLINE: 95350630.

FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F.,
FLEISCHMANN R.D., BULT C.J., TOMB J.-F., DOUGHERTY B.A., MERRICK J.M.,
MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D.,
SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M.,
WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D.,
WILDMAN J.E., PHILLIPS C.A., FORGYEN D.M., BRANDON R.C.,
FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M.,
GNEHM C.L., MCDONALD D.A., SMALL K.V., FRASER C.M., SMITH H.O.,
   ö
  Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
   DB 1; Length 411;
  4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
                                      GCRDB; GCR_0954; --
GCRDB; GCR_0955; --
PROSITE; PS00237; G_PROTEIN_RECEPTOR; FALSE_NEG.
PFAM; PF00001; 7tm_1; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein;
Alternative splicing.
   0; Indels
  EXTRACELLULAR (POTENTIAL).
  7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
  EXTRACELLULAR (POTENTIAL)
   3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
   (POTENTIAL).
   MISSING (IN CLONE 80A)
299918C2 CRC32;
   01-NoV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
HYPOTHETICAL PROTEIN HI1655.
  1 (POTENTIAL).
CYTOPLASMIC (POT
2 (POTENTIAL).
   Score 34; DB ]
Pred. No. 22;
2; Mismatches
  575 AA.
  PRT;
  45600 MW;
   Query Match 58.6%;
Best Local Similarity 77.8%;
Matches 7; Conservative ;
  EMBL; U04275; AAA17414.1;
EMBL; U04276; AAA17415.1;
  STANDARD;
   390 4
411 AA;
   [1]
SEQUENCE FROM N.A.
  ||:|:||||
| 343 LLLRKILLR 351
   3 LLIRRILLR 11
  RESULT 15
YRAM_HAEIN
ID YRAM_HAEIN
   TRANSMEM
DOMAIN
TRANSMEM
  DOMAIN
TRANSMEM
  DOMAIN
TRANSMEM
DOMAIN
  DOMAIN
TRANSMEM
   VARSPLIC
SEQUENCE
  DOMAIN
TRANSMEM
   DOMAIN
CARBOHYD
  VARSPLIC
VARSPLIC
  VARSPLIC
VARSPLIC
   CARBOHYD
  CARBOHYD
  DISULFID
  FRANSMEM
   VARSPLIC
   DOMAIN
   VARIANT
  P45299;
   ò
  g
   SOTION STATES OF
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   ö
  Gaps
   ö
   Score 34; DB 1; Length 575; Pred. No. 31; 3; Mismatches 2; Indels
  TIGR; H11655; -. PROKAR_LIPOPROTEIN; UNKNOWN_1
   Hypothetical protein.
SEOUENCE 575 AA; 63436 MW; 90038AEB CRC32;
   Search completed: February 8, 2000, 00:59:55 Job time: 3784 sec
  58.68;
54.58;
  EMBL; U32838; AAC23299.1; -.
  Query Match 58.6
Best Local Similarity 54.5
Matches 6; Conservative
   1 YRLLIRRILLR 11
   |:|| |:|:|
65 YKLLAARVLIR 75
```

THIS PAGE BLANK (USPTO)

anabaena sp chlamydia p methanobact

026858 045433 095843 096797 026797 0972007 0922663 092385

026658 methanobact 04543 bacilius st 09593 streptonella 02697 methanobact P72007 mycobacteri 09714 schizosacteri 09285 tolypocladi 05974 schizosacch 011875 dengue viru 00234 unidentifie 092378 bacilius an 004396 oryza sativ 09579 saccharomyc 06593 accetaromyc 
011875 009234 0903378 0043378 092RDB P72295 000503 096917 056779 048733

```
MSV021.
Melanoplus sangulnipes entomopoxvirus.
Viruses: dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
  STRAIN-TUCSON;
MEDLINE; 99102612.
AFDOSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
The genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73:533-552(1999).
  STRAIN-TUCSON;
AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AFO613865, AAC97850.1; --.
SEQUENCE Z60 AA, 31180 WW; AB880E14 CRC32;
  01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-MAY-1999 (TrEMBLrel. 10, Last annotation update) ORF MSV021 MTG MOTIF GENE FAMILY PROTEIN.
  (TrEMBLrel. 07, Created)
(TrEMBLrel. 07, Last sequence update)
   65.58;
  21325
   01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
  Query Match
Best Local Similarity 66.
   PRELIMINARY;
  PRELIMINARY;
245
  1 YRLLIRRILLRY 12
  SEQUENCE FROM N.A.
   1 ||| :||| |
234 YYLLIEKILLNY
   SEQUENCE FROM N.A.

    CO    C
  066951
066951;
01-AUG-1998 (
01-AUG-1998 (
    Q9YW71
Q9YW71;
   RESULT
066951
    RESULT
   29YW7.
   125H
  ò
  g
  Q9yw71 melanoplus
C66951 aquifex aeo
084647 chlamydia t
094887 homo sapien
005052 heemophilus
Q77591 drosophila
06487 arabidopsis
096160 plasmodium
P91495 ceenorhabdi
  Q85331 vaccinia vi
Q85383 variola vir
P97213 clostridium
Q9xb05 myxococcus
000326 homo sapten
   43162 homo saplen
Q9zvc8 arabidopsis
  015191 homo sapien
09y136 drosophila
076912 drosophila
043162 homo sapien
  homo sapien
drosophila
  8, 2000, 13:17:42; Search time 209.03 Seconds (without alignments) 3.980 Million cell updates/sec
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
   Description
                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
   hits satisfying chosen parameters:
  225878 seqs, 69334122 residues
  SUMMARIES
   summaries
  OM protein – protein search, using sw model
  064487
  P91495
Q85383
Q85383
P97213
Q9XB05
O00326
  015191
Q9X136
076912
043162
Q9ZVC8
  Q9YW71
O66951
O84647
  Gapop 10.0 , Gapext 0.5
   094887
005052
Q27591
  sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
   sp_archea:*
sp_bacteria:*
sp_fung1:*
sp_fung1:*
sp_human;*
sp_invertebrate:*
sp_mammal:*
   sp_mhc:*
sp_organelle:*
sp_phage:*
   1 YRLLIRRILLRY 12
   222
  Post-processing: Minimum Match 0%
Listing first 45
   US-08-653-294-16
58
  10
   sp_plant: *
   8
   Minimum DB seq length: 0
Maximum DB seq length: 1000000
  1847
179
185
325
325
393
402
454
735
777
777
  SPTREMBL_12:*
   Length
  February
   BLOSUM62
  Query
Match
   662.1
662.1
662.1
662.1
662.1
662.1
662.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
663.1
   Total number of
   Score
  Title:
Perfect score:
   Scoring table:
   ••
   Seguence:
  Searched:
   Database
  Run on:
  Result
   Š
```

260 AA

PRT;

Created)

ALIGNMENTS

ô

Gaps

ö

Length 260; 3; Indels

Score 38; DB 12; Pred. No. 14; 1; Mismatches 3;

408 AA

PRT;

```
NAGASE T., ISHIKAWA K., SUYAMA M., KIKUNO R., MIYAJIMA N., TANAKA A., KOTANI H., NOMURA N., OHARA O.; "Preddiction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."; Pfor large proteins in vitro.";
   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
  [3]
SEQUENCE OF 1-754 FROM N.A.
SEQUENCE OF 1-754 FROM N.A.
SUN H., STONEKING T., LANGSTON Y., LAPLANT Y.;
The sequence of Homo sapiens BAC clone RG442F18.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
   WATERSTON R.H.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL, AB018336; BAA34513.1; -. BEMBL; AC06104; AAD12224.1; -. HSSP; P08567; 1PLS.
   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
TYPE I RESTRICTION ENZIME ECOR124/3 R PROTEIN (HSDR).
   Created)
Last sequence update)
Last annotation update)
  Score 36; DB 4; Le
Pred. No. 1.2e+02;
2; Mismatches 3;
  3BA89171 CRC32;
  [2]
SEQUENCE OF 1-754 FROM N.A.
MEDLINE; 99063792.
SULSTON J.E., WATERSTON R.;
"TOWARG a COMPlete human genome sequence.";
Genome Res. 8:1097-1108(1998).
   1054 AA
  PRT; 1055 AA.
   1054 AA; 119888 MW;
   01-MAY-1999 (TEEMBLEEL 10, 01-NOV-1999 (TEEMBLEEL 10, MIAAAO) PROTEIN.
  62.1%;
58.3%;
   SEQUENCE OF 1-754 FROM N.A.
  SEQUENCE OF 1-754 FROM N.A.
   SEQUENCE OF 1-754 FROM N.A.
  PRELIMINARY;
   7; Conservative
   01-MAY-1999 (TrEMBLrel.
  PRELIMINARY;
                   409 YRLLLTRVLKR 419
  688 YRLLLRRLCGHY 699
  1 YRLLIRRILLRY 12
   SEQUENCE FROM N.A.
   Query Match
Best Local Similarity
Matches 7; Conserv
   MEDLINE; 99087487
   TISSUE-BRAIN
   WATERSTON
  KIAA0793
   SEQUENCE
   094887
   005052
   Ŋ
  RESULT
094887
  RESULT
005052
  DDT TO DE TO
                   셤
   셤
  ò
  ö
  ö
   STRAIN-D/UW-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
  SEQUENCE FROM N.A.
STRAIN-D/UN-3/CX;
STEPHENS R.S., KALMAN S., LAMMEL C.J., FAN J., MARATHE R., ARAVIND L.,
MITCHELL W.P., OLINGER L., TATUSOV R.L., ZHAO Q., KOONIN E.V.,
  MEDLINE; 98196666.

DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L.,
GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R.,
FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
   DECKERT G., WARREN P.V., GAASTERLAND T., YOUNG W.G., LENOX A.L., GRAHAM D.E., OVERBEEK R., SNEAD M.A., KELLER M., AUJAY M., HUBER R., FELDMAN R.A., SHORT J.M., OLSON G.J., SWANSON R.V.; SHORT J.M., OLSON G.J., SWANSON R.V.; EMBLITEG (JUL-1997) to the EMBL/GenBank/DDBJ databases.

EMBL: AE000705; AAC06902.1; --
PFAM: PF00482; GSPII_F: 1.

SEQUENCE 408 AA: 45763 MW; 2E2A7221 CRC32;
   Gaps
  Gaps
   "Genome Sequence of an Obligate Intracellular Pathogen of Humans: Chlamydia trachomatis.";
Science 0:0-0(1998).
   ö
   ó
   63.8%; Score 37; DB 2; Length 408; larity 72.7%; Pred. No. 33; Conservative 1; Mismatches 2; Indels
  Query Match 62.1%; Score 36; DB 2; Length 559; Best Local Similarity 63.6%; Pred. No. 68; Matches 7; Conservative 2; Mismatches 2; Indels
   DAVIS R.W.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AEO01334; AAC68245.1; ...
SEQUENCE 559 AA: 61931 MW; 618B74E1 CRC32;
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
FIMBRIAL ASSEMBLY PROTEIN PILC.
   Last sequence update)
Last annotation update)
   Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
  Aquifex aeolicus.
Bacteria: Aquificales; Aquificaceae; Aquifex.
   559 AA
  Created)
   PRT;
   08,
08,
08,
   Nature 392:353-358(1998).
   PRELIMINARY;
   01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
  :| || || || || || || 250 FRALIHRILLR 260
  1 YRLLIRRILLR 11
   Ouery Match
Best Local Similarity
Matches 8; Conserv
   1 YRLLIRRILLR 11
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   EFFLUX PROTEIN.
  DAVIS R.W.;
  084647
084647;
   ო
```

ò

ö

Gaps

ö

Indels

Haemophilus influenzae

Length 1054;

the

ö

Gaps

ö

MEDLINE;

,

```
STRAIN-CV. COLUMBIA,
VYSOTSAIA V.S., OSBORNE B.I., SCHWARTZ J.R., TORIUMI M., KWAN A.,
VYSOTSAIA V.S., OSBORNE B.I., SCHWARTZ J.R., TORIUMI M., BRENDEL V.,
BUCHLER E., CONWAY A.B., CONWAY A.R., DEWAR K., FENG J., KIM C.,
KURTZ D., LI Y., PALM C.J., SHINN P., SUN H., DAVIS R.W., ECKER J.R.,
SUDMITTED N.A., THEOLOGIS A.,
SUDMITTED (AUG-1997) to the EMBL/GenBank/DDBJ databases.
  "A novel, tissue-specific integrin subunit, beta nu, expressed in the midgut of Drosophila melanogaster.";
Development 118:845-858(1993).
-!- FUNCTION: INTEGRINS ARE A LARGE FAMILY OF CELL SURFACE GIACOPROTEINS THAT MEDIATE CELL TO CELL & CELL TO MATRIX ADHESION.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: WITH OTHER BETA CHAINS FROM THE INTEGRIN FAMILY OF CELL-SURFACE RECEPTOR.
EMBL: L13305; AAC37169.1;
--- HSSP; P00750; 17FG.
  Arabidopsis thaliana (Mouse-ear cress).
Bubryophyta; Tracheophyta; Embryophyta; Tracheophyta; Streptophyta; Embryophyta; Expermatophyta; euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
tissue-specific integrin subunit, beta nu, expressed
   FLYBASE; FBGN0010395; beta-Int-nu.
PROSTIE; PS00243; INFEGRIN, BETA; 1.
PFAM: PF00362; integrin, B. 1.
Integrin; Cell adhesion; Transmembrane; Glycoprotein; Repeat.
   Length 799;
   Score 35; DB 10; Length 81
Pred. No. 1.5e+02;
3; Mismatches 1: Indels
  4; Indels
  Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC002411; AAC16741.1; -.
SEQUENCE 814 AA; 92446 MW; AE8AF982 CRC32;
  THEOLOGIS A.; Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
   to the EMBL/GenBank/DDBJ databases
  Created)
Last sequence update)
Last annotation update)
   Score 35; DB 5;
Pred. No. 1.5e+02;
  0F909972 CRC32
   814 AA
  0; Mismatches
   PRT;
  90741 MW;
  60.3%;
   66.3%;
  07,
07,
   Ouery Match
Best Local Similarity 66...
18. Conservative
   Conservative
   PRELIMINARY;
  01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
01-AUG-1998 (TrEMBLrel.
F20D22.3 PROTEIN.
   Query Match
Best Local Similarity
  STRAIN-CV. COLUMBIA;
THEOLOGIS A.;
  Submitted (AUG-1997)
   61 YRCLSRROLLNY 72
   SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
   1 YRLLIRRILLRY 12
   STRAIN-CV. COLUMBIA;
  799 AA;
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   Arabidopsis
   NON_TER
NON_TER
SEQUENCE
   064487
  RESULT
064487
  g
         STATES
  à
   ö
   "Whole-genome random sequencing and assembly of Haemophilus influenzae
   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
   Gaps
   PELSICHMAN N.A. PARAS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., FELSCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., MERRICK J.M., MCKELAVAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCANNE J.D., SCOTT J.D., SHIRLEY R., LIU L., GLODEK A., KELLEY J.M., WHIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOW E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., VENTER J.C., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O., VENTER J.C.;
  KERLAYAGE A.R., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAYAGE A.R., BULT C.J., TOMB J.F., DOUGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FILIAUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIELEY R., LIU L.I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRITCHMAN J.L., FUHRMANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
   L TATUSOV R., MUSHEGIAN A.R., BORK P., BROWN N.P., HAYES W.S., BORODOVSKY M., RUDD K.E., KOONIN E.V.; Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coll."; Curr. Biol. 6:279-291(1996).
   ö
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
  Length 1055;
  WHITE O., CLAYTON R.A., KERLAVAGE A.R., FLEISCHMANN R.D.; Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases. EMBL; U32808; AAC22934.1; -. TIGR; H11285; --
   2; Indels
   Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases
  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
INTEGRIN BETA SUBUNIT (FRAGMENT).
   1055 AA; 120709 MW; 9F1C0713 CRC32;
  Score 36; DB 2; I
Pred. No. 1.2e+02;
2; Mismatches 2;
   799 AA.
   <BETA>INT.
Drosophila melanogaster (Fruit fly).
  62.1%;
63.6%;
   Science 269:496-512(1995).
   7; Conservative
  PRELIMINARY;
  SEQUENCE FROM N.A.
TISSUE=MIDGUT ENDODERM;
MEDLINE; 94357079.
YEE G.H., HYNES R.O.;
   ||||:|| | :|
|1017 RLLVRRALQKY 1027
  2 RLLIRRILLRY 12
  Best_Local Similarity
Matches 7; Conserv
  SEQUENCE FROM N.A. MEDLINE; 96398784.
  SEQUENCE FROM N.A. MEDLINE; 95350630.
  SEQUENCE FROM N.A.
  VENTER J.C.;
```

SEQUENCE

Query Match

ô qq

Q27591 Q27591; 9

RESULT Q27591

0

Gaps

ö

Length 814;

```
SEQUENCE
  Q85383
Q85383;
   085331
  RESULT 11
085383
AC 085383
AC 085383
AC 085383
DT 01-NOV
DT 01-NOV
DT 01-NOV
DE HOMOLO
GN Variol
OC Viruse
OC Viruse
OC Viruse
RR SEQUEN
RR SEQUEN
RR MASSUN
RR MASSUN
RR RA MASSUN
RR RA MASSUN
RR REDILIP
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RASUN
RR RR RASUN
RR RR RR RR RR RR RR RR RR RR R
   RESULT
  셤
   ò
  셤
  ŏ
   ö
  MILSON R., ALNSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
MILSON R., ALNSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDINER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
LIGHTAING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SAUNDERS D., SHOWNKEEN R.,
THIERRY-MIEG J., THOMAS K., VADDIN M., VADGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
   Gaps
  MEDILIRE; 99021743.

MEDILIRE; 99021743.

MEDILIRE; 99021743.

KOONIN E.V., SHALLOM S., MASON T., YU K., FUJII C., PEDERSON J.,

SHEN K., JING J., ASTON C., LAI Z., SCHWARTZ D.C., PERTEA M.,

SALZBERG S., ZHOU I., SUTTON G.G., CLAYTON R., WHITE O., SMITH H.O.,

FRASER C.M., ADAMS M.D., VENTER J.C., HOFFMAN S.L.;

"Chiconosome 2 sequence of the human malaria parasite Plasmodium
  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida; Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
  01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
SIMILARITY TO RAI INTEGRAL MEMBRANE GLYCOPROTEIN GP120 PRECURSOR.
   ö
  plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
  60.3%; Score 35; DB 5; Length 1712; 50.0%; Pred. No. 3e+02; ive 3; Mismatches 3; Indels
   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL 204.0 KD PROTEIN.
  EMEL: AE001386; AAC71852.1; -.
Hypothetical protein.
SEQUENCE 1712 AA; 204013 MW; E8B0BD71 CRC32;
   PRT; 1847 AA.
   1712 AA
   01-WAY-1997 (TrEMBLrel. 03, Created)
01-WAY-1997 (TrEMBLrel. 03, Last seq
01-NOV-1998 (TrEMBLrel. 08, Last ann
  PRT;
  Science 282:1126-1132(1998).
  Query Match
Best Local Similarity 50...
Best Local 6; Conservative
  PRELIMINARY;
   PRELIMINARY;
   r23Hz.ı.
Caenorhabditis elegans.
  Nature 368:32-38(1994).
   |:::|||| |
| 1316 YKIYLRRILFGY 1327
  1 YRLLIRRILLRY 12
                              |::||:|| |
263 LVVRRLLLNY 272
3 LLIRRILLRY 12
   SEQUENCE FROM N.A.
   STRAIN=BRISTOL N2;
MEDLINE; 94150718.
   SEQUENCE FROM N.A.
   falciparum.
   PFB0315W.
   P91495
P91495;
  096160
   g
   ò
     ò
   g
```

```
ö
  ö
  Gaps
   AEQUENCE FROM N.A.
MEDLINE: 89094998.
THOMPSON C.L., HOODA-DHINGRA U., CONDIT R.C.;
"Fine structure mapping of five temperature-sensitive mutants in the 22-and 147-kilodalton subunits of vaccinia virus DNA-dependent RNA
  Gaps
   Vaccinia virus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
  dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
   MASSONS R.F., ESPOSITO J.J., LIU L.I., QI J., UTTERBACK T.R., KNICHT J.C., AUBIN L., YURAN T.E., PARSONS J.M., LOPAREV V.N.; "Potential virulence determinants in terminal regions of variola
  ö
  ö
  Length 1847;
   Length 179;
   Score 35; DB 5; Length 184
Pred. No. 3.2e+02;
2; Mismatches 3; Indels
  Indels
STRAIN-BRISTOL N2;
WAMSLEY P., BRADSHAW H.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, U80033; AAC48199.1; -
SEQUENCE 1847 AA; 199637 MW; BOA25E0F CRC32;
   Last sequence update)
Last annotation update)
  Last sequence update)
Last annotation update)
  3;
   DB 12;
54;
  smallpox virus genome.";
Nature 366:748-751(1993).
EMBL; L22579; AAA60829.1; -.
SEQUENCE 185 AA; 21355 MW; 3B9F48DE CRC32;
   179 179 179 AW; 7E103F8D CRC32;
  185 AA
  3; Mismatches
   RNA POLYMERASE 22 KD SUBUNIT (FRAGMENT).
   Score 34;
Pred. No.
   (TremBLrel. 01, Created)
(TremBLrel. 01, Last seq
(TremBLrel. 08, Last ann
   Created)
  PRT;
  HOMOLOG OF VACCINIA VIRUS CDS J4R
  5
   58.68;
   60.3%;
58.3%;
   01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
   polymerase.";
J. Virol. 63:705-713(1989).
EMBL; M24216; AAA48277.1; -.
NON_TER 179 179
   Query Match
Best Local Similarity 50.0
Matches 6; Conservative
  Conservative
  PRELIMINARY;
  PRELIMINARY;
  [1]
SEQUENCE FROM N.A.
STRAIN-BANGLADESH-1975;
MEDLINE; 94088747.
   24 YAVINRNVLLRY 35
   ||| : |:|| |
19 YRLNVPRVLLPY 30
   1 YRLLIRRILLRY 12
   1 YRLLIRRILLRY 12
   Query Match
Best Local Similarity
Matches 7; Conserv
  Orthopoxvirus.
   Variola virus.
   Viruses; dsDNA
Orthopoxvirus.
   01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
```

P97213 P97213;

ô g

```
TISSUE-UTERUS;
MEDLINE: 97230456.
KOTANI M., TANAKA I., OGAWA Y., USUI T., TAMURA N., MORI K.,
NARUMIYA S., YOSHIMI T., NAKAO K.;
"Structural organization of the human prostaglandin EP3 receptor
   MEDLINE; 97230456.
KOTANI M., TANDRA I., OGAWA Y., USUI T., TAMURA N., MORI K., NARUMIYA S., YOSHIMI T., NAKAO K.;
"Structural organization of the human prostaglandin EP3 receptor
  ..
0
  ÷
   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TREMBLrel. 12, Last annotation update)
PROSTAGLANDIN EPJ RECEPTOR SUBTYPE ISOFORM.
HOMO sapiens (Human).
Elwaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   58.6%; Score 34; DB 4; Length 393; 77.8%; Pred. No. 1.1e+02; ive 2; Mismatches 0; Indels
  Query Match 58.6%; Score 34; DB 4; Length 402; Best Local Similarity 77.8%; Pred. No. 1.2e+02; Matches 7; Conservative 2; Mismatches 0; Indels
  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
PROSTAGLANDIN EP3 RECEPTOR SUBTYPE ISOFORM.
   4EC7995B CRC32;
   6A6BE279 CRC32;
   402 AA
   393
   PRT;
   PRT;
  subtype gene (PTGES3).";
Genomics 40:425-434(1997).
Genomics 40:425-434(1997).
FPML. D86097; BAA19958.1; -...
FPAM; PF00001; 7tm_1; 1.
PRINTS; PR00428; PRCSTAGLNDNR.
PRINTS; PR00584; PRSTNOIDEB3R.
SEQUENCE 402 AA; 44937 MW; 6
  subtype gene (PTGER3).";
Genomics 40:425-434(1997).
EMEL, D86098; BAAJ1959.1; -.
PFAM; PF00001; 7tm_1; 1.
PRINTS; PR00428; PROSTAGLMDNR.
PRINTS; PR00682; PRSTNOIDEP3R.
PRINTS; PR00584; PRSTNOIDEP3R.
   393 AA; 43683 MW;
   Query Match
Best Local Similarity 77.8
Matches 7; Conservative
   PRELIMINARY;
   PRELIMINARY;
  Homo sapiens (Human).
   [1]
SEQUENCE FROM N.A.
  347 LLLRKILLR 355
   SEQUENCE FROM N.A. TISSUE-UTERUS;
   347 LLERKILER 355
  3 LLIRRILLR 11
  3 LLIRRILLR 11
   SEQUENCE
   000326
   RESULT 15
000325
AC 000325, DT 01-JUL-
DT 01-JUL-
DT 01-JUL-
DT 01-NUL-
DT 01-NUL-
DT 01-NUL-
DE PROSTAC
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C EUKARYS
C
   000325
   HD DT THE BEACH OF
  ò
  g
   ö
   g
   ö
  ö
  ö
  STRAIN-ER-15;
PAITAN Y., ORR E., RON E.2., ROSENBERG E.;
"Genetic and functional analysis of genes required for the post-
modification of the Polyketide antibiotic TA of Myxococcus xanthus.";
submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ132503; CAB46503.1; -...
SEQUENCE 325 AA; 35985 MW; 4CC64E85 CRC32;
   Gaps
   Gaps
  Gaps
   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-1997 (TrEMBLrel. 03, Last annotation update)
CDU2, CDU1, TCDD, TCDB, TCDE, TCDA, TCDC, CDD1, CDD2, CDD3, AND CDD4
GENES.
  Clostridium difficile.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
Clostridium.
  ö
  ö
  Query Match 58.6%; Score 34; DB 2; Length 313; Best Local Similarity 41.7%; Pred. No. 92; Matches 5; Conservative 5; Mismatches 2; Indels
   Bacteria; Proteobacteria; delta subdivision; Myxobacteria;
Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
  Score 34; DB 2; Length 325;
Pred. No. 95;
  Indels
   SEQUENCE FROM N.A.
STRAIM-VPI10463;
VON EICHEL-STREIBER C.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X92982; CAA63559.1; ...
EMBL; X92982; CAA63558.1; ...
SEQUENCE 313 AA, 33380 MM, 4F20347A CRC32;
  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN.
                                       Score 34; DB 12;
Pred. No. 56;
3; Mismatches 3;
   313 AA.
  325 AA
  1; Mismatches
   PRT;
                               58.6%;
  58.6%;
58.3%;
Ouery Match
Best Local Similarity 50.00
The conservative
  7; Conservative
   PRELIMINARY;
  PRELIMINARY;
   ||:: ||: ::|
259 YRVVARRLSIKY 270
   202 YRLTVDRFPLRY 213
  | :: | :||||
24 YAVINRNVLLRY 35
  1 YRLLIRRILLRY 12
   1 YRLLIRRILLRY 12
   1 YRLLIRRILLRY 12
  Query Match
Best Local Similarity
```

Myxococcus xanthus.

Q9XB05; Q9XB05

RESULT Q9XB05

ô g SEQUENCE FROM N.A.

Matches

à qq

ö

Gaps

ö

Gaps

Search completed: February 8, 2000, 13:17:44 Job time: 32493 sec

us-08-653-294-16.rspt

us-08-653-294-16.rge

```
AF134389 Uncultured archaeon AF134390 Uncultured archaeon AJ133622 Uncultured archaeo
   http://webace.sanger.ac.uk/cgi-
bin/display?db-wormaccéclass=Sequence &object=F14B6
Current sequence finiahing criteria for the C. elegans genome
sequencing consortium are that all bases are either sequenced
unambiguously on both strands, or on a single strand with both a
dye primer and dye terminator reaction, from distinct subclones.
Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is NOT necessarily the entire insert of
the specified clone. It may be shorter because we only sequence
overlapping sections once, or longer because we arrange for a small
impoRTANT: This sequence is not the entire insert of clone F14B6.
It may be shorter because we only sequence
overlapping sections.
It may be shorter because we only sequence overlapping sections
once, or longer because we only sequence overlapping sections
neighbouring submissions.
The true left end of clone F41D3 is at 2917 in this sequence. The
true right end of clone F41D3 is at 19221 in this sequence. The
start of this sequence (1. .109) overlaps with the end of sequence
   Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Caenorhabditis elegans.
Eukaryota, Metazoa; Nematoda; Secernentea; Rhabditida;
Bukaryota, Matazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditiodea; Rhabditidae; Peloderinae; Caenorhabditis.
Caenor, Rhabditina; Rhabditidae, Rhabditidae; Peloderinae; Caenorhabditis.
Caenor, Aniscough, R., Anderson, K., Baynes, C., Berks, M.,
Bonfledd, J., Burton, J., Connell, M., Copsey, T., Cooper, J.,
Coulson, A., Caraton, M., Dear, S., Du, Z., Durbin, R., Favello, A.,
Colson, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M.,
Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N.,
Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.,
Saunders, D., Shownkeen, R., Sanladon, N., Smith, A., Sonnhammer, E.,
Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,
Vaughan, K., Wateston, R., Watson, A., Weinstock, L.,
Wilkinson-Sproat, J., and Wohldman, P.,
C. Mo of contiguous nucleotide sequence from chromosome III of C.
   The end of this sequence (29177. .29283) overlaps with the start of sequence Z81337.
   Direct Submission
Submission
Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.wustl.edu
fon Jan 28, 1998 this sequence version replaced gi:1665918.
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
   For a graphical representation of this sequence and its analysis
   Caenorhabditis elegans cosmid F14B6, complete sequence. 281502.1 G1:2814053
   complement(947, .2169)
/gene="F14B6.1"
complement(join(947, .1390,1835, .2063,2114, .2169))
  901
902
1296
  /organism="Caenorhabditis elegans"
  114.88
115.02
169.89
  Nature 368 (6466), 32-38 (1994)
   /db_xref="taxon:6239"
  Location/Qualifiers
120.09
120.08
117.04
   /chromosome="I"
   (bases 1 to 29283)
  39.00
39.00
39.00
   seq_documentation_block:
LOCUS CEF14B6
   seq_name: gb_in1:CEF14B6
   elegans
   White, S
  gb_ba2:AF134389
gb_ba2:AF134390
gb_ba1:UAR133622
   DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  REFERENCE
AUTHORS
TITLE
  gene
   JOURNAL
  REFERENCE
  JOURNAL
  FEATURES
  COMMENT
  Len i Documentation ...
29283 1 281502 Caenorhabditis elegans 296589 1 295311 Caenorhabditis elegans 296589 1 295311 Caenorhabditis elegans 296589 1 295312 Caenorhabditis elegans 306999 1 AL121256 Home sapiens chromos 59865 1 AC014422 Drosophila melanogas 7150 1 AB007931 Home sapiens mRNA for 86130 1 AC013482 Genomic sequence for 86130 1 AC013472 Home sapiens chromos 97906 1 AL108912 Home sapiens chromos 135305 1 AL080317 Human DNA sequence 142796 1 AC013772 Home sapiens chromos 375 1080134 Human immunoglobulin head 550 1 AL115310 Botrytis cinerea strain 1 AL115311 Botrytis cinerea strain 1 AF142982 Uncultured archaeon 2 1047 1 AF015992 Uncultured archaeon 2 1045 1 AC01543 Prosophila melanogas 104365 1 AC01543 Prosophila melanogas 104367 1 AC01545 Home sapiens DNA se 105726 1 AF03352 Mus musculus T cell 130435 1 AC008464 Home sapiens chromos 25532 1 AC0084
   1 Uncultured archaeon BU
4 uncultured euryarchaec
4 uncultured euryarchaec
2 uncultured euryarchaec
5 uncultured euryarchaec
   AC017155 Drosophila melanoga
AC011085 Homo sapiens chrome
AC006377 Homo sapiens clone
AC016259 Homo sapiens chrome
AL132800 Homo sapiens chrome
  AC009602 Leishmania major chu
AC008413 Homo sapiens chromos
AC002453 Human BAC clone GS44
AC006300 Arabidopsis thallana
AC006300 Arabidopsis thallana
   AC011180 Homo sapiens clone
AF165139 Homo sapiens chromo
   -MODEL-frame+_p2n.mcdel -DEV=xlp
-Q=/cgnl_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-Q=/cgnl_1/USPTO_spool/US08653294/runat_04022000_160701_15779/app_query.fasta.1
-Q=/cgnl_1/USPTO_spool/USO8653294/runat_040200_GGAPDTT=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GGAPDF4.500
-QGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-UST=45 -DOCALIGN=200 -THR_SCORE=pct -ALIGN=15 -MODE=LOCAL
-OUTPMT=pfs -NORM=ext -MINLEND -MARKIX-END=1000000 -USER-US08653294
  ! Documentation
   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993–2000 Compugen Ltd.
   130435
265232
40000
63934
  176332
176463
179656
191442
  89885
145531
   155664
  70319
  ren
     out_format
  311.20
3.8e+03
6.2e+03
1.7e+03
   76+03
16+04
36+03
16+03
96+03
96+04
76+04
  EScore
  269.92
3.8e+03
   .9e+03
.5e+03
.4e+03
.8e+03
  6e+03
7e+03
   6e+03
7e+03
8e+03
   8e+04
0e+04
1e+04
  .2e+04
.3e+04
   .1e+04
   32.32
32.32
32.32
35.54
43.96
46.42
53.93
53.98
  250076
112.32
89.02
113.9.17
113.9.17
99.17
99.25
99.25
99.25
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120.29
120
   80.43
79.99
79.38
79.22
79.22
78.69
122.34
120.44
120.44
     OM of: US-08-653-294-16 to: GenEmbl:*
  Database sequences: 821193
Database length: -1518192014
Search time (sec): 11370.480000
  Strd Orig
   쮼
   Search information block:
  Command line parameters:
  Date: Feb 8, 2000 4:41
  Query: US-08-653-294-16
Query length: 12
  Database: GenEmbl:*
  gb_pl2:cNS01CBA
gb_pl2:cNS01CBA
gb_bal:AF142982
gb_bal:AF142982
gb_bal:AF015992
gb_bal:AF015978
gb_btg:AF015978
gb_htgs:AC015445
gb_htgs:AC015445
gb_htgs:AC004464
gb_htg3:AC004464
gb_htg3:AC008463
gb_htg3:AC008463
gb_htg3:AC008463
gb_htg4:AF01180
gb_htg4:AF011180
gb_htg4:AF011180
   gb_pri:AB007931
gb_pl3:AC013482
gb_pr3:AC005365
gb_hrg1:HS1141E20
gb_pr3:HSJ1112D6
gb_htg7:AC013772
  9b_pr4; AC006377
9b_ht96: AC016259
9b_ht91: CNS01DTM
9b_ba1: AF142981
9b_ba1: AF142981
   gb_htg1:CEY47H10
gb_htg2:HSDJ655C5
  gb_htg5:AC014422
   gb_ba1:UEU131272
gb_ba1:UEU131265
  gb_pr3:HSU80134
   gb_in1:CEF14B6
  Seguence
```

```
jóin(17155. 17218,17267. 17455,17898. 18232,18389. 18591,
19031. 19178,19319. 19537)
/gene="fil486.6"
/note="cDNA EST yk549c2.3 comes from this gene"
  jóin(20434. .20524,21137. .21250,21298. .21659,21969. .22168,
22218. .22344,22393. .22482,22538. .22684)
   /translation="MKARKILITVAILASLLAYRYYSORTMEFLIEEDOMCLOREWYE
SEFFCQHSEILNVFNKFKFSLKFFKKSNIFNNIIYSRFTISSOINSTADYGNSYQISF
SDVOGSTFWHIHIPKISGSPEILLIVISRPDDFSRRNYIRHTWMSQENEIKYLFLIGLG
ANDGKIKEVWAAEAKLFGOIVVTRADRYSKSKLSFFTLTLLEGVSKVPSAQLIGKID
GDVLFFPNLFFSTIRKENSMINVTSASYYGRAAFAYPIVSNCKRFKYNFRSNSLI
SFGCTRYAFYLAGPFYLVTRSAALRLEASKHRNFHKIEDTLITGVLADDTDVSRVQL
  /translation="MLSFLQSFFKSLGYEDYFKPIAPSSPRFFTKYCNETQKKITIVI
DSNNIIRPFVFDESNEREPLFVAHLGCSECMRWNRMYGENIAENNEPETDSEDETDYE
  NSFLQNENLTVDD1STGACALLNETAEKLKQMFSSSG1SGRKESSEGTNKDLIKFGEL
EIRGDEEEDDDDESYVEGEEEDSSDEDLDDEDQEGESSIEPRLSETFKKSEARESLSS
  /proteIn_id="CaB04107.1"
| DateIn_id="CaB04107.1"
| DateIn_id="G1:387581"
| Ab xref="SPTRENE.:067163"
| At xrenslation="MEISLQKKLIFLFLFANASSVSGCGSFDYYLLKSISGLLNYQID
   RKVVMEEARIYGDMVVVDLKDIYEELPFKSLTTLLYGTSKASEFKLIGKIDEDIMFFP
DKILPLLEQUALIDPSSESIYGMLFABGGYVYRDKEHRWFVDGSTYGCDMFPPYTGGLF
YLYTQDAAKKILNATKHRIFIPIEDALINGILANDCKIPRIHLPEIYGDHSLTDEDT
RGYLAWHTGKNDQOFLDYFYRKLSESRLKKRILDEKNHHLFY"
   /translation-"MSVAAKPRRLDLOGIRGLAILSVLGFHFYPALFPNGYLGVDGFF
VLGGFLAGALLKRABNEPTCTLITLYSKRRKRILDFYLLITLLSMISLYTIPEDTSI
PINOKSAMRALLFVSNAPKSVODDYFTMLABAVDIFFHTWSLSVEVOFYFLVFFIFLF
AIKLEGELLSYAFFFTPSNTSFNSVFARIWOFLIGMIVFLLSSHSKKSPFAEKNIEEC
NKIEDDEBWYTORAQKPSILHLISYPPLISTILICIIPYOFUNDFVRPLYTLAMGALM
LISBNMILLSKWILTSYTGDISSYSYLIHWPYYAYWKLAFDGDVNLITISLLSSILLAI
IVFEFFEKWYILKSSYSIGLLIVFLFFLNVILLINKDELIPDREENNNHNSSMNTDDAI
  SETSDSELGODSPNPNLSEALNNCIENFDQLVDEVVRHKDFHERSQLLRVLEECLGNM
  KEAPVKDLVIYQKFRDEHEDLEESENEPRMSDEAEKLVEDKIIEESDEDSFDIIGRDE
   KNLQKEHEEHKLALTNCMKSGRIFNSSVPETKDFGSSFTISFADIQKTHSWLYLPKFQ
NSMSSEILMIVASRTDSFARRNVLRKTWMNPENSEIIKDGRMKALFLVGMTDGDDSRM
   jón(23603. .23727,23784. .24048,24104. .24209,24287. .2
24425. .24635,24799. .24965,25030. .25343,25388. .25514,
25566. .25680,25729. .25933,25988. .26251)
/gene="Fi486.5"
  HRINLGQEKGTDLVFAWHSPLNDPEYKDLYYKTMSSQQFKEKLRLQEINVT"
   Length: 12
Gaps: 0
Percent Identity: 66.667
   ELDDDSNGKEEEELELDVTQEDSEDDEQFFSL"
   1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
      /protein_id="CAB04104.1"
/db_xref="G1:3875878"
/db_xref="SPTREMBL:062160"
   /protein_id="CAB04109.2"
/db_xref="GI:582444"
/db_xref="SPTREMBL:062165"
  /db_xref-"SPTREMBL:062164"
  to: 29283
   /protein_id="CAB04108.1"
/db_xref="G1:3875882"
   from: 1
  20434. .22684
/gene="F14B6.4"
   17155. .19537
/gene="F1486.6"
   /gene="F14B6.4"
   23603. .26251
/gene="F14B6.5"
   /codon_start=1
   45.00
4.091
91.667
  to: CEF14B6
   alignment_block:
US-08-653-294-16 x CEF14B6
   Quality:
Ratio:
  Percent Similarity:
   alignment_scores:
   Align seg 1/1
  gene
  gene
  gene
   CDS
   CDS
   // yeare-fredicted using Genefinder; cDNA EST yk329e12.5 comes from this gene; cDNA EST EMBL:C08202 comes from this gene; cDNA EST EMBL:C08202 comes from this gene; cDNA EST EMBL:C0873 comes from this gene; cDNA EST yk198f11.3 comes from this gene; cDNA EST yk198f11.5 comes from this gene; cDNA EST yk329e12.3 comes from this gene; cDNA EST yk338a7.3 comes from this gene; cDNA EST yk404g5.5 comes from this gene; cDNA EST yk404g5.5 comes from this gene; cDNA EST yk415a6.5 comes from this gene; cDNA EST yk415a6.5 comes from this gene; cDNA EST yk415a0.3 comes from this gene; cDNA EST yk404g5.3 comes from this gene; cDNA EST yk404g5.3 comes from this gene; cDNA EST yk509c5.3 comes from this gene; cDNA EST yk509c5.3 comes from this gene;
   LIEIDSSGRVOPFVSITVEEGSRFYFSPHVGCARCMOWNDVYGROPHRYEETEDDDTDE GVEESSEIEDSDFDDQITFVKPTTPAPLSPETENFIEDKMKFHFQATDIINSYLGKGT DMGIVSNLIRISQTYGVQLKQVSSGRSSMKEIEGILKSLQKEFFQEIEGLNGEISEAE ENNESDIDESFEFVENLELDSDFE"

complement (2938 . 3345)
/gene="F1486.7"
   /protein_id="CAB04105.1"
| Dab_xraf="G1:8975879"
| Abb_xref="SPREMBL:062161"
| Aranslation="MFSVFEWILIFFGILNWFKFTQPSTPEPASRFFTRVCQQLRETV
   /protein_id="CAB54218.1"
/db_xref="G1:5824443"
/translation="MGICYPRWSLFVLHIVFDFLFLVVGFVTSLTIAIMSSIMYFLID
EMTSDSLFEFLLVAFYIDIVILILYAIVYGIAYRCCCRLVDNSIKETSINYSVSSNGEA
  /protein_id="cab04106.1"
/db_xref="G1:3875880"
/db_xref="G1:3875880"
/db_xref="SPTREMBL:062162"
/translation="MSTSSVLPTTPIGKQQVIDLKAGAILRENARKSVLFFGCPLSVVLIVLIKCLCISFWIRRHIRPBFFDFRCAANNGGOPTDYMYAAKRSTAFEKSDPRKFSKIPDDDDDDDNSKTDVINKDKKKKPLYGRSTSPANDIISDAPKIDPRLDFPFPFQ
   DEEQFIEIDIANAPRIYUSKIKSRHGGEEEEHFDLKELKKDEEEKEKKKEKKGKG
LKKAKKLTEAFRLLINSTSTSYIPDPAVSRKPKGKGLKKSKKLINGKRSDEETTROPR
HLVGKSSLEAFTTPRRKSSWMGYLDPODPNFSNGGIRGYPWGASRKPSATTASPS
BKEDEEKLKJESTRWMDDELKYTTFLAPKTTEGTKQVEEGVKEVIQEAHERSQV
PMLKEFEEATTSTEKRLPGGMSKOOMEKKREAFEATTPPISLSDLQPBHSSHGGPAO
APQHIHFESASSTPSTPPAFHFIPPSSEAPYYVEINDADTETVYVSSYTPMYRPVFEN
  RKIDSNHIPAVPPYEPDDDLPMTTMVTLTNTQIVQLSGEETGVVKMKTIRNRVEKVGS
/note="cond EST yk242e8.5 comes from this gene; cDNA EST yk242e8.3 comes from this gene; cDNA EST yk471b10.5 comes from this gene; cDNA EST yk477b2.3 comes from this gene; cDNA EST yk477b2.5 comes from this gene; cDNA EST yk608e9.3 comes from this gene;
   MCHLESTTAKSYDELHLEVSFESFECCVGOLLCHFVFDP.
Complement(9869..9940)
//gene="Filab6.t2"
/note="CAT Met M-tRNA; predicted using tRNAscan-SE-1.11;
preliminary prediction; similar to tRNA-Met"
/complement(9869..9940)
/gene="Filab6.t2"
13752..13823
  complement(join(2938. .3065,3115. .3212,3260. .3345))
/gene="F14B6.7"
/codon_start=1
   complement(join(4016. .4423,4517. .5309,5485. .5820,6093. .675,6563. .6657)
/gene="F1486.2"
   join(15024. .15079,15134. .15329,15847. .16695)
/gene="F14B6.3"
  complement(4016. .6657)
   /gene="F14B6.t1"
  'gene="F14B6.3"
   /codon_start=1
  /codon_start=]
   gene
  gene
  gene
  trna
   gene
  gene
  CDS
   CDS
  CDS
```

```
Direct Submitted (26-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire, Calbilled (26-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 27, 1999 this sequence version replaced gi:6066017.
IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Ordig_LD: 00008 Length: 1036bp
Contig_LD: 00013 Length: 1998bp
Contig_LD: 00039 Length: 1898bp
Contig_LD: 00039 Length: 1840bp
   Length:
   enath:
   Length:
                                 Submission
  00679
  00940
  01212
  00638
   00812
  00892
  01017
   01085
   0097
   CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIGNED
CONTIG
  Contig_ID:
Contig_ID:
  AUTHORS
TITLE
JOURNAL
  COMMENT
  Submitted (07-5EP-1999) Nematode Sequencing Project, Sanger Centre, Hinkton, Cambridge CB10 1RO, UK and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
Washington University, St. Louis, MO 63110, USA. E-mail:
Des@sanger.ac.uk or rewematode wustl.edu
On Aug 10, 1999 this sequence version replaced g1:4938508.
Order of segments is not known: 800 n's separate segments.
IMPORTANT: This sequence is unfailished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the content and the release of this data is based on the sequence may be contained with foreign sequence from E.coli, yeast, vector,
  07-SEP-1999
*** SEQUENCING IN
   Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 296589)
   seq_documentation_block:
LOCUS
HSDJ655C5 306999 bp DNA
LOCUS
DEFINITION Homo sapiens chromosome 6 clone RP4-655C5, *** SEQUENCING IN
PROGREES ***, in unordered pieces.
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 306999)
  NOTE: This is a 'working draft' sequence.
This record will be updated with the finished sequence as soon as it is available and the accession number will
  2401 others
  Gaps: 0
Percent Identity: 66.667

    1. .296589
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"

  188134 TACCGACTACTATCGCGTAGAGTATTAATACAATAT 188169
to: 296589
   /clone="Y47H10"
55009 c 53606 g 92582 t
   1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
  Location/Qualifiers
  from: 1
  295311
295311.10 GT:5725202
HTG: HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans.
  /chromosome="I"
   AL121956
AL121956.2 GI:6469398
HTG: HTGS_PHASE1.
human.
   McLay, K.
Direct Submission
   4.091
  Align seg 1/1 to: CEY47H10
  alignment_block:
US-08-653-294-16 x CEY47H10
  45.00
   seq_name: gb_htg2:HSDJ655C5
  * as soon as it
   seq_name: gb_htg1:CEY47H10
   Homo sapiens
  ø
  phage etc.
   alignment_scores:
Quality:
  Ratio:
  Percent Similarity:
   92991
   ORGANISM
  AUTHORS
TITLE
JOURNAL
  BASE COUNT
ORIGIN
  ORGANISM
   ACCESSION
   REFERENCE
  VERSION
KEYWORDS
   KEYWORDS
SOURCE
   REFERENCE
  FEATURES
  COMMENT
  PERSION
  SOURCE
```

1648bp 1175bp 1781bp 10365bp

458bp

196bp

1722bp 1260bp 1606bp 299bp

1083bp 1408bp 1477bp 1742bp 1888bp

```
2 (sites)
Seki,N., Ohira,M., Nagase,T., Ishikawa,K., Miyajima,N.,
Nakajima,D., Nomura,N. and Ohara,O.
Characterization of cDNA clones in size-fractionated cDNA libraries
from human brain
DNA Res. 4 (5), 345-349 (1997)
   Submitted (08-0CT-1997) to the DDBJ/EMBL/GenBank databases. Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail.codnainfo@kazusa.or.jp, Tel:+81-438-52-3913, Fax:+81-438-52-3914)
                Direct Submission
Submitted (16-007-1999) Celera Genomics, 45 West Gude Drive,
Submitted (16-007-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
This sequence was identified as CDM:10210882 by the submitter.
This sequence will sequence e-mail to fly@celera.com.
* NOTE: This is a "working draft" sequence.
* This sequence will be replaced
* by the flished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
  AB007931.1 GI:3413885
KIAA0462 protein.
Homo sapiens male brain cDNA to mRNA, clone_lib:pBluescriptII SR
plus clone:HG0891.
Homo sapiens
   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 7150) Obara.0. Direct Submission
   seq_documentation_block:
Locus AB007931 7150 bp mRNA PRI 13-AUG-1998
DEFINITION Homo sapiens mRNA for KIAA0462 protein, partial cds.
ACCESSION AB007931
  to: 59865
  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
16683 a 13092 c 13361 g 16729 t
  Length: 12
Gaps: 0
Gaps: 0
Percent Identity: 66.667
  /clone_lib-"pBluescriptII SK plus"
/sex-"male"
  49675 TATCGACTACTTTTGCAATCGATTCTTGTTCGATAC 49640
  from: 1
  1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
   /organism="Homo sapiens"
/db_xref="taxon:9606"
  /tissue_type="brain"
   Location/Qualifiers
1. .7150
  to reverse of: AC014422
   <i. .6832
/gene="KIAA0462"
  /gene="KIAA0462"
  /clone="HG0891"
   Adams, M. and Venter, J.C.
   /chromosome="1
   alignment_block:
US-08-653-294-16 x AC014422/rev
  43.00
3.909
91.667
   .6832
   seq_name: gb_pr1:AB007931
  Quality:
Ratio:
Percent Similarity:
   alignment_scores
  Align seg 1/1
   source
  source
   BASE COUNT
   ORGANISM
AUTHORS
TITLE
JOURNAL
   ACCESSION
VERSION
KEYWORDS
SOURCE
  REFERENCE
AUTHORS
TITLE
JOURNAL
   REFERENCE
AUTHORS
   gene
  MEDLINE
  JOURNAL
   CDS
  FEATURES
   FEATURES
  TITLE
   COMMENT
  ORIGIN
  AC014422 59865 bp DNA HTG 16-NOV-1999
Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
  Drosophija melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 59865)
   th the finished sequence
the accession number will
   /clone_lib-"RPCI-4"
48318 c 46393 g 68867 t 71293 others
   Gaps: 0
Percent Identity: 75.000
  sednence
  to: 306999
  Length:
   * NOTE: This is a 'working draft's
* This record will be updated with
* as soon as it is available and th
* be preserved.
  Location/Qualifiers
1. .306999
/organism="Homo sapiens"
/db_xref="taxon:9606"
  1372bp
1097bp
2927bp
1190bp
3272bp
  1704bp
1071bp
1081bp
   2110bp
1126bp
  8584bp
1827bp
2693bp
  1334bp
1861bp
1912bp
1884bp
1208bp
6578bp
   1168bp
   3890bp
   /chromosome="6"
/clone="RP4-655C5"
  from: 1
  Length:
   ength:
  ength:
  Length:
   Length:
  ength:
   AC014422
AC014422.1 GI:6436913
HTG; HTGS_PHASE2.
fruit fly.
  Align seg 1/1 to: HSDJ655C5
  Contig_ID: 01487
Contig_ID: 01519
Contig_ID: 01524
Contig_ID: 01534
Contig_ID: 01532
Contig_ID: 01532
Contig_ID: 01532
Contig_ID: 01632
Contig_ID: 01745
Contig_ID: 01746
Contig_ID: 01746
Contig_ID: 01746
Contig_ID: 01746
Contig_ID: 01822
Contig_ID: 01823
Contig_ID: 01824
Contig_ID: 01834
Contig_ID: 01984
  alignment_block:
US-08-653-294-16 x HSDJ655C5
  01413
01427
01430
01435
01453
  44.00
4.000
91.667
  seq_name: gb_htg5:AC014422
   seq_documentation_block:
LOCUS AC014422
                  Contig_ID:
Contig_ID:
Contig_ID:
Contig_ID:
Contig_ID:
Contig_ID:
Contig_ID:
  ี่๗
  Quality:
Ratio:
Percent Similarity:
  72128
  pieces
   alignment_scores:
   source
  BASE COUNT
ORIGIN
   DEFINITION
   ACCESSION
VERSION
KEYWORDS
  ORGANISM
   REFERENCE
  FEATURES
   SOURCE
```

Streptophyta;

```
Eukaryota; Viridiplantae;
  chromosome
  Ecker, J.R
   Direct
   source
   REFERENCE
AUTHORS
   REFERENCE
AUTHORS
   TITLE
   REFERENCE
AUTHORS
   TITLE
JOURNAL
   TITLE
JOURNAL
  REFERENCE
  JOURNAL
   COMMENT
   CDS
  TITLE
  PVEDBSWFYTELSTIMMOTOTORY

PVEDBSWFYTELSTIMMOTOTORY

KLLEEGGIFLRASYVTASSGALQYDTISLWELLKACAELAGRITUMSKETF

VLYFLLQVSFLVDEGVSPYVROOTISLWELKACAELAGRITUMGKFCIKDDS

VLYFLLQVSFLVDEGVSPYLLQLLSCALCGSKULAALAASSGSSSSSSSSSPAASSG

QATTOSKSSTKKSKREREKREGSTGSOSDOLCTALVNOLUKFADKFTLIOFLRCF

LLESNSSSVRWQAHCLTLHIYRNSKSQOELLLDLMWSIWPELPAYGRKAAQFVDLLG

YFSLKTPQTEKKLKETSSQRAVELLRTQNHILTHNHPNSTYTTTGCSTVETOGYTLESDP

CLUNNNEYVOATTELSTKATTTGQVKLIGSHISKYTKKVIGLLKRTKWYT

INLYNNRTYOATTELSTKATTTGQVKLIGSHISKYTVGLDELRKTKWYTT

INLYNNRTYOATTELGCSSVPANPGYCGNCGENVYQCHKCRSINYDEKDPFLCNACGF

CKYNREADERKPODDSGTAGSTSANNWYILQLAQEYCGDCKNSPDELSKIIGKVY

LCKYNREADERKPODDSGTAGGISSTGASVNRYILQLAQEYCGDCKNSPDELSKIIGKVY

FEHCTILLAALANTALKRISKISSTGASVNRYILQLAQEYCGDCKNSPDELSKIIGKVY

FEHCTILLAALANTALKRISKISSTGASVNRYILQLAQEYCGDCKNSPDELSKIIGKVY

FEHCTILLAALANTALKRISKISSTGASVNRYILQLAQEYCGDCKNSPDELSKIIGKVY

FEHCTILLAALANTALKRISKISTGASTGASVNRYILGLAQEXCAGCHTSSTKCYGCASAV

FEHCTILLAALANTALKRISKISTGASGASTGASCAANTALTANGTGASTACTGASTA
  EATQONNDLIIGKVSTALKGHWANDDLASSLOYEMLLITDSISKEDSGWELRICALS
AQAQUALKRPPVVBNITLMCLRILQKLIRPPAPTSKKNRDVPVBALTTVRFPVCNEIH
AQAQUALKRPPRASYDRAKKCLPIRGIDGNGRAPSKSELRHLYLTTVRFPVCNEIH
RGKRTSPLDLKLGHNNALKCLPIRGIDGNGRAPSKSELRHLYLTTSTYVWRNKQFLSR
LDELSIAGECAAEY LALYQVLTTSAHWKVYLAARGVLPYVGNLITKEIARLLALEEAT
ETDLQQGATALKSLIGLLSSFEVERSTKRPKSREVOTVLPVGTSLCHLUSPT
ETQDMLLEMLEDMTGTSSFEVERSTKRPKSREVOTVLTKEIARLSLIYPER
ETQDMLLEMLEDMTGTSSFEVERSKANVOIFFRLIS
ETQDMLLEMLEDMTGTSSFEVERSKANVOIFFRLIS
ETGDMLLEMLEDMTGTSSFEVERSKANVOIFFRLIS
ETGDMLLEMLEDMTGTSSFEVERSKANVOIFFRLIS
ETGDMLLEMLEDMTGTSSFEVERSKANVOIFFRRIS
ETGTSSFEVERSKANVOIFFRRIS
ETGTSSFEVER
  SEGEGEGETEGDVHTSNRLHMYRLMLLERLLQTLPQLRNYGGVRAIPYMQVILMLTTD
LDGEDEKDKGALDNLLSQLIAELGMDKKDVSKKNERSALNEVHLVVMRLLSVFMSRTK
SGSKSSICESSSLISSATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLL
   DDSGMELLVNNKIISLDLPVÄEVYKKVWCTTNEGEPMRIVYRMRGLLGDÄTEEFIESL
DSTTDEEDEDEDEVKRAGVAQCGELECEMLNRLAGIRDFKOGRHLLTVLLKLESYCVK
VKVNRQQLVKLEMNTLAVWAGTLNALVAEDESKDSGAAVAEDVLSIMEIIDESNA
EPLSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLLRIIPYLSFGEVEKWOI
  GWTTNEKGOVVTKTALLKQMEELIEEPGLTCCICREGYRFQPTKVLGIYTFTKRVALE
EMENKPRKQOGYSTVSHFNIVHYDCHLAAVRLARGREEWESAALQNANTKCNGLLPVW
   LVERFKPYCNFDKYDEDHSGDDKVFLDCFCKIAAGIKNNSNGHQLKDLILQKGITQNA
  LDYMKKHIPSAKNLDADIWKKFLSRPALPFILRLLRGLAIOHPGTOVLIGTDSIPNLH
KLEOVSSDEGIGTLAENLLEALREHPDVNKKIDAARRETRAEKKRMAMAMROKALGTL
  VLALHILPPEGWRATRVEILRRLLVTSGARAVAPGGATRLTDKAVKDYSAYRSSLLFW
ALVDLIYNMFKKVPTSNTEGGWSCSLAEYIRHNDMPIYEAADKALKTFGEEFMPVETF
  KPHTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQIKKITDTNSRIPF
   GPHVPESAFATCLARHNTYLQECTGQREPTYQLNIHDIKLLFLRFAMEQSFSADTGGG
  GRESNIHLIPYIIHTVLYVLNTTRATSREEKNLQGFLEQPKEKWVESAFEVDGPYYFT
  seq_documentation_block:
LOCUS AC013482 82875 bp DNA PLN 09-DEC-1999
DEFINITION Genomic sequence for Arabidopsis thaliana BAC T26F17 from
  translation="EHSVSGRSSAYGDATAEGHPAGPGSVSSS/
  to: 7150
  42.00 Length: 12
3.818 Gaps: 0
91.667 Percent Identity: 58.333
  SEFLDVAGLLSEITDPESFLKDLLNSVP"
  2058 TACAGGTTGATGGTCCGCACCATCTTGGTCCGTTTC 2023
  Align seg 1/1 to reverse of: AB007931 from: 1
  1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
  chromosome I, complete sequence. AC013482
  1861 q
   AC013482.2 GI:6478885
   alignment_block:
US-08-653-294-16 x AB007931/rev
  thale cress.
Arabidopsis thaliana
   1916 c
   seq_name: gb_pl3:AC013482
  ø
  Ratio:
Percent Similarity:
  Quality:
  1797
   alignment_scores:
   SOURCE
ORGANISM
  BASE COUNT
   ACCESSION
   VERSION
KEYWORDS
  ORIGIN
```

```
ECKET.J.R.

Direct Submission

L. Submitted (30-00V-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

(Dases 1 to 82875)
ES Ahinn,P., Brooks,S., Buehler,E., Chao,O., Johnson-Hopson,C.,
Khan,S., Kim,C., Altafi,H., Babi,B., Chin,C., Chiou,J., Choi,E.,
Conn,L., Conway,A., Gonzalez,A., Hansen,N., Howing,B., Koo,T.,
Lam,B., Lee,J., Lee,J., Lee,J., Liu,A., Liu,J., Liu,J., Liu,S.,
Mukharsky,N., Nguyen,M., Palm,C., Pham,P., Sakano,H., Schwartz,J.,
Southwick,A., Thevelly, Palm,C., Pham,P., Sakano,H., Schwartz,J.,
Federspiell,N., Theologis,A. and Ecker,J.
Direct Submission
L. Submitted (09-DEC-1999) Arabidopsis thaliana Genome Center,
Department of Balology, University of Pennsylvania, 38th and
Hamilton Walk, Philadelphia, Pa 19104-6018, USA
On Nov 30, 1999 this sequence version replaced gi:6403470.
  /protein_dd="AAF15527.1"
/db_xref="G1.6552728"
/db_xref="G1.6552728"
/db_xref="G1.6552728"
/db_xref="G1.6552728"
/db_xref="G1.6552728"
/db_xref="G1.6552728"
/db_xref="G1.65527278"
/db_xref="G1.655278"
/db_xref="G1.65527
  LALYRNVTINYLILTLICEMHSIFLHVRKLRRMAGIRDSNTALVKLEWVLNWTAFVFA
RCIPHILITIKLIKDAHKFGKGVELPLALSGMAGMNILNVGLGLDLFHAFRRERSHRR
NOENGNLHDHGE"
   IIKKLAKLEAECRKLRILAKTSSSLSSNQSVDSHSDGGRERVEGSCSDSWASSAFISE
LDQIKNEKGGNRSLQGTTSSTEIDLMDDFLEMERLVALPTETQAKNSKDGYELSLMEK
   LEKIQAEKDDLEREVKCCREAEKRLSLEIEAVVGDKMELEDMLKRVEAEKAELKTSFD
VLKDKYQESRVCFQEVDTKLEKLQAEKDELDSEVICCKEAEKRFSLELEAVYGDKIEM
  Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Chan, S., Kim, C., Altafi, H., Bel, Q., Chin, C., Chlou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lee, J., Liu, A., Liu, R., Liu, S., Mukharsky, M., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Torlumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J.R. Genomic sequence for Arabidopsis thaliana BAC T26F17 from
  KOKLEDAADKNIVLEDRVSHLDGALKECVROLROFRDEQEKNIQAAVTESTKELHSAN
  TGLEKRVLELQKEAEAAKSENMMLRREFLTQREDLEIVMIERDLSTQAAETASKQHLD
  euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
   /translation="MMTGTTLILEPVMDSKDELVKQHAKVAEDAVAGWEKAENEVVEL
Embryophyta; Tracheophyta
   Submitted (13-NOV-1999) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th Street Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (bases 1 to 82875)
   complement(join(2361. .2747,2834. .4239,4324. .4420))
/note="hypothetical protein"
  join(140. .398,676. .953,1145. .1474)
/note="unknown; similar to EST gb|H74506"
/codon_start=1
   1. .82875
/Organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/chromosome="1"
  /evidence=not_experimental/product="T26F17.2"
  /evidence=not_experimental
/product="T26F17.1"
   /protein_id="AAF16547.1"
/db_xref="GI:6552748"
  /clone-"T26F17"
  Unpublished
2 (bases 1 to 82875)
  Submission
```

CDS

CDS

CDS

```
/translation="MAVQVSKKICRVLMIVILFAMMFSAHSNSIDVCVKNCVVNQCMK
ASKKATPAICDNPCKIICDPLNNERYIVPRGNGGPIKRFCRAFSMICSA"
join(23991. .24104,24201. .24450,24546. .24753,24936. .25167,
DYTLLVGDWYKTNHKDLKAQLDNGGKLPLPDGILINGRSSGATLNIEPGKTYRLRISN
VGCNSLDWFRIQHTWKLVEYEGRYTIQNLFSSLDVHYGGSYSVLITADQPAKDXYVY
VSSRTSKILTTTGVLHYSNVAPVSGPIPDGPRIKLSWFRINGARAIRTNLTASGPRPN
POGSYRYGYTNITETITALANNLGHIEGKQRYAVNSASFYPADTPLKLVDYFKIDGVYR
PGSISDQPTNGAIFPTTSVMQADFRAFVEVIFENSEDIVQSWHLDGYSFYVVGMELGK
  /product-"r26F17.10"
/product-"r26F17.10"
/db_xref-"d1.652732"
/translation-"MKIPEKPIFLIFVSLILASSLFTATAKSTIEPCSSNDTCNALL
STLYTYTHYSEVASLFOYDETSILLANDIDLSSPDVENHILDSKLEFKIPITGSCVD
GIRKSVSTHYKTRESONLGSTADSVYGGLVSAROJOGANSVNDPSLLDVGTSLYJPIPP
CACFNGTDNSLPAVYLSYVKEIDTLVGIARRYSTTITDLMNVNAMGAPDVSSGDILA
   WSPASRKYVINDAILRCTIÖVYPRSWTAIYIALDNVGMWNMRSEIWEROYLGOOFYM
RVYTTSTSLRDEYLIPKNALLCGRASSSHR"
21348. .21629
/note="hypothetical protein"
   RIIPVSFMQTIKSLIPATTVVLOWLVWRKYFDWRIWASLVPIVGGILLTSITELSFNV
FECAALEGCLATSTKTILESELLHOYKTEDSITHVYTYMAFFANYLGIEDPSLLERNGI
LDWFFRHPSPWSALIIENSSYLAFCLNFSTFYVJOSTTAVTFNVAGNLKVAVFVYS
WMIFRNPISPWNAVGCGITLVGCTFYGYVRHMLSOQOPGTPRTPRTPRNKMELIPLVN
  /translation-"meegslwrqwtwfrsllsilqwwgfnvtviimnkwifqKldFKF
PLSVSCVHFICSSIGAIIVIKVLKLKPLIVVDPEDRWRRIFPMSFVFCINIVLGNISL
  join(23991. .24104,24201. .24450,24540. .44755,25259. .25480)
/note="similar to phosphate/phosphoenolpyruvate translocator protein gPlAAD20711; similar to ESTS gplA1881401., gplAA172874.1, gplAA660386, dbjlC27462, gblA1725635.1, dbjlAT001755.1, and gblA1998102.1"
   01-AUG-1998
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
  P1 clone 79-2A (LANL), complete
   to: 82875
   Length: 12
Gaps: 0
Percent Identity: 66.667
   31870 TACTCTTTATTGGTACGATACATTTTGATTCGTTAT 31835
  to reverse of: AC013482 from: 1
  1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
   /evidence-not_experimental/product-"T26F17.10"
  /evidence=not_experimental
/product="T26F17.9"
/proteln_id="AAF16530.1"
/db_xref="G1:6552731"
  /evidence=not_experimental
/product="T26F17.8"
   /protein_id="AAF16529.1"
/db_xref="G1:6552730"
   DNA
16,
   seq_documentation_block:
LOCUS AC005365 86130 bp
DEFINITION Homo sapiens chromosome
sequence.
ACCESSION AC005365
   /codon_start=1
   AC005365.1 GI:3367509
   alignment_block:
US-08-653-294-16 x AC013482/rev
  42.00
4.200
83.333
  seq_name: gb_pr3:AC005365
  Homo sapiens
   Quality:
   Percent Similarity:
   human.
  alignment_scores
  Align seg 1/1
   ORGANISM
  ACCESSION
VERSION
KEYWORDS
SOURCE
   CDS
  CDS
  CDS
   /evidence=not_experimental
/product="126F17.7"
/protein_id="AAR16543.1"
/db_xref="C1:66544"
/db_xref="C1:66544"
/translat_ion="MKVYKSMWTRAMITTLIFLISLAFAEDPYRFFEWHYTYGNISPLG
VAQOGILINGKFPGPDIISITNDNLIINVFNHLDEPFLLSWNGIRNWKNSFQDGVYGT
MCPIPPGKNYTYALQVKDQIGSFYXFPSLGFHKAAGGFGGIRISSRALIPVPFPTPAD
   VAQQGILLINGKEPGPDIAAVTHONLIINVENHLDEPFLISWSGIRNWRNSYQDGVYGT
TCPIPPGKNYTYALQVKDQIGSFYIFPSLGFHKAAGGFGAIRISSRPRIPVPFPAPAG
TCPIPPGKNYTYALQVKDQIGSFYIFPSLGFHKAAGGFGAIRISSRPRIPVPFPAPAG
TYULIGDWYKTNHKDLLYVUEGTHTIQTPESSLDVHVGGSYSVLITADQPAKDYYIV
VSCAPTSKILITAGALHYSNSAGPYSGPIPEAPIQLRMSFDQARAIKINLAASGPRPN
PQGTYHYGKIKVTRTIKLASSAGNINGKQRYAVNSASFYPTDTPLKLADYFKIAGVYN
  PGSIPDQPTHGAIYPVTSVMQTDYKAFVEIVFENWEDIVQTWHLDGYSFFVVGMELGK
WSAASRKVYNLNDAVSRCTVQVYPRSWTAIYVSLDNVGMWNLRSELWERQYLGQQFYM
RVYTPSTSLRDEYLIPKNALLCGRATGHHTTTPGPLSEGSERF"
   EDELEKMEAEKAELKISFDVIKDQYQESRVCFQEVEMKLEAMKRELKLANESKTQAES
SYTRAMEAEVSKERIVSDGLKEKCEFFEERELEENETEKTMIKREKVEPKINGEDTATAA
GKFADCQKTIASLGKQLQSLATLEEFLIDTASIPGSARSVHNKEALLGKDPHECIKTI
NGRSLEFLAIONSNNKTSPPCSSSDSTTVSLIMSSNRGSSEKNRNGFATVFTRSRNS
   /translation-"MINLKSFMFCSDSFISIKFENDGNASWEKKAVVTKVCVDNNNNN
TINSTCKKQQSPITSNTSIVEHNSAKSSLRWRKRIGHLFHVIKLKSGSSTSSCHVAPS
  SSKASMSOGSALFRIAASVFTEVPNLKMIRDASLGSKNVCFHHAPIFGLVCGLLGMDS
TSCRALYTLRDVLSAATRLNIVGPMGASVMQHRIAIVTETVLEKMNNREAGEACQ
TSPLLDVVGCHGYLFSRLFCS
COMPLEMENT ( JOHN (13586 . .13828, 13930 . .14008, 14146 . .14511,
   /translation="MDMYKDDSSPYCYFHPKEEYVGVCPLCLNERLLVLASKQRSSRT
   /translation="meederrdivmsrasscmowsowolldsilptggfahsfglerar
IQTRLVSSPEDLETHIIHVLDNTASLLLDFVYSALKSPDIETWHKLDGILNATLTNQV
   complement(join(13586. 13828,13930. 14008,14146. 14511,
14642. 14984,15072. 15171,15388. 15658,15975. 16084,
16170. 16313)
   /note="similar to urease accessory protein UREF sp|Q07402"
  /translation="MEVKSVNTTAMILGLFFLISFVAAEDPYKFFEWHVTYGNISPLK
   complement(join(16811. 17014,17112. 17190,17407. 17772, 18036. 18378,18463. 18562,18737. 19007,19646. 19755,
   lol70. .16313))
/note="similar to pollen-specific protein precursor emb|CpA23065; similar to ESTS emb|F14023, gb|A1491058.1, gb|R30156, gb|A174044.1, gb|A1730478.1, gb|A1726799, and gb|A1992516.1"
   KHSSSSPIISLPKIFALSSLLSRLDLRHRKFHPSSDLDVSTSQEGTVFL"
  ESTS gb/T21171 and
  EST gb|AA586241"
   KVEGTKVRKQGWMVRTLTRKKSRKSKS"
   complement(8023. .8304)
/note="unknown; similar to
  complement(7212. .7601)
/note="unknown; similar to
  /evidence=not_experimental
/product="T26F17.3"
/protein_id="AAF16546.1"
/db_xref="G1:6552747"
  /evidence=not_experimental
/product="T26F17.4"
/protein_id="AAF16545.1"
/db_xref="G1:6552746"
   /evidence=not_experimental
/product="T26F17.5"
/protein_id="AAF16528.1"
/db_xref="G1:6552729"
   /evidence=not_experimental
/product="T26F17.6"
/protein_id="AAF16544.1"
/db_xref="G1:6552745"
  complement(7212.
  /codon_start=1
  gb|AI992884.1"
   /codon_start=1
```

CDS

CDS

| 2805928174 /note="GRAIL 2 excellent exon, frame 0" 2897529221 /rpt_family="Alu" 2940829459 /rpt_family="MIR" 304630276 /rpt_family="Alu" 3051330631 /note="GRAIL 2 excellent exon, frame 1" 3051330631 /note="GRAIL 2 excellent exon, frame 1" 3791931186                                                                                                                                                                                                                                                      | 3160832152                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | /rpc_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continue_continu | complement(5305853720)  /rpt_family="Li" 5495855829  /rpt_family="Alu" 5555655848  /rpt_family="Alu" 5655556848  /rpt_family="Alu" 5655659183  /rpt_family="Alu" 5892659183  /rpt_family="Alu" 5892659183  /rpt_family="Alu" 5949060014  /rpt_family="Alu" 6098861273  /rpt_family="Alu" 6098861273  /rpt_family="Alu" 6098161275                                                                                                                                                                                             |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| misc_feature repeat_region repeat_region repeat_region misc_feature repeat_region                                                                                                                                                                                                                                                                                                                                                                                                                              | repeat_region repeat_region repeat_region misc_feature repeat_region                                                                                                                                                                                                                                                                                                                                                                                                            | repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | misc_feature repeat_region misc_feature repeat_region repeat_region repeat_region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | repeat_region repeat_region repeat_region misc_feature repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
| Eutheria; Primates; Catarrhini; Hominidae; Homo.  AUTHORS Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., Saunders, E., Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Thompson, S., White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Maltble, M., Misra, M. and Deaven, L.  TITLE Sequencing of Human Chromosome 16 JOURNAL Unpublished REFERENCE 2 (bases 1 to 86130) AUTHORS Ricke, D.O.  AUTHORS Ricke, D.O.  AUTHOR FIRE Calcal Sequence Analysis and Annotation with the Sequence | Comparison Analysis (SCAN) System AL Unpublished To be seen to 8(130) RS Ricke, D.O., Bruce, D., Mundt, M., Doggett, N., Munk, C., SRobinson, D., Jones, M., Buckingham, J., Chasteen, L., The Goodwin, L., Bryant, J., Tesmer, J., Meincke, L., Longmir White, S., Ueng, S., Tatum, O., Campbell, C., Fawcett, J., Misra, M. and Deaven, L. Direct Submission AL Submitted (01-MUG-1998) Center for Human Genome Studie Genome Institute, Los Alamos National Laboratory, MS 1 | Alamos, NM 87545, USA Location/Qualifiers 1 Location/Qualifiers 1 Location/Qualifiers 1 Location/Qualifiers 2 Location/Suref="taxon:9606"    Ab_xref="taxon:9606"     Ab_xr | repeat_region (1542. 10563                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | repeat_region /rpt_family="Alu" 17124. 17355 repeat_region complement(1844818747) repeat_region /rpt_family="Alu" repeat_region /rpt_family="Alu" repeat_region /rpt_family="Alu" repeat_region /rpt_family="Alu" /rpt_type=tandem /rpt_unit=A repeat_region /rpt_unit=A repeat_region /rpt_unit=A repeat_region /rpt_unit=A /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_unit=A /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_type=tandem /rpt_family="Alu" repeat_region /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" /rpt_family="Alu" |

us-08-653-294-16.rge

```
REFERENCE
   23-NOV-1999
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
  /note="67All 2 excellent exon, frame 0"
complement(66679. 66796)
/rpt_family="Alu"
66995. 6726?
   /note-"GRAIL 2 excellent exon, frame 64707. .64992
   seq_documentation_block:
LOCUS HS1141E20 97906 bp DNA
DEFINITION Homo sapiens chromosome 6 clone RP5-1141E20,
PROGRESS ***, in unordered pieces.
   Percent Identity: 58.333
   21591 TATAAGTTAATGGTTTATAAGATACTTTTAAGATAT 21626
  /rpt_family="MER46"
complement(72760..72985)
/rpt_family="MER46"
complement(73181..73243)
/rpt_family="MIR"
  from: 1 to: 86130
          complement(63604. .63875) /rpt_family="Alu"
                                       complement(63894. .64098)
/rpt_family="MER1"
64463. .64588
   complement(69213. .69456)
/rpt_family="Alu"
70077. .70906
   complement(74246. .74532)
rpt_family="Alu"
4601. .74899
  /4915. .75035
/rpt_family="L1"
75843. .76122
/rpt_family="Alu"
/6105. .7614
  /rpt_family="L1"
/2758. .72045
  /rpt_family="Alu"
57741. .68036
/rpt_family="Alu"
   rpt_family="Alu"
4915. .75035
  /rpt_family="Alu"
76635. .76655
   'rpt_type=tandem
'rpt_unit=A'6163. .76652
  6105. .76145
   AL109912
AL109912.4 GI:5870369
HTG; HTGS_PHASE1.
human.
  /note="(A)21
   42.00
3.818
91.667
  Align seg 1/1 to: AC005365
   alignment_block:
US-08-653-294-16 x AC005365
   seq_name: gb_htgl:HS1141E20
   Percent Similarity:
  Quality:
Ratio:
             repeat_region
  repeat_region
  repeat_region
  repeat_region
   repeat_region
   repeat_region
  repeat_region
   repeat_region
  repeat_region
   repeat_region
  repeat_region
  repeat_region
   repeat_region
   repeat_region
  repeat_region
  repeat_region
   repeat_region
  repeat_region
  repeat_region
   misc_feature
   alignment_scores
  ORGANISM
   ACCESSION
VERSION
   KEYWORDS
SOURCE
```

```
Direct Submission

Submitted (10-SEP-1999) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 15A, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
on Sep 12, 1999 this sequence version replaced gi:5777438.
IMPORTANT This sequence version replaced gi:5777438.
IMPORTANT This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments. Unfinished: dJ1141E20 Contig_ID: 00340 acc-AL109912
Length: 64235 bp Unfinished: dJ1141E20 Contig_ID: 00679
acc-AL109912 Length: 18869 bp Unfinished: dJ1141E20 Contig_ID:
00679. acc-AL109912 Length: 13202 bp.
* NOTE: This is a 'working draft' sequence
* as soon as it is available and the accession number will
* be preserved:
   Submitted (09-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk requests: clonerequest@sanger.ac.uk clones controled this sequence version replaced gi:5791529.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with the following abbreviations are used to associate primary accession
   DNA PRI 23-NOV-1999 clone 1112D6 on chromosome 6q21-22.2,
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 135305)
   1602 others
  to: 97906
  Percent Identity: 58.333
   to reverse of: HS1141E20 from: 1
  /clone_lib="RPCI-5"
18298 c 18016 g 29795 t
  Gaps:
   1 TyrargleuleulleargarglleleuleuargTyr 12
  /organism="Homo sapiens'/db_xref="taxon:9606"
   /clone-"RP5-1141E20"
  Location/Qualifiers
1. .97906
  HSJ1112D6 135305 bp
Human DNA sequence from
complete sequence.
   AL080317.11 GI:5830430
HTG; CpG Island.
   US-08-653-294-16 x HS1141E20/rev
(bases 1 to 97906)
   42.00
3.818
91.667
   Direct Submission
   seq_name: gb_pr3:HSJ1112D6
  seq_documentation_block:
LOCUS HSJ1112D6 1:
  Homo sapiens
  30195 a
   Quality:
Ratio:
   Percent Similarity:
   Patel, R
   uman.
   alignment_scores:
  alignment_block
  Align seg 1/1
   DEFINITION
   BASE COUNT
  ORGANISM
  TITLE
JOURNAL
   REFERENCE
AUTHORS
  TITLE
  ACCESSION
                            AUTHORS
   KEYWORDS
   FEATURES
   COMMENT
  COMMENT
   ORIGIN
```

```
Location/Qualifiers
1. .142796
  /clone="RP11-7024"
   alignment_block:
US-08-653-294-16 x AC013772/rev
  4.200
  42.00
   seq_name: gb_pr3:HSU80134
  2143
  9212
  4835
  25158
   66209
   Percent Similarity:
  Quality:
   47989
  Ratio
  alignment_scores:
   Align seg 1/1
  source
   BASE COUNT
  TITLE
   FEATURES
  COMMENT
numbers given in the feature table with their source databases:
Em:, FMBEL; Swi. SWISSPROT; Tr:, TREMBL; Wp:, WORNPEP; Information
on the WORNPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is
the entire insert of clone 1112D6. This sequence has been finished
according to sequence map criteria as follows. An attempt is made
to resolve all sequencing problems, such as compressions and
repeats, but not necessarily within known annotated human repeat
sequence elements (e.g. Alu). Where the sequence is ambiguous,
there is an annotation using the 'unsure' feature key.
This sequence was generated from part of bacterial clone contigs of
human chromosome 6, constructed by the Sanger Centre Chromosome 6
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr6
1112D6 is from the library RPCI-5 constructed at the Roswell Park
Cancer Institute by the group of Pieter de Jong. For further
contains see thit processed.
  Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Bockerly, R., Boquelavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Daarellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardynas, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollaraw, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
  seq_documentation_block:
LOCUS AC013772 142796 bp DNA HTG 09-DEC-1999
DEFINITION Homo sapiens clone RP11-7024, WORKING DRAFT SEQUENCE, 6 unordered
pieces.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 142796)
   Align seg 1/1 to reverse of: HSJ1112D6 from: 1 to: 135305
   Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-7024
   Gaps: 0
Percent Identity: 58.333
   101493 TATAAGTTAATGGTTTATAAGATACTTTTAAGATAT 101458
   /clone_lib="RPCI-5"
/clone="RP5-1112D6"
26002 c 26091 g 42041 t
  Length:
   1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
  Location/Qualifiers
1. 135305
   ÅC013772
AC013772.2 GI:6553994
HTG: HTGS_PHASE1; HTGS_DRAFT.
  US-08-653-294-16 x HSJ1112D6/rev
   42.00
3.818
91.667
  seq_name: gb_htg7:AC013772
  Homo sapiens
   Unpublished
   Percent Similarity:
  Quality:
   Ratio:
  41171
  human.
   alignment_scores:
  alignment_block:
  source
   BASE COUNT
  ORGANISM
   AUTHORS
TITLE
  JOURNAL
REFERENCE
AUTHORS
  ACCESSION
   VERSION
KEYWORDS
   REFERENCE
   FEATURES
   SOURCE
```

```
Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.

Direct Submission

L. Submitted (15-YoV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 10, 1999 this sequence version replaced gi:6425750.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center: Whitehead Institute/ MIT center for Genome Research
Center code: WIBR
Web site: http://www.seq.wi.mit.edu
Conter: sequence_submissions@genome.wi.mit.edu
Center project name: L2959
Center project name: L2959
Center project name: L2959
  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
  NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is
  Insert size: 138000; agarose-fp
Insert size: 142796; sum-of-contigs
Quality coverage: 5.7 in Q20 bases; agarose-fp
Quality coverage: 5.5 in Q20 bases; sum-of-contigs
   Sequencially vectors. M13, M77815; 100% of reads Sequencial vectors. M13, M77815; 100% of reads Chemidstry: Dye-terminator B19 Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 127112 bases at least Q40 Consensus quality: 147112 bases at least Q20
  2142: contig of 2142 bp in length gap of unknown length 4834: contig of 2692 bp in length gap of unknown length 9211: contig of 4377 bp in length gap of unknown length 25157: contig of 15946 bp in length gap of unknown length
  /clone_11b="RPCI-11 Human Male BAC"
a 24580 c 24540 g 45686 t 1 others
   66208: contig of 41051 bp in length gap of unknown length 142796: contig of 76588 bp in length.
  to: 142796
   12
0
.667
  Percent Identity: 66.
  to reverse of: AC013772 from: 1
   Length:
   /organism="Homo sapiens"
/db_xref="taxon:9606"
```

```
cDNA library; nitrogen deprivation.
Botryotinia fuckeliana.
Botryotinia fuckeliana
  alignment_block:
US-08-653-294-16 x CNSOICBA/rev
   Ratio: 3.417
Percent Similarity: 100.000
   Submission
   Direct Submission
  41.00
  seq_name: gb_p12:CNS01CBB
   ีฟ
  Genoscope
   Genoscope
  Quality:
   193
   vector.
   Direct
   alignment_scores:
KEYWORDS
SOURCE
ORGANISM
  BASE COUNT
ORIGIN
  REFERENCE
AUTHORS
TITLE
JOURNAL
  AUTHORS
TITLE
  TITLE
JOURNAL
  AUTHORS
TITLE
JOURNAL
   JOURNAL
   REFERENCE
   REFERENCE
  FEATURES
  COMMENT
   COMMENT
  S. (bases 1 to 375)
Glas,A.M., Nottenburg,C. and Milner,E.C.B.
Direct Submission
Submitted (29-NOV-1996) Immunology, Virginia Mason Research Center,
1000 Seneca Street, Seattle, WA 98101, USA
   /map="14q32-q33"
/note="CD19+ peripheral blood B cells obtained from a bone
marrow transplant recipient 1 year post transplant; clone
59 in reference 1"
   /product-"immunoglobulin heavy chain variable region"
/protein_id-"AAC51049.1"
/db_xref-"G1:1791111"
/tanslation-"QVOLOQUGAGLIKPSETILSLTCAVYGGSFSGYYWSWIRQPPGKG
LEWIGEINHSGSTYWNPSIKSRYTISVDTSKNQFSIKLSSYTAADTAVYYCARGQTIG
RWYGSYYYGMDVWGQGTTVTVSS"
106 c 111 g 75 t
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eukheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 375)
Glas,A.M., Nottenburg,C. and Milner,E.C.
Analysis of rearranged immunoglobulin heavy chain variable region genes obtained from a bone marrow transplant (BMT) recipient
Clin. Exp. Immunol. 107 (2), 372-380 (1997)
               HSUB0134 375 bp DNA PRI 19-FEB-1997 Human immunoglobulin heavy chain variable region (V4-34) gene, partial cds.
  CNSOICEA 650 bp mRNA PLN 02-SEP-1999
Botryiis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.
ALL15310 ALL15310.1 GI:5829929
  Gaps: 0
Percent Identity: 58.333
   /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="CD19+ B cells"
/tissue_type="peripheral blood"
/clone="312a3"
/chromosome="14"
   300 CAICGGTCGTTGGTACGGAAGCTACTACTACTGGTAT 335
  1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
  /gene="V4-34"
/note="Ig VH4 heavy chain"
  from: 1 to: 375
  /codon_start=1
   1. .375
/gene="V4-34"
  U80134.1 GI:1791110
  41.00
3.727
91.667
  Align seg 1/1 to: HSU80134
   alignment_block:
US-08-653-294-16 x HSU80134
   seq_name: gb_pl2:CNS01CBA
                 seq_documentation_block:
Locus HSU80134
  seq_documentation_block:
   Quality:
Ratio:
Percent Similarity:
   97182739
   83
   human.
   alignment_scores
  source
   DEFINITION
   ORGANISM
   DEFINITION
   AUTHORS
TITLE
   MEDLINE
REFERENCE
  TITLE
JOURNAL
   BASE COUNT
   ACCESSION
  VERSION
KEYWORDS
SOURCE
  gene
  REFERENCE
   AUTHORS
   ACCESSION
  JOURNAL
   CDS
   FEATURES
   VERSION
  ORIGIN
```

```
Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage: CP 5706 91057 EVRX cedex - FRANCE (E-mail: seqref@genoscope.cns.fr web: www.genoscope.cns.fr)
The conal library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
  Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage: CP 5706 91057 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
The CDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal
Eukaryota; Fungi; Ascomycota; Euascomycetes; Discomycetes; Leotiales; Sclerotiniaceae; Botryotinia.

[ (Dases 1 to 650)
Bitton,F., Levis,C., Fortini,D., Pradier,J.M. and Brygoo,Y. Direct Submitsion
Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 650)
   Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78026 Versailles, France
2 (bases 1 to 710)
  seq_documentation_block:
LOCUS
CNSOICEB 710 bp mRNA PLN 02-SEP-1999
DEFINITION BOLIVILS cinered strain T4 cDNA library under conditions of nitrogen deprivation.
ALI15311. GI:5829930
VERSION ALI15311. GI:5829930
SOURCE BOLIVOLINIA fuckellana.
ORGANISM BOLIVOLINIA fuckellana.
ELECTROPES BOLIVOLINIA fuckellana.
ORGANISM BOLIVOLINIA fuckellana.
ELECTROPES BOLIVOLINIA fuckellana.
ELECTROPES BOLIVOLINIA fuckellana.
ORGANISM BOLIVOLINIA fuckellana.
ELECTROPES BOLIVOLINIA fuckellana.
ELECTROPES BOLIVOLINIA SCOMPOCA: ENASCOMPOCA: ELECTROPES: LECTROPES: Lectrales: Sclerotiniaceae; Bolivolinia.

REFERENCE 1 (Dases 1 to 710)
AUTHORS BILCON, Levis.C., Fortini,D., Pradier,J.M. and Brygoo,Y.
TITLE Direct Submission.
   /note="Genoscope sequence ID : W60E121"
121 c 169 g 167 t
   650
   Length: 12
Gaps: 0
Percent Identity: 50.000
  /organism="Botryotinia fuckeliana'
/strain="T4"
   ;
;
   Align seg 1/1 to reverse of: CNS01CBA from: 1
  /db_xref="taxon:40559"
  Location/Qualifiers
1. .650
```

```
source
  ORGANISM
   BASE COUNT
ORIGIN
   REFERENCE
AUTHORS
   ACCESSION
   rRNA
  VERSION
KEYWORDS
SOURCE
  JOURNAL
  FEATURES
  TITLE
situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII
  Submitted (27-NOV-1998) Jurgens G.N., Applied Chemistry & Microbiology, Dept. Microbiology, University of Helsinki, P.O.Box 56, Biocenter 1 A, Vilkinkaari 9, Helsinki, 00014 Helsinki University, FINLAND C. Chases 1 to 865)
Jurgens, G.N., Glokner, F.O., Saano, A., Amann, R. and Munster, U. Freshwater Archaeal diversity and FISH in boreal forest lake in
   Archaea; Euryarchaeota; unclassified Euryarchaeota; environmental
   /note="From surface water of freshwater Finnish forest lake Valkea Kotinen"
  1 .865
/orgam="uncultured euryarchaeote VAL147"
/db.xref="taxon:85395"
/clone="VAL147"
   /organism="Botryotinia fuckeliana"
/strain="r4"
/db_xref="taxon:40559"
/note="Genoscope sequence ID : W60E122"
135 c 178 g 181 t 1 others
   to: 710
   Quality: 41.00 Length: 12
Ratio: 3.417 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
   Gaps: 0
Percent Identity: 50.000
  443 TITCGGATCTTGGTTCGCAAGATATTACTAAAGTTT 408
   /evidence=experimental
/product="16S ribosomal RNA"
   from: 1
  1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
   Length:
   VAL147.
AJ131275.1 GI.3955079
AJ181275.1 GI.3955079
I6S ribosomal RNA; 16S rRNA gene.
uncultured euryarchaeote VAL147.
uncultured euryarchaeote VAL147.
  Location/Qualifiers
   Location/Qualifiers
   to reverse of: CNS01CBB
  271 g
   /gene="16S rRNA"
   /gene="16S rRNA"
178 c 271
   alignment_block:
US-08-653-294-16 x CNS01CBB/rev
   1 (bases 1 to 865)
Jurgens, G.N.
  Direct Submission
   Ratio: 3.417
Percent Similarity: 100.000
   41.00
  seq_name: gb_bal:UEU131275
   Unpublished
  Quality:
   215
  223
   sambles
  Finland
  alignment_scores
  alignment_scores:
   Align seg 1/1
   VERSION
KEYWORDS
SOURCE
ORGANISM
  source
  BASE COUNT
ORIGIN
   BASE COUNT
   AUTHORS
TITLE
JOURNAL
  ACCESSION
  gene
   AUTHORS
   JOURNAL
  rRNA
  REFERENCE
   REFERENCE
   FEATURES
  FEATURES
  TITLE
  ORIGIN
```

```
uncultured archaeon BURTON20_A.
uncultured archaeon BURTON20_A
uncultured archaeon BURTON20_A
uncultured archaeon BURTON20_A
(bases: Euryarchaeota: Thermoplasmales: environmental samples.
( (bases 1 to 510)
BOWMEN.J.P., McCammon,S.A. and McMeekin,T.A.
BOWMEN.J.P., McCammon,S.A. and McMeekin,T.A.
floresity and community structure of Antarctic maritime lake and Unpublished
  LOCUS AF142982 910 bp DNA BCT 06-JUL-1999
DEFINITION Uncultured archaeon BURTON20_A 16S ribosomal RNA gene, partial
   archaeon BURTON20_A"
   to: 865
  to: 910
  Length: 12
Gaps: 0
Percent Identity: 50.000
  Align seg 1/1 to reverse of: UEU131275 from: 1
   230 TACAACCIGATAGICCGCAGACITAICCITAGGCAC 195
   <1. .>910
/product="16S ribosomal RNA"
185 c 287 g 204 t
   229 TACAACCTGATAGTCCGCAGACTCATCCTAAGGCAC 194
  Align seg 1/1 to reverse of: AF142982 from: 1
  1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
  1 TyrargLeuLeuIleargargIleLeuLeuargTyr 12
  /organism="uncultured a /db_xref="taxon:97847" /clone="BURTON20_A"
   Location/Qualifiers
   AF142982.1 GI:5359964
alignment_block:
US-08-653-294-16 x UEU131275/rev
  alignment_block:
US-08-653-294-16 x AF142982/rev
   Quality: 41.00
Ratio: 3.417
Percent Similarity: 100.000
   seq_name: gb_bal:AF142982
  seq_documentation_block:
LOCUS AF142982
   sequence.
   234
   alignment_scores:
```

THIS PAGE BLANK (USPTO)

us-08-653-294-16.rng

```
Streptococcus pneumoniae gen
Sequence for a synthetic la
1941 HIV envelope protein c
Synthetic p41 gene with p12
   New Lucilia cuprina ecdysteroid receptor, its fragments and related nucleic acid - vectors, transformed cells, ligands and antisense sequences, used as insecticides also in inducible gene therapy systems and for recombinant protein production

Example 2; Fig 4; 50pp; English.

Example 2; Fig 5; 
   0.2-FEB-1999 (first entry)
Lucilia cuprina ecdysteroid receptor cDNA.
Ecdysteroid receptor; insecticide; biological control;
godysteroid Australian blowfly; ds.
Lucilia cuprina.
   to: 2812
   Length: 11
Gaps: 0
Percent Identity: 72.727
876
1199
1199
1204
   20-AUG-1998.
16-FEB-1998; NZ0018.
14-FEB-1997; NZ-314239.
(NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.
(NZWO-) NEW ZEALAND WOOL BOARD.
   Align seg 1/1 to reverse of: V60302 from: 1
  Location/Qualifiers
104.35
101.62
101.62
101.59
   V60302 standard; cDNA; 2812 BP. V60302;
35.00
35.00
35.00
   us-08-653-294-16 x V60302/rev
   seq_name: N_Geneseq_36:V60302
   39.00
3.900
90.909
   Heath ACG, Huang SQ;
WPI; 98-520754/44.
   seq_documentation_block:
   Quality:
Ratio:
N_Geneseq_36:X30865
N_Geneseq_36:Q55183
N_Geneseq_36:Q62660
N_Geneseq_36:N90797
  Percent Similarity:
   P-PSDB; W71297
  WO9835550-A2
  alignment_scores
  alignment_block:
  1332 | Entercocccus faecalis genome of thuman secreted protein gene 30 3279 | Sequence encoding protein L. I 3279 | Sequence encoding protein L. I 564 | Arabidopsis Golgi glycosyltran 5892 | BRCA2 cancer susceptibility genome of the sequence encoding protein L. I 564 | Arabidopsis Golgi glycosyltran 5892 | BRCA2 cancer susceptibility genome of the sequence of the 
  Recombinant heat-resistant tree Sequence of BAR 1 gene contg.
Nucleotide Sequence of the S.
Barrier protein BAR1 gene. DWA
BAR1 barrier protease gene. PWA
Recombinant heat-resistant tree Drosophila para voltage-activa Drosophila para voltage-activa Calcium permeable voltage sens i Total base sequence of rice i Total base sequence of rice Oyster derived CDNA encoding F
   Documentation ... i Lucilia cuprina ecdysteroid re l' Lucilia cuprinture HUMGS00405 ! Human gene signature HUMGS00405 ! Enterococcus faecalis genome c
  EST clone GX909. New polynucied
Streptococcus pneumoniae genomi
   software, version 4.5,
  2686
2723
2750
2750
2750
2756
6513
6513
134525
134525
  Len ! 1 2812 1119 1332 1366 3279 1564 5550 5892 7240 7902
  142.52
219.81
388.43
388.43
388.43
1.1e+03
1.1e+03
1.6e+03
1.6e+03
2.2e+03
2.2e+03
3.2e+03
4.6e+03
4.6e+03
4.6e+03
  633.53
633.53
633.53
633.53
749.96
749.96
758.24
758.24
758.24
778.20
2.0e+03
2.0e+03
5.5e+04
417.94
   12.44
   .54
  Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
OM of: US-08-653-294-16 to: N_Geneseq_36:*
  ZSCOTE
1107 .71
1110 .82
1110 .82
1103 .01
103 .01
105 .07
94 .55
89 .55
89 .55
   90.30
64.03
64.03
102.43
115.02
  88.83
126.73
113.75
  97.65
90.31
90.31
90.30
   112.67
   Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
Search time (sec): 590.520000
                                      Date: Feb 8, 2000 1:28 PM
  Search information block:
Query: US-08-653-294-16
Query length: 12
   Command line parameters:
  About: Results were
  Geneseq_36:V74278
   0896
  N_Geneseq_36:T79668
N_Geneseq_36:V52245
  _Geneseq_36:V60302
   :X04340
  N_Geneseq_36:x13074
N_Geneseq_36:T79680
   N_Geneseq_36:X30258
   N_Geneseq_36:Q81920
  N_Geneseq_36:V88615
N_Geneseq_36:X30742
  Geneseq_36:X13394
   N_Geneseq_36:X30256
N_Geneseq_36:X30257
  N_Geneseq_36:X30255
  N_Geneseq_36:V86355
  N_Geneseq_36:X23322
   Geneseq_36:T09355
  N_Geneseq_36:V82467
  N_Geneseq_36:T18986
   N_Geneseq_36:V82500
   36:T84841
  Geneseq_36:T69707
   N_Geneseq_36:V37711
  N_Geneseq_36:T79630
   Geneseq_36:T19381
   Genesed_36
   N_Genesed_36
  N_Genesed_36
   N_Geneseq_36
N_Geneseq_36
  N_Geneseq_36
N_Geneseq_36
  N_Genesed_36
  N_Geneseq_36
   N_Geneseq_36
   N_Geneseq_36
   N_Genesed_36
  -THREADS=1
  Genesed_
  N_Geneseq_
   Genesed
   N_Geneseq_
```

Wed Feb

```
WO9856804-A1.
   Homo sapiens
  13-JUN-1997;
   13-JUN-1997;
13-JUN-1997;
   13-JUN-1997;
   alignment_scores:
  infection.
  alignment_block
   Sequence
       DD TO THE PERMINANT OF 
   Claim 1; Page 372; 2245pp; Japanese.

A single-stranded DNA (or its complementary strand or the corresp.

double-stranded DNA) which comprises one of the 7837 "GS" sequences
given in T19001-T26837 and which is able to hybridise to part of
human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
sequences were obtained from 3'-directed CDNA libraries prepared
from various human tissues; synthesis of CDNA was initiated from the
untranslated sequence is unique to a particular mRNA species, almost
all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
is constructed so as to reflect accurately the relative abundance of
different mRNAs in the particular tissue from which it was derived.
The appearance frequency of a given GS in a cDNA library can be
determined (esp. using primers and probes derived from the GS
sequences) as a means of diagnosing abnormal cell function or for
recognising different cell types.
Sequence 119 BP; 37 A; 34 C; 24 T;
   Identifying gene signatures in 3'-directed human cDNA library - e.g. for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
  19381;
04-070L-1996 (first entry)
Human gene Signature HUGS00405.
Gene Signature; messenger RNA; mRNA; relative abundance; frequency;
Human; cloning; mapping; non-biased library; diagnosis; detection;
eall typing; abnormal cell function; ss.
Homo sapiens.
  Enterococcus faecalis genome contig SEQ ID NO:457.

Enterococcus faecalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.

Enterococcus faecalis.
  Length: 11
Gaps: 0
Percent Identity: 72.727
   to: 119
   Align seg 1/1 to reverse of: T19381, from: 1
   110 AGGCTCTTTATTAGACGGTTATTGCTGTACTAC 78
76 AGGTTACTTCTGAGGAGGATTCTTCTAACATTT 44
  2 ArgLeuLeuIleArgArglleLeuLeuArgTyr 12
  I19381 standard; cDNA to mRNA; 119 BP
  seq_documentation_block:
ID x13394 standard; DNA; 1332 BP.
AC X13394;
DT 19-MAR-1999 (first entry)
  alignment_block:
US-08-653-294-16 x T19381/rev
  38.00
3.800
90.909
  seq_name: N_Geneseq_36:T19381
  seq_name: N_Geneseq_36:X13394
   01-JUN-1995.
11-NOV-1994; J01916.
12-NOV-1993; JP-355504.
(MATS/) MATSUBARA K.
   US-044031.
   (OKUB/) OKUBO K.
Matsubara K, Okubo K;
WPI; 95-206931/27.
   12-NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066000
06-MAY-1997; US-04403.
   seg_documentation_block:
  Quality:
Ratio:
Percent Similarity:
  W09514772-A1.
  WO9850555-A2.
  alignment_scores:
  tissues
  NEW MARKET OF THE PART OF THE
```

```
Here Har-1997; US-046655.

(HUMA-) HUMAN GENOME SCI INC.

Barash SC. Dillon PJ, Kunsch CA;

WHI: 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides.

New isolated Enterococcus faecalis polynucleotides and polypeptides.

The computer readable medium has been developed which has recorded on it a computer readable medium has been developed which has recorded on it.

A computer readable medium has been developed which has recorded on it.

A computer readable medium has been developed which has recorded on it.

A computer readable medium has been developed which has recorded on it.

A computer readable medium has been developed which has recorded on it.

A computer readable medium has been developed which has recorded on it.

A computer faedances is also known as conlige. The computer based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcus faecalis, no modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the polypeptides encoded by the Enterococcus faecalis nucleotide sequences or in the contract of the computer or attenuate an Enterococcal
  Human secreted protein gene 30 clone HTLAB25.

Human secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foctal deficiency; blood; allergy; renal; immune system; asthms; lymphocytic disease; brain; hepatic; lymphoma; inflammation; isothemia; prostate; obesity; osteoclast; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
   38.00 Length: 12
3.800 Gaps: 0
83.333 Percent Identity: 58.333
  227 G;
   801 TATCGTATTATATGAAGAAAATACTTATTAAGGTAT 836
  Align seg 1/1 to: X13394 from: 1 to: 1332
  190 C;
  seq_documentation_block:
ID X04340 standard; DNA; 1966 BP.
  479 A;
  seq_name: N_Geneseq_36:X04340
  US-049549.
US-049550.
US-049606.
US-049607.
US-049608.
   US-049547
   US-08-653-294-16 x x13394
  1332 BP;
   Percent Similarity:
   Quality:
```

```
Disclosure: Figure 1: 28pp; English.

Disclosure: Figure 1: 28pp; English.

The synthetic immunoglobulin binding proteins derived from protein L comprise repeated sequences from protein L which bind immunoglobulin kappa 1ight chains. They can be used in protein analysis, purification procedures and other biochemical processes e.g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell wall binding (The repeat regions commencing at nucleotide numbers 1045, 1261, 1483 and 1705).

Sequence 3279 BP; 1505 A; 481 C; 625 G; 668 T;
   /*tag= c
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide position 757"
  /*tag- d
/note- "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 1162, 1375
and 1597"
  /*tag= e
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 1261, 1483
and 1705
   /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347, 2545 and 2731"
  New immunoglobulin binding proteins derived from Protein {\tt L} -which bind immunoglobulin kappa light chains but not albumin or
  /*tag= g
/note= "Repeat units are adjacent, repetitions
of this sequence are not 100% homologous and
ogin at nucleotide positions 2935, 2953,
2968, 2986, 3001, 3019 and 3034"
of this sequence are not 100% homologous and
begin at nucleotide positions 673 and 856"
574. .672
   Align seg 1/1 to reverse of: Q50946 from: 1 to: 3279
  Trowern AR;
   Gaps: 0
Percent Identity: 50.000
  2746 TITCGCCTGGTTTTTCAGCGTGTGCTTTTAAGATT 2711
  TyrargLeuLeuIleargArgIleLeuLeuArgTyr 12
  Length:
   11-NOV-1993.
07-MAY-1993. G00950.
07-MAY-1992. GB-0009804.
24-DEC-1992. GB-026928.
(PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
Atkinson A. Duggleby CJ, Murphy JP, Trown WPI: 93-368798/46.
   seq_documentation_block:
ID Q51556 standard; cDNA; 3279 BP.
  1045. .1158
   1822. .1938
   alignment_block:
US-08-653-294-16 x Q50946/rev
  Quality: 38.00
Ratio: 3.167
Percent Similarity: 100.000
  seq_name: N_Geneseq_36:Q51556
   *tag=
  alignment_scores:
                                       repeat_unit
   WO9322439-A.
  repeat_unit
  repeat_unit
  repeat_unit
   repeat_unit
 New isolated human genes and the secreted polypeptides they encode -

"Seful for diagnosis and treatment of e.g. cancers, neurological

"Gasorders, immune diseases, inflammation or blood disorders

"Inflammation or blood disorders

"Claim 1; Page 195-196; 380pp; English.

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents a nucleic acid molecule which encodes a secreted

"This sequence represents to the gene number, and the clone it is derived from, are

"The invention relates to the stability of the fused protein as

"The invention relates to 86 novel genes and their fragments (nucleic acid

"Sequences: X04311-X04410; amino acid sequences W78126-W78225) which

are useful for preventing, treating or ameliocating medical conditions

"Sequences by determining the amount of the new polypeptides in a sample

or by determining the presence of mutations in the new polynucleotides.

"Specific uses are described for each of the 86 polynucleotides, based on

which tissues they are most highly expressed in (see X04311 for described
   /*tag* b
/note= "Repeat units are not adjacent, repetitions
   18-MAY-1994 (first entry)
Sequence encoding protein L.
Peptide: immunoglobulin; binding; analysis; purification; ELISA; enzyme linked immunoabsorbant assay; ss.
  (HUMA-) HUMAN GENOME SCI INC.
Brewer LA, Ebner R, Ferrie AM, Feng P, Greene JM, Lafleur DW,
Moore PA, Ni J, Olsen HS, Rosen CA, Ruben SM, Shi Y, Young P,
  to: 1966
   Gaps: 0
Percent Identity: 72.727
  584 G;
   Length:
  to reverse of: X04340 from: 1
  2 ArgLeuLeulleArgArglleLeuLeuArgTyr 12
  545 C;
  /*tag= a /product= Protein L. 490. .573 /*tag= b
  Location/Qualifiers
103. .3185
   seq_documentation_block:
ID Q50946 standard; cDNA; 3279 BP.
  440 A;
   38.00
3.800
90.909
   alignment_block:
US-08-653-294-16 x X04340/rev
   12-SEP-1997; US-058668
12-SEP-1997; US-058668
12-SEP-1997; US-058750.
12-SEP-1997; US-058971.
12-SEP-1997; US-058972.
12-SEP-1997; US-060897.
02-0CT-1997; US-060844.
02-0CT-1997; US-060844.
02-0CT-1997; US-060844.
02-0CT-1997; US-060844.
02-0CT-1997; US-060864.
  seq_name: N_Geneseq_36:Q50946
  Seguence 1966 BP;
  Peptococcus magnus.
   99-080881/07.
  alignment_scores:
Quality:
   Ratio:
Percent Similarity:
   P-PSDB; W78155
  repeat_unit
  Align seg 1/1
  Key
```

ID DI DE DE FH FH FT FT

It

```
alignment_scores:
  SSSS
  /*tag= c
//ote= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide position 757"
949 .104
//tag= d
//note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1162, 1375
and 1597"
   /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 673 and 856" 574. .675.
   /*tag= e
//note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide positions 1261, 1483
and 1705"
   1822. .1938
//tag- f
//otbe="Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347 and 2545"
1939. .2007
   /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2479, 2665 and 2851"
   /*tag- h
/note= "Repeat units are not adjacent, repetitions
of this sequence are not 100% homologous and
begin at nucleotide position 2209"
  /note- "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2269"
  Immunoglobulin binding polypeptide, protein L - used for prodn. of pharmaceuticals and for immobilising antibodies e.g. on columns, in diagnostic tests and in assays bisclosure; Figure 1; 29pp; English. Protein L forms a complex with immunoglobulin Kappa light chain. Purified protein can be used as a reagent for immobilising
         18-MAY-1994 (first entry)
Sequence encoding protein L.
Protein; immunoglobulin; binding; immobilisation; light chains; antibodies; diagnosis; pharmaceutical; ss.
Peptococcus magnus.
  /note= "Repeat units are adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2935, 2953, 2968, 2986, 3001, 3019 and 3034"
   07-MAY-1992; GB-009804.
(PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.
Artinson A. Duggleby CJ, Murphy JP, Trowern AR;
WPI: 93-388797/46.
P-PSDB: R43699.
  /product- Protein L.
  Location/Qualifiers 103. .3185
  . 2094
  1045. .1158
  490. .573
/*tag= b
   /*tag= a
  /*tag=
   /*tag=
  11-NOV-1993.
07-MAY-1993; G00949
Q51556;
18-MAY-1994
   repeat_unit
  repeat_unit
   repeat_unit
  repeat_unit
  repeat_unit
   repeat_unit
   repeat_unit
   WO9322438-A
  repeat_unit
   repeat_unit
```

```
P-PSDB; W90488.

Transform plants to alter the properties or composition of cell transform plants to alter the properties or composition of cell walls, e.g. for modifying foodstuffs or wood pulp products

Claim 8; Fig 1A-0; 66pp; English.

Claim 8; Fig 1A-0; 66pp; English.

Claim 8; Fig 1A-0; 66pp; English.

This is the nuclectide sequence of clone gil6, which encodes a novel glycosyltransferase (see W90188) of Arabidopsis thallana.

A thaliana expressed sequence tag (EST) clones were identified when searching an EST database with the Schizosaccharomyces pombe gmal2p and the related Saccharomyces cerevisiae mnnl0p proteins.

An iterative process was then performed to isolate further clones, and 5 different genes were identified, i.e. gil1 (gma twelve-like 1), gil2, gil4, gil5 and gil6 (see V14278-83). The longest clone, gil6, identified from EST H36383, encoded a predicted truncated contain, and 5 'ARAE was performed using RNA from A. thaliana callus cells to obtain the full-length clone. The predicted protein has the characteristics of a Golgi glycosyltransferase, i.e. a short colone. Niterminus, and sharmane domain, and a larger lumenal C-terminal domain with conserved cysteines. The plant clumenal C-terminal domain with conserved cysteines. The plant clumenal conserved systeines of complex non-cellulosic colone who may also catalyse the colone when may also catalyse the colone when the colone when may also catalyse the colone when the colone when may also catalyse the colone when the colone when may also catalyse the colone when the colone when may also catalyse the colone when the colone when may also catalyse the colone when the colone when may also catalyse the colone when the colone when may also catalyse the colone or man may also catalyse the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone when the colone or colone when the colone when th
   plant cell wall polysaccharides. They may also catalyse the glycosylation of plant cell wall protein and/or the transfer of saccharide moteties from nucleotide sugar precursors to oligosaccharide precursors. Nucleic acids encoding the glycosyltransferases can be used to transform plants to alter the properties or composition of the cell wall. The plants produced can be used in the preparation of e.g. food or wood pulp products
antibodies e.g. on columns, in diagnostic tests and in assays. may also be used in the production of pharmaceuticals. Sequence 3279 BP; 1505 A; 480~\rm C; 626~\rm G; 668~\rm T;
   Arabidopsis Golgi glycosýltransferase clone gtl6.
Glycosyltransferase; Golgi, gtl6 gene; transgenic plant;
glycosylation; plant cell wall; paper; pulp; food; ss.
Arabidopsis thaliana.
  434
  Align seg 1/1 to reverse of: Q51556 from: 1 to: 3279
   Length: 12
Gaps: 0
Percent Identity: 50.000
   2746 TITCGCCTGGTTTTCAGCGTGTGCTTTTAAGATTT 2711
   1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12 :::|||||||||||:::
   30-JUN-1997; GB-013852.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
Dupree P. Mogelsvang S;
WPI; 99-106058/09.
  306 C;
  Location/Qualifiers
100. 1449
/*tag= a
   V74278 standard; cDNA; 1564 BP
  such as paper or cardboard
Sequence 1564 BP; 474
  10-MAY-1999 (first entry)
  alignment_block:
US-08-653-294-16 x Q51556/rev
   seq_name: N_Geneseq_36:V74278
   Percent Similarity: 100.000
  38.00
   3.167
  30-JUN-1998; G01911
  seq_documentation_block:
  Quality:
Ratio: 3
   alignment_scores:
```

20

Length:

37.00

Ouality:

X13074:

```
(UYDU-) UNIV DUKE.

PR (GANC-) CANCER RES CAMPAIGN TECHNOLOGY.

(UYDU-) UNIV DUKE.

MAINOTTH A, FULTEAL PA, STRATTON MR, WOOSTER RF;

WIT; 97-261884/24.

DR P-PSDB; W25049.

NUCLEIC acid molecules comprising part or all of the BRCA2 cancer susceptibility gene - useful for diagnosis, prognosis or therapeutic treatment of cancer represents exon 11 and the intron boundaries of the SC Claim 10; FT8 7; 124pp; English.

The present sequence represents exon 11 and the intron boundaries of the BRCA2 cancer susceptibility gene. The nucleic acid molecule can be used to construct probes for screening cDNA or genomic libraries, sequencing positive clones obtained, and assembling the full length BRCA2 concerts of method of medical treatment, preferably gene therapy, especially for treating cancer, where the cancer is female or male breast cancer, ovarian, prostate or colorectal cancer, ocular melanoma or lawkamia. In particular antisense oligonuclecities coular melanoma or lawkamia. In particular antisense oligonuclecities capable of prevented. The BRCA2 nucleic acid, pre-mRNA or mature mRNA are used so that the expression of the BRCA2 nucleic acid is reduced or prevented. The nucleic acid molecules are also useful in a method for diagnosing susceptibility or predisposition to cancer in a patient. The nucleic acid molecules are used to design probes or primers for PCR to determine or detect the presence of mutations in a sample of nucleic control of the promoter. Antibodies are used to determine the presence, amount or location in a cell of a BRCA2 polypeptide or its mutant forms. The properties are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used and partners are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, the partners for problement the partners for
BRCA2 cancer susceptibility gene exon 11 and intron boundaries. RCA2 cancer susceptibility gene; breast cancer; ovarian cancer; gene therapy, prostate cancer; colorectal cancer; ocular melanoma; leukaemia; human; ss.
  polypeptide, which can be used as cancer therapeutics. Sequence 5892 BP; 2146 A; 967 C; 1046 G;
   5413. .5892
/*tag= c
/number= 11
/note= "Start of intron 11"
  /number- 10
/note- "End of intron 10"
481. .5412
   Location/Qualifiers
1. .480
/*tag= a
   /*tag= b
/number= 11
  37.00
3.700
90.909
   seq_name: N_Geneseq_36:T79668
  28-AUG-1996; GB-017961.
23-NOV-1995; GB-023959.
14-DEC-1995; GB-025555.
   to: T79680
   alignment_block:
US-08-653-294-16 x T79680
  28-MAY-1997.
25-NOV-1996; 024453
   Percent Similarity:
  Quality:
   Ratio:
  Homo sapiens
   alignment_scores:
   .Malign seg 1/1
   intron
  intron
  exon
  Claim 1: Page 813-816; 2084pp; English.

A computer readable medium has been developed which has recorded on it
Computer readable medium has been developed which has recorded on it
X12938 to X13919 represent these nucleotide sequences which are primary
nucleotide sequences; also known as contigs. The computer-based system
can identify fragments of the Enterococcus faecalis genome with
commercial importance. The products can be used to detect the presence
of Enterococcus faecalis in samples. They can also be used for
configuration of disease, and for identifying agents which can be used to
modulate the growth or pathogenicity of Enterococcus faecalis, or
conclusted organism, in vivo or in vitro. In particular the
polypeptides encoded by the Enterococcus faecalis nucleotide sequences
can be used in vaccines to prevent or attenuate an Enterococcal
   WPI; 99-045171/04.

New isolated Enterococcus faecalis polynucleotides and polypeptides used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
  19-MAR-1999 (first entry) abterococcus faccalis genome contig SEQ ID NO:137. Enterococcus faccalis; contig; detection; Enterococcal infection; vaccine; attenuation; computer readable medium; ds.
  1041 G;
  Gaps: 0
Percent Identity: 80.000
   Percent Identity: 58.333
  Align seg 1/1 to reverse of: X13074 from: 1 to:
   Length:
   Gaps:
  1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
  806 C;
  Align seg 1/1 to: V74278 from: 1 to: 1564
   12-NOV-1998. U08985. 04-MAY-1998; U08985. 06-MAY-1997; US-066009. 06-MAY-1997; US-044031. 16-MAY-1997; US-046655. (HUMA-) HUMAN GENOME SCI INC. Barash SC, Dillon PJ, Kunsch CA;
   1940 A;
  seq_documentation_block:
ID X13074 standard; DNA; 5550 BP.
  seq_documentation_block:
ID T79680 standard; DNA; 5892
AC T79680;
  alignment_block:
US-08-653-294-16 x X13074/rev
   03-FEB-1998 (first entry)
   37.00
3.364
91.667
  seq_name: N_Geneseq_36:X13074
Ratio: 3.700
Percent Similarity: 100.000
  seq_name: N_Geneseq_36:T79680
  Enterococcus faecalis. WO9850555-A2.
  alignment_block:
US-08-653-294-16 x V74278
   Ratio:
Percent Similarity:
  Quality:
   alignment_scores:
   infection.
   infection.
```

Sequence

AC PT

```
1730 T;
   Percent Identity: 54.545
   Gaps:
  Length:
   2 ArgLeuLeulleArgArglleLeuLeuArgTyr 12
   from: 1 to: 5892
```

```
Claim 1; Page 814-819; 1409pp; English.

The present invention describes a computer readable medium which has the present invention describes a computer readable medium which has the nucleotide sequences SEO ID NO: 1 to 391 (V52134 to V52524) recorded on it, or a representative fragment or a sequence at least 95% identical to SEO ID NO: 1 to 391 (V52134 to V52524) are genomic fragments from Streptococcus pneumoniae. The present invention also describes an isolated nucleic acid molecule encoding a homologue of any of the fragments of the S.pneumoniae genome (SEO ID NO: 1 to 391) where the nucleic acid molecule is produced by a process comprising: (a) screening a genomic DNA library using as a probe a target sequence defined by any of the sequences in SEO ID NO: 1 to 391, identifying members of the library which contain sequences that hybridise to the target sequence and isolating mRNA, DNA or CDNA produced
   from an organism, amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from the fragment of the S. pneumoniae genome to prime the amplification and isolating the amplified sequences. The computer readable medium can used in a computer-based system for identifying fragments of the S. pneumoniae genome of commercial importance, or expression modulating fragments of the S. pneumoniae genome. Products from the present invention can be used in diagnosis kits and assays, and pharmaceutical compositions and vaccines for S. pneumoniae.
  Computer-readable medium with recorded Streptococcus pneumoniae polynucleotide sequences - useful in diagnostic kits and assays, and pharmaceutical compositions and vaccines for Streptococcus
   Streptococcus pneumoniae genome fragment SEQ ID No:112.
Streptococcus pneumoniae; S. pneumoniae; genome; diagnosis; assay;
computer readable medium; vaccine; pharmaceutical composition; ds.
  07-SEP-1995 (first entry)
Hepatitis C virus gene HC-G9 cDNA.
Hepatitis C virus; HCV; non-A non-B; HC-G9; treatment;
Hepatitis C virus.
  (HUMA-) HUMAN GENOME SCI INC.
Barrash SC, Chol GH, Dillon PJ, Dougherty BA, Fannon Kunsch CA, Rosen CA, Rosen CA, WPI: 98-272252/24.
   Ratio: 3.700 Length: 10 Percent Similarity: 100.000 Percent Identity: 60.000
   342. .937
/*tag= a
/transl_except= pos:7947. .7949,
/transl_except= pos:7950. .7952,
/transl_except= pos:7953. .7955,
  1307 C;
   Align seg 1/1 to: V52245 from: 1 to: 7902
  7791 TITCGTATGCTAGTTCGGAGATTGTTGCTA 7820
   1 TyrArgLeuLeulleArgArglleLeuLeu 10
   Location/Qualifiers
   seq_documentation_block:
ID 079140 standard; cDNA; 9487 BP.
AC 079140;
  2482 A;
  entry)
   Streptococcus pneumoniae
  seq_name: N_Geneseq_36:Q79140
  30-OCT-1997; U19588.
31-OCT-1996; US-029960.
   US-08-653-294-16 x V52245
  (first
  7902 BP;
   WO9818931-A2.
   07-MAY-1998.
   alignment_scores:
                                       23-OCT-1998
  pneumoniae
  aliqnment_block
   Sequence
NAME OF THE PROPERTY OF THE PR
   The present sequence represents the partial sequence of the BRCA2 cancer susceptibility gene. The nucleic acid molecule can be used to construct probes for screening cDNA or genomic libraries, sequencing construct probes for screening cDNA or genomic libraries, sequencing construct probes for screening cDNA or genomic libraries, sequencing construct probes for and assembling the full length BRCA2 constructed in a method of medical treatment, preferably gene therapy, especially for treating cancer, where the cancer is female or male breast cancer, ovarian, prostate or colorectal cancer, ocular melanoma or latexaemia. In particular antisense oligonucleotides capable of by bridising to the BRCA2 nucleic acid, pre-mRNA or mature mRNA are used so that the expression of the BRCA2 nucleic acid is reduced or prevented. The nucleic acid molecules are also useful in a method for prevented. The nucleic acid molecules are used to design probes or primers for PCR to determine or detect the presence of mutations in a sample of nucleic caid molecules are used to design probes or primers for PCR to determine or detect the BRCA2 promoter region is useful for screening for substances which modilate the expression of nucleic acid under control of the promoter. Antibodies are used to determine the presence of mutations or determine or a cell of a BRCA2 polypeptide or its mutant forms. The polypeptides are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding partners, these are used to screen for binding
  P-PSDB; W25038.

Nucleic acid molecules comprising part or all of the BRCA2 cancer susceptibility gene - useful for diagnosis, prognosis or therapeutic treatment of cancer creatment of cancer Claim 3; Fig 4; 124pp; English.
   Partial BRCA2 cancer susceptibility gene.
RCA2 cancer susceptibility gene; breast cancer; ovarian cancer;
gene therapy; prostate cancer; colorectal cancer; ocular melanoma;
leukaemia; human; ss.
   1995 T;
  /product= BRCA2_fragment
/transl_except= (pos:3800. .3801,aa:Glu)
/transl_except= (pos:3802. .3803,aa:Lys)
  polypeptide, which can be used as cancer therapeutics. Sequence 7240 BP; 2735 A; 1188 C; 1322 G;
  Ashworth A, Futreal PA, Stratton MR, Wooster RF; WPI; 97-261854/24
   Ouality: 37.00 Length: 11
Ratio: 3.700 Gaps: 0
Percent Similarity: 90.909 Percent Identity: 54.545
  Align seg 1/1 to: T79668 from: 1 to: 7240
   2 ArgleuleulleArgArglleLeuLeuArgTyr 12
   28-AUG-1996; 024453.
28-AUG-1996; GB-017961.
23-NOV-1995; GB-023959.
14-DEC-1995; GB-025555.
(CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
(UYDU-) UNIV DUKE.
  Location/Qualifiers
2. .6989
seq_documentation_block:
ID T79668 standard; cDNA; 7240 BP.
   02-FEB-1998 (first entry)
   /*tag= a
  alignment_block:
US-08-653-294-16 x T79668
   Homo sapiens.
  alignment_scores:
  GB2307477-A.
```

1634 G;

aa:Glu aa:Glu aa:Ala

seq\_documentation\_block:
ID V52245 standard; DNA; 7902 BP.

seq\_name: N\_Geneseq\_36:V52245

```
(ONCO-) ONCORMED INC
   WO9909164-A1.
   alignment_scores:
   Key
 F 13-MAY-1993; 147133.
F 13-MAY-1994; 147133.
F 13-MAY-1995; 147133.
A (IMMO) IMMUNO JAPAN KK.
R PPEDS); R67588.
T A hepatitis C virus gene and oligo-nucleotide(s) - used for the retarment of hepatitis C (Jaim 1); Pages 10-15; 41pp; Japanese.
C Claim 1; Pages 10-15; 41pp; Japanese.
C (79140 is the hepatitis C virus (HCV) gene HC-G9 cDNA, it encodes the protein described in R67588. Both the cDNA and protein can be used in the treatment of HCV infection
Sequence 9487 BP; 1905 A; 2798 C; 2687 G; 2097 T;
   21-JUN-1999 (first entry)

Human BRCA2 (omi2) encoding cDNA.

Human BRCA2; genetic testing; protein therapy; haplotype; detection; genet therapy; breast cancer; ovarian cancer; ds.

Homo sapiens.
                                 aa Pro
aa Pro
aa Sta
aa Sa
aa Sa
aa Lys
aa Lys
aa Tyr
aa Asp
aa Tyr
aa Asp
aa Yal
aa Sa
aa Gln
  aa:Leu
aa:Pro
   aa:Ile
aa:Ala
   aa:Val
aa:Met
   Length: 12
Gaps: 0
Percent Identity: 58.333
   Align seg 1/1 to reverse of: Q79140 from: 1 to: 9487
  .8024,
  8009,
  .8018,
  .8012,
   .7979,
   .8000,
   .8003,
  .8006,
  .8015,
  1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
   pos:8004.
pos:8007.
pos:8010.
pos:8013.
pos: 7956.
pos: 7959.
pos: 7965.
pos: 7968.
pos: 7971.
pos: 7977.
pos: 7980.
pos: 7983.
pos: 7983.
pos: 7983.
   pos:7995.
pos:7998.
pos:8001.
  pos:8016.
pos:8019.
   Location/Qualifiers
229. .10485
/*tag= a
/transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
  /transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
   /transl_except= p
/transl_except= p
/transl_except= p
/transl_except= p
   /transl_except=/transl_except=
   /transl_except=
/transl_except=
   /transl_except=/transl_except=
  /transl_except=
/transl_except=
   seq_documentation_block:
ID X30256 standard; cDNA; 10485 BP.
AC X30256;
   /transl_except=
   Quality: 37.00
Ratio: 3.700
Percent Similarity: 83.333
  alignment_block:
US-08-653-294-16 x Q79140/rev
  seq_name: N_Geneseq_36:x30256
  25-FEB-1999.
14-AUG-1998; U16905.
   WO9909164-A1.
  alignment_scores:
   J06319563-A.
   Key
```

```
PR 12-70X-1999; US 004471.

PR 10-70X-1997; US 005784.

PR 11-70X-1997; US 005784.

PR 11-70X-1997; US 005784.

PR 07-70X-1997; US 005526.

PR 07-70X-1997; US 005527.

PR
```

```
PP-PSDB: Y04356.

PP Avelop products for determining susceptibility to, detection and develop products for determining susceptibility to, detection and treatment of breast or ovarian cancer.

PP Claim 13: Page 97-111: 226pp; English.

CC Tase present invention describes genomic DNA which contains a BRCA2 gene where the first 12 nucleotides beginning exon 5 are 5-TCCTGTTGTTGT-3' as in sequence (I) (see X03249), where nucleotides numbers (I) (see X03249), where nucleotides beginning exon 5 are 5-TCCTGTTGTTGTT-3' as in sequence (II) (see X30251) and the first 20 nucleotides beginning con a sequence (II) (see X30551) and the first 20 nucleotides beginning exon 15 are 5-CTGGTGTTGTTGTTGTTG-3' as in sequence (III) (see X30551).

CC last 20 nucleotides encoding exon 15 are 5-CTGGTGTTGTTGATAAACAG-3' as in sequence (III) (see X30551) and the first 20 nucleotides beginning exon 16 are 5'-CTGTATAGCTATGGTTGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGCTATGGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGCTATGGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGCTATGGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGCTATGGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGCTATGTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGTTG-3' as in sequence (III) (see X30253).

CF con 16 are 5'-CTGTATAGTTG-3' as in sequence or quantifying the amount of a tumour growth inhibitor following such therapy. The BRCA2 protein, polypeptides, their contains and canceristics of BRCA2 proteins, such as structure and cunction of BRCA2 in oncogenesis or subcellular localisation of BRCA2 contains cells. The present sequence encodes
   21-JUN-1999 (first entry)
Human BRCA2 (om14) encoding cDNA.
Human BRCA2; genetic testing; protein therapy; haplotype; detection;
gene therapy; breast cancer; ovarian cancer; ås.
  coding sequence haplotypes of the human BRCA2 gene - used to elop products for determining susceptibility to, detection and
  2870 T;
  Eskandari T, Jackson GM, Murphy PD, Olson SJ, Park M, Rabin MB, Schryer B, White MB, Yoshikawa M; WPI; 99-190163/16.
Eskandari T, Jackson GM, Murphy PD, Olson SJ, Park M,
Rabin MB, Schryer B, White MB, Yoshikawa M;
WPI; 99-190163/16.
  1965 G;
  37.00 Length: 11
3.700 Gaps: 0
90.909 Percent Identity: 54.545
  1842 C;
  Align seg 1/1 to: X30257 from: 1 to: 10485
   2 ArgleuLeulleArgArglleLeuLeuArgTyr 12
   Location/Qualifiers
229. .10485
/*tag= a
  3808 A;
   X30258 standard; cDNA; 10485 BP. X30258;
   seq_name: N_Geneseq_36:X30258
   22-MXY-1998; US-084471.
15-AUG-1997; US-055784.
07-NOV-1997; US-064926.
12-NOV-1997; US-065567.
01-MAY-1998; US-071715.
  alignment_block:
US-08-653-294-16 x X30257
  orocein ...
numan BRCA2 (omi3).
numance 10485 BP;
  (ONCO-) ONCORMED INC.
   016905
  seq_documentation_block:
   Quality:
Ratio:
   Percent Similarity:
   P-PSDB: Y04357
  14-AUG-1998;
  alignment_scores:
  sapiens
  WO9909164-A1
   25-FEB-1999
  develop
  Homo
   Key
```

```
PT treatment of breast or ovarian cancer.

PS Claim 14: Page 119-133; 256pp; English.

CC The present invention describes genomic DNA which contains a BRCA2 gene content of the present invention describes genomic DNA which contains a BRCA2 gene content of titst 12 nucleotides beginning exon 5 are 5'-TCCTGTTGTTGTT-3' as a sequence (IV) (see X30249), where nucleotides numbers content of the content of BRCA2 in oncogenesis or succeillular localisation of BRCA2 (inhibitor following such therapy The BRCA2 protein, polypeptides, their continuous leginal and cancerous cells, polypeptides, their content of BRCA2 in oncogenesis or subcellular localisation of BRCA2 (inhibitor of BRCA2 in oncogenesis or subcellular localisation of BRCA2 (onid).

CC function of BRCA2 in oncogenesis or subcellular localisation of BRCA2 (onid).

Sequence 10485 BP; 3809 A; 1841 C; 1964 G; 2871 T;

alignment_block:

CR protect Similarity: 90.909 Percent Identity: 54.545

Align seg 1/1 to: X30258 from: 1 to: 10485

Align seg 1/1 to: X30258 from: 1 to: 10485
```

```
A1927435 w075f12.x1 NCI_CGAP
AA591962 v150b07.r1 Beddingt
AQ632742 RPCI-11-475D13.TJ R
   Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda: Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis;
1 (bases 1 to 300)
Kohara, Y., Shin-1, T., Thierry-Mieg, J., Thierry-Mieg, D., Mitsuki, H., Nishiqaki, A., Motohashi, T., Zeng, Q., Watanabe, H., Sugimoto, A., Sano, M., Miyata, A., Mitani, Y., Iida, K., Uesugi, H., Sugiyama, Y. and Nomoto, H.
Expressed genes in C.elegans
   seq_documentation_block:
LOCUS AV182551 300 bp mRNA EST 21-JUL-1999
DEFINITION AV182651 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk64097 3', mRNA sequence.
ACCESSION AV182651
  Homo
  seq_documentation_block:
LOCUS AQ137850 461 bp DNA GSS 24-SEP-1998
DEFINITION HS_3058_B2_C09_MF CIT Approved Human Genomic Sperm Library D Pserivition HS_3058_B2_C09_MF CIT Approved Human Genomic Sperm Library D Pserivity Sapiens genomic clone Plate=3058 Col=18 Row=F, genomic survey
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
   /db_xref="taxon:6239"
/clone="yk64097"
/clone=lib="yuji Kohara unpublished cDNA:Strain N2
hermaphrodite embryo"
/sex="hermaphrodite"
  Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189500.
Contact: Yuji Kohara
Gene Library Lab
   others
   ~
  Length: 12
Gaps: 0
Percent Identity: 66.667
  Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. 300
/organism="Caenorhabditis elegans"
  National Institute of Genetics
Yata 111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
  ų
  1 TyrArgLeuLeulleArgArgIleLeuLeuArgTyr 12
216.33
231.69
250.80
   71
   Align seg 1/1 to: AV182651 from: 1 to: 300
  /dev_stage="embryo"
68 c 54 g
128.49
127.96
127.34
  Caenorhabditis elegans.
   AV182651.1 GI:5562552
   AQ137850.1 GI:3528503
   /strain-"N2"
39.00
39.00
  45.00
4.091
91.667
  alignment_block:
US-08-653-294-16 x AV182651
   seq_name: gb_est36:AV182651
   seq_name: gb_gss9:AQ137850
   Homo saplens
   ø
  sequence.
AQ137850
  Ratio:
Percent Similarity:
   Quality:
   105
   human.
gb_est36:AI927435
gb_est16:AA591962
gb_gss15:AQ632742
  alignment_scores
  BASE COUNT
ORIGIN
  ORGANISM
   ORGANISM
   TITLE
JOURNAL
COMMENT
  ACCESSION
VERSION
KEYWORDS
SOURCE
  REFERENCE
AUTHORS
   VERSION
KEYWORDS
SOURCE
  FEATURES
   | Documentation | N182651 Yuji Kohara u | A0182651 AV18651 Yuji Kohara u | A0137860 Was 2009_MF CIT | A0835306 HS_4815_A1_D12_TA CIT | A748739 Ny06612.51 NCI_CGAP_GC | A0253565 HS_3026_A1_A07_MF CIT | AA103036 mo21dil: Ti_Life_Tech | AA103036 mo21dil: Ti_Life_Tech | A0569045 HS_5344_A1_F08_TA RPG | A0259553 nbxb0023512r CUGI Rice | D37193 CELK041G6F V****
   A0869567 nbeb0035056 CuGI Rich
A0869567 nbeb0035056 CuGI Rich
A1774609 EST255709 tomato resis
B70241 CIT-HSP-2028112.TR CIT-H
A1775248 EST255648 tomato mixed
A1162936 A027932U Hybrid aspen
A0097888 HS_3035_B2_A06_MF CIT
B60584 CIT-HSP-2013F20.TRC CIT-H
A0097888 HS_3035_B2_A06_MF CIT
A1163552 A044P30U Hybrid aspen
A1163545 A044P30U Hybrid aspen
A1163545 A044P30U Hybrid aspen
A1163545 A044P30U Hybrid aspen
A163545 A044P30U Hybrid aspen
A1163545 A044P30U Hybrid aspen
A1163545 A044P30U Hybrid aspen
A1163543 CONSTREEL-2591A11.TF CI
A161741 A006P30U Hybrid aspen
A1161931 A006P30U Hybrid aspen
A1161931 A006P30U Hybrid aspen
A1161093 A006P80U Hybrid aspen
A221068 A1160005005005 CUGI Rice
AQ210689 AU006893 SCHIZOSACCHAI
  D37193 CELK041G6F Yuji Kohara v
AQ311590 RPCI11-1A13.TJ RPCI-11
  -MODEL-frame+_p2n.model -DEV-x1p
-Q-fqqn1_J/OSFPQ_SPO.1/VOSP8653294/runat_04022000_160700_15770/app_query.fasta.1
-DB=EST -OPRMT=fastap -SUFFIX-rst -GAPOP=12.000 -GAPOP=4.000
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -GGAPOP=6.000
-FGAPDP=6.000 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cd1
-LIST=45 -DOCALIGN=200 -THR_SCORE=PCt -ALIGN=15 -MODE=LOCAL
-OUTPWT=pfs -NORM=ext -MINLEN=0 -MAXIEN=1000000 -USER=USO8653294
-NCPU=6 -ICPU=3 -NO_XLPXY -WAIT -THREADS=1
   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format :
  EScore
   54.70
73.10
95.80
96.80
96.80
110.22
110.22
110.22
110.22
110.22
110.22
110.22
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
110.23
  241.25
245.62
268.48
269.45
279.22
289.50
307.66
394.93
212.68
  236.41
237.38
237.86
  125.00 123.00 12
  EST:*
   Query: US-08-653-294-16
Query length: 12
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.360000
  OM of: US-08-653-294-16 to:
   Search information block:
   Command line parameters:
  Strd
  Date: Feb 8, 2000 4:03
  gb_estl:D37193
gb_gss11:AQ311590
gb_gss6:AQ869567
gb_est37:A1960153
gb_est33:AI774609
   gb_est24:A1161931
gb_est24:A1162067
gb_est37:A1966443
gb_est44:A1966443
gb_est44:AN219466
gb_gss11:AQ328194
gb_gss11:AQ328194
gb_gss11:AQ291628
gb_est18:AA709270
gb_est22:AU006893
   9b_gss9.A0137850
9b_gss6.AQ835306
9b_est10:AA748739
9b_est20:AA748739
9b_est20:AA103036
9b_gss14:AO569045
9b_gss14:AO569045
   gb_est41:Av263447
gb_gss9:Ab097888
gb_gss9:Ab094
gb_est37:A1960040
gb_est24:A1163552
gb_est24:A1163552
gb_est24:A1163545
  gb_est18:AA690244
gb_gss13:AQ476031
gb_est8:AA012276
gb_gss12:AQ339784
   gb_est24;Ai161741
gb_gss8:AQ055939
gb_est24:AI162058
  gb_gss3:B70241
gb_est33:A1775248
  gb_est38:AW096409
gb_est24:AI162936
   Sequence
gb_est36:AV182651
   gb_est37:AI966327
  score_list:
```

```
High quality sequence stop: 605.
Location/Qualifiers
1, .605
  107 9
  Align seg 1/1 to: AQ835306 from: 1
   mRNA sequence.
AA748739
AA748739.1 GI:2788697
  112 c
  43.00
3.909
91.667
  alignment_block:
US-08-653-294-16 x AQ835306
   Class: BAC ends
  seq_name: gb_est19:AA748739
   seq_documentation_block:
LOCUS AA748739
   Percent Similarity:
  Quality:
  178
   naman.
  alignment_scores
  source
  KEYWORDS
SOURCE
ORGANISM
  source
  DEFINITION
  BASE COUNT
ORIGIN
   REFERENCE
AUTHORS
TITLE
   ACCESSION
   JOURNAL
  FEATURES
   FEATURES
  VERSION
   COMMENT
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
Abhairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
   Adams, M.D. and
  HOMO
   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="Plate=3058 Col=18 Row=F"
/clone="Plate=3058 Col=18 Human Genomic Sperm Library D"
/sex="male"
  1 (bases 1 to 605)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
  /note-"Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
  Sequence-tagged connectors: A sequence approach to mapping and
  seq_documentation_block:
LOCUS
LOCUS
AQ835306
605 bp DNA
BEFINITION HS_4815_Al_D12_T7A CIT Approved Human Genomic Sperm Library D
sapiens genomic clone Plate=4815 Col=23 Row=G, genomic survey
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
  scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 308 row: F column: 18
Class: BAC ends
  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
  Length: 12
Gaps: 0
Percent Identity: 75.000
  to: 461
   High quality sequence stop: 461:
Location/Qualifiers
   102 g
   Align seg 1/1 to: AQ137850 from: 1
   AQ835306
AQ835306.1 GI:5801368
  4.300
  43.00
   alignment_block:
US-08-653-294-16 x AQ137850
  seq_name: gb_gss6:AQ835306
   Homo sapiens
  Quality:
  Ratio:
   Percent Similarity:
   alignment_scores:
   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
   BASE COUNT
   JOURNAL
MEDLINE
COMMENT
  REFERENCE
AUTHORS
  MEDLINE
COMMENT
                    REFERENCE
                                      AUTHORS
   JOURNAL
   FEATURES
  TITLE
  TITLE
  ORIGIN
```

```
Sequencing Center
Information can be
  AA748739 309 bp mRNA EST 22-JAN-1998 ny06e12.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1270990 3',
Tel: (206) 616-3618

Fax: (206) 616-3887

Email: jwallaced.washington.edu

Clones may be purchased from Research Genetics (info@resgen.com).

BAC end Web Server: http://www.htsc.washington.edu

Plate: 4815 row: G column: 23
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutherla; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 309)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NAI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
   /organism="Homo sapiens"
/db_xref="tabe.g506"
/clone="Plate=4815 Col=23 Row=G"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DB108"
   Tumor Gene Index
Onpublished (1997)
On Jan 14, 1998 this sequence version replaced gi:1797612.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenth.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D., David Allman, Ph.D., Gerald Marti, M.D.
CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
  7 others
  CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/ELNL at:
   Length: 12
Gaps: 0
Percent Identity: 58.333
  Insert Length: 674 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 256.
Location/Qualifiers
1. 3309
   ww-bio.llnl.gov/bbrp/image/image.html
  201 t
  1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
   to: 605
```

```
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Mammalia,
Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 519)
Marran, Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
  /note="Organ: whole embryo; Vector: pCMV-SPORT2; Site_1: Sali; Site_2: Not1; Cloned unidirectionally. Primer: 011go dr. 13 5dpc embryos. pCMV-SPORT2 vector."
/db_xref="taxon:9606"
/clone="plate=3026 Col=13 Row=A"
/clone_llb="CIT Approved Human Genomic Sperm Library D"
/sex="male"
   Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:801493.
On May 8, 1995 this sequence version replaced gi:801493.
Ontact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: mouseest@watcon.wustl.edu
This clone is available royalty-free through LLNL; contact the
   seq_documentation_block:
LOCUS AA103036 519 bp mRNA EST 29-OCT-1996
DEFINITION mo21d11.rl Life Tech mouse embryo 13 5dpc 10666014 Mus musculus CDNA clone IMAGE:554229 5', mRNA sequence.
  /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
   /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:554229"
/closne=lib="tife Tech mouse embryo 13 5dpc 10666014"
/closue_type="embryo"
/dev_stage="13.5dpc embryos"
/lab_host="DH10B"
/lab_host="DH10B"
  1 others
   Gaps: 0
Percent Identity: 80.000
  Seq primer: -28M13 rev1 from Amersham High quality sequence stop: 444.
Location/Qualifiers
1. .519
/organism="Mus musculus"
/strain="C57BL/65"
  132 t
  Length:
  Waterston, R.
The WashU-HHMI Mouse EST Project
   1 TyrArgLeuLeuIleArgArgIleLeuLeu 10
   25 TATCGACTACTACTAGGCGACTTCTATTA 54
  р
   81
  from: 1
  AA103036.1 GI:1649195
   o 66
  to: AQ253565
   Quality: 42.00
Ratio: 4.200
Percent Similarity: 100.000
  alignment_block:
US-08-653-294-16 x AQ253565
  seq_name: gb_est9:AA103036
   house mouse.
  Mus musculus
  150 a
   177
   alignment_scores
  Align seg 1/1
  VERSION
KEYWORDS
SOURCE
ORGANISM
  BASE COUNT
ORIGIN
   BASE COUNT
ORIGIN
  TITLE
JOURNAL
COMMENT
   REFERENCE
AUTHORS
  FEATURES
  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
Mahahiras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
   seq_documentation_block:
LOCUS AQ233565 490 bp DNA GSS 10-OCT-1998
DEFINITION HS_3026_A1_A07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=13 Row-A, genomic survey
  Sequence-tagged connectors: A sequence approach to mapping and
  constructed by Bento Soares and M. Fatima Bonaldo." 52\ c 55\ g 107\ t
   scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
   High quality sequence stop: 13 class: BAC ends. High quality sequence stop: 400. Usa to the sequence stop: 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887
Email: jwallace@u.washington.edu Sequence Tagged Connector Sequence Tagged Connector Sequence Tagged Connector Sequence Tagged Connector Class: BAC ends. High quality sequence stop: 490.
  /clone="IMAGE:1270990"
/clone_lib="NGI_GGAP_GGB1"
/tissue_type="germinal center B cell"
/lab_host="DH10B"
  to: 309
   Length: 12
Gaps: 0
Percent Identity: 66.667
   Contact: Mahairas GG, Wallace JC, Hood L
  Align seg 1/1 to reverse of: AA748739 from: 1
  1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
   /organism="Homo sapiens"
  AQ253565
AQ253565.1 GI:3724919
  alignment_block:
US-08-653-294-16 x AA748739/rev
   4.200
   42.00
   seq_name: gb_gss10:AQ253565
   Homo sapiens
  Ratio:
Percent Similarity:
   sequence.
  Quality:
   95
   Hood, L
  human.
   alignment_scores:
   source
   BASE COUNT
   ORGANISM
  REFERENCE
AUTHORS
   MEDLINE
COMMENT
  ACCESSION
   VERSION
KEYWORDS
SOURCE
  JOURNAL
   FEATURES
  TITLE
   ORIGIN
```

```
/organism="crypta sativa"
/organism="crypta sativa"
/dutivar="Nipponiar="
/dutivar="Nipponiar="
/dutivar="Nipponiar="
/dutivar="nipponiar="
/clone="lib="canigate"
/clone="lib="cuci Rice BAC Library"
/clone="lib="cuci Rice BAC Library"
/clone="lib="cuci BeloBAC11; Site_1: HindIII: Site_2:
/lab_host="E. col; DH10B"
/note="Wector: pBeloBAC11; Site_1: HindIII: Site_2:
HindIII; Rice ne of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
/Arumquanthan and Earle, 1991). The relatively small
genome of rice, three times larger than that of
Arabidopsis, makes it suitable for genomic studies. In
order to facilitate positional cloning, physical mapping
and genome sequencing of rice, we have constructed a BAC
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
library from Oryza sativa, Nipponbare variety. The
sequence with a probability of 99.9 % Two high density
filters, each containing 18,432 clones (doubly spotted),
represent the whole-library for colony screening."
   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
  seq_documentation_block:
LOCUS AQ259553 685 bp DNA GSS 23-OCT-1998
DEFINITION nbxb0023E12r CUGI Rice BAC Library Oryza sativa genomic clone nbxc0023E12r, genomic survey sequence.
   1 (bases 1 to 685)
Ming.R.A. and Dean.R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
  to: 596
  0 12
  Contact: Wing RA
Clemson University Genomics Institute
Clemson University
Clemson University
ToU Jordan Hall; Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
  210 TATAAGTTAATGGTTTATAAGATACTTTTAAGATAT 175
  to reverse of: AQ569045 from: 1
  1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
   Length:
Gaps:
  /organism="Oryza sativa"
   High quality sequence start: 71
High quality sequence stop: 310.
Location/Qualifiers
1. 685
   Email: rwing@clemson.edu
Seg primer: GGAAACAGCTATGACCATG
Class: BAC ends
   AQ259553.1 GI:3784035
US-08-653-294-16 x AQ569045/rev
   42.00
  seq_name: gb_gss11:AQ259553
  Poaceae; Oryza.
   Oryza sativa.
  Oryza sativa
   Quality:
Ratio:
   195
  alignment_scores:
   Align seg 1/1
   VERSION
KEYWORDS
SOURCE
ORGANISM
   source
   REFERENCE
AUTHORS
TITLE
JOURNAL
  BASE COUNT
  FEATURES
   COMMENT
  ORIGIN
  On Mar 23, 1999 this sequence version replaced gi:3324756.

Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (207) Factor Contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://www.htsc.washington.edu
Plate: 920 row: K column: 15
Seq primer: 17
  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 596)
Mahalras, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
   /note="Vector: pBACe3.6; Genomic sequence of BAC ends"
116 c 93 g 161 t 22 others
  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
   AQ569045 596 bp DNA GSS 01-JUN-1999 HS_5344_A1_F08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=920 Col=15 Row=K, genomic survey sequence.
   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=920 Col=15 Row=K"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
  Length: 12
Gaps: 0
Percent Identity: 58.333
   Length: 12
Gaps: 0
Percent Identity: 58.333
   ä
  from: 1
   1 TyrArgLeuLeuIleArgArgIleLeuLeuArgTyr 12
   High quality sequence stop: 596.
Location/Qualifiers
   Align seg 1/1 to reverse of: AA103036
   AQ569045.1 GI:4962265
  alignment_block:
US-08-653-294-16 x AA103036/rev
   42.00
3.818
91.667
   42.00
3.818
91.667
  seq_name: gb_gss14:AQ569045
   Class: BAC ends
  Ratio:
Percent Similarity:
   Quality:
Ratio:
Percent Similarity:
  AQ569045
  204
   human.
   alignment_scores:
  alignment_scores:
   alignment_block:
```

MEDLINE COMMENT

JOURNAL

TITLE

BASE COUNT ORIGIN

FEATURES

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

```
Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Eutheria; Primates; Catarrhin; Hominidae; Homo.

Sed finama Date Catarrhin; Hominidae; Homo.

Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.

Contact: Shaying Zhao, William Nierman, Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

Fal: 301 838 0200

Fax: 301 80200

Fax: 40000

Fax: 400000

Fax: 400000

Fax: 400000

Fax: 400000

Fax: 400000

Fax: 4000000

Fax: 4000000

Fax: 4000000

Fax: 4000000

Fax: 400000

Fax: 400
   Oryza sativa Sukaryota; Embryophyta; Iracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza; Oryza; I (bases 1 to 438) I (bases 1 to 438) I (bases I to 4
  Oryza sativa genomic
   On Mar 23, 1999 this sequence version replaced gi:3324665.
  seg_documentation_block:
LOCUS A0869567 438 bp DNA
DEFINITION nbeb0035D05f CUGI Rice BAC Library (ECORI) On a10ne nbeb0035D05f, genomic survey sequence.
ACCESSION A0869567
   Length: 10 Gaps: 0 Percent Identity: 80.000
  to: 420
  /organism="Homo sapiens"
   /db_xref="GDB:7500012"
/db_xref="taxon:9606"
/clone="RPCI-11-1A13"
  3 LeuLeulleArgArglleLeuLeuArgTyr 12
   /clone_lib="RPCI-11"
   Location/Qualifiers
  Align seg 1/1 to: AQ311590 from: 1
   AQ869567.1 GI:6220018
   Ratio: 4.100
Percent Similarity: 100.000
  alignment_block:
US-08-653-294-16 x AQ311590
  seq_name: gb_gss6:AQ869567
   Oryza sativa.
   Homo sapiens
   ಥ
   Quality:
   133
  alignment_scores
  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  source
   ORGANISM
   BASE COUNT
  TITLE
JOURNAL
COMMENT
   AUTHORS
TITLE
JOURNAL
COMMENT
  REFERENCE
  AUTHORS
   REFERENCE
   FEATURES
           SOURCE
  D37193 360 bp mRNA EST 24-OCT-1994 CELKO41G6F Yuji Kohara unpublished cDNA Caenorhabditis elegans CDNA clone yk41g6 5', mRNA sequence.
   Caenorhabditis elegans.
Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota, Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 360)
Kohaza,Y., Mitsuki,H., Nishigaki,A., Motohashi,T., Sugimoto,A. and
   seq_documentation_block:

LOCUS AQ311590 420 bp DNA GSS 04-MAY-1999
DEFINITION RPCIII-1A13.T RPCI-11 Homo sapiens genomic clone RPCI-11-1A13,

GENOMIC SURVEY SEQUENCE.

ACCESSION AQ311590 GI:4043339
KERMORDS GSS 04-MAY-1999
  1 others
   /clone="yk41g6"
/clone=lib-"ruji Kohara unpublished cDNA"
/sex="hermaphrodite, male"
/tissue_type="whole animal"
  Toward an expression map of the C.elegans genome
  Length: 12
Gaps: 0
Percent Identity: 58.333
Identity: 75.000
  /organism="Caenorhabditis elegans"
  Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
  /strain="CB1489 him-8(e1489)
/db_xref="taxon:6239"
  ų
   1 TyrArgLeuLeulleArgArglleLeuLeuArgTyr 12
  6
  to: 685
   Unpublished (1994)
Contact: Yuli Kohara
Gene Library Lab
National Institute of Genetics
  Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
  /dev_stage="varied"
76 c 80 q
  80 g
           Percent
  from: 1
   from: 1
   D37193 D37193.1 GI:525575
  41.00
3.727
91.667
  Align seg 1/1 to: AQ259553
           83,333
  alignment_block:
US-08-653-294-16 x AQ259553
   seq_name: gb_gss11:AQ311590
   Align seg 1/1 to: D37193
  US-08-653-294-16 x D37193
  seq_documentation_block:
LOCUS D37193
   seq_name: gb_est1:D37193
  rabara, H.
   Percent Similarity:
  Quality:
Ratio:
           Percent Similarity:
  106
   alignment_scores:
   alignment_block:
```

source

FEATURES

BASE COUNT ORIGIN

```
eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
  /lab_host-"DH10B"
   John Erpelding
106 c 1
  alignment_block:
US-08-653-294-16 x AI960153/rev
                             (bases 1 to 457)
   4.100
  seq_name: gb_est33:AI774609
   grown
  seq_documentation_block:
  Quality:
   Ratio:
Percent Similarity:
  alignment_scores:
  source
   TITLE
JOURNAL
   BASE COUNT
                             REFERENCE
   AUTHORS
  FEATURES
   COMMENT
   A1960153 457 bp mRNA EST 20-AUG-1999 sc39b03.x1 Gm-c1014 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1014-1458 3', mRNA sequence.
  Glýcine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
   2 others
   Percent Identity: 90.000
                       Clemson University
ToU Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Fax: 864 656 4293
Small: rwing@clemson.edu
Seg primer: ryATAACGACTCACTATAGGG
Class: BAC ends
Contact: Wing RA
Clemson University Genomics Institute
   Gaps:
   /organism="Oryza sativa"
   Resource Center
c 65 g 10
  High quality sequence start: 24
High quality sequence stop: 397
Location/Qualifiers
1. 438
  /strain="Japonica"
/cultivar="Nipponbare"
   3 LeuLeuIleArgArgIleLeuLeuArgTyr 12
  /db_xref="taxon:4530
   from: 1
  A1960153.1 GI:5752866
  457 bp
  4.556
   Align seg 1/1 to: AQ869567
   US-08-653-294-16 x AQ869567
   seq_name: gb_est37:A1960153
   seq_documentation_block:
   Percent Similarity:
   Quality:
  Ratio:
   soybean.
   121
  alignment_scores
   alignment_block
   source
  DEFINITION
  BASE COUNT
ORIGIN
  ORGANISM
   ACCESSION
  FEATURES
  KEYWORDS
  VERSION
   SOURCE
```

```
/note="Vector: pT7T3Pac (pT7T3, Pharmacia); Site_1: ECORI; Site_2: HindIII; This cDNA library was constructed from mRNA isolated from leaves of 2-3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a 3' anchored poly (dT) primer. ECORI adapters were ligated to the blunt-ended cDNA fragments followed by digestion with ECORI and HindIII. The CDNA fragments were directionally cloned into the ECORI-HindIII restriction were transformed into DH10B host cells (Gibco BRL). This library was constructed by Dr. Randy Shoemaker and Dr.
Shoemaker, R., Rein, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J.,
Beck, C., Wylle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
On Mar 10, 1998 this sequence version replaced gi:2948010.
On Mar 10, 1998 this sequence version replaced gi:2948010.
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
  Email: estéwatson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
This clone is available through: Genome Systems, Inc. 4633 World
This clone (1900) 430-0030 or (1914) 427-3222 FAX: (888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
Info@genomesystems.com web_site: www.genomesystems.com
   /tissue_type="Leaves, 2-3 week old seedlings, greenhouse
   LOCUS A1774609 578 bp mRNA EST 29-JUN-1999
DEFINITION EST255709 tomato resistant, Cornell Lycopersicon esculentum cDNA
ACCESSION A1774609
   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
   /organism="Glycine max"
/db_xref="taxon:3847"
/clone="cBNOME SYSTEMS CLONE ID: Gm-c1014-1458"
/clone_lib="Gm-c1014"
   Length: 10
Gaps: 0
Percent Identity: 80.000
   Align seg 1/1 to reverse of: AI960153 from: 1
   Seq primer: primer name ambiguous
   High quality sequence stop: 364,
Location/Qualifiers
   236 CGCCTCCTCGTTCGACGACTTCTCCTCCGA 207
  11
  160 g
  2 ArgleuleulleArgArglleLeuLeuArg
```

Wed Feb

```
100 Jordan Hall, Člemson, SC 29634, USA
   ø
  Percent Similarity:
  Quality:
  Ratio:
   238
   tomato.
   alignment_scores
   source
  BASE COUNT
ORIGIN
  ORGANISM
  TITLE
JOURNAL
COMMENT
   JOURNAL
  VERSION
KEYWORDS
SOURCE
  REFERENCE
  AUTHORS
  FEATURES
                                       TITLE
  COMMENT
   Potatoe; Lycoperside.

E (bases 1 to 578)

S D'Ascenzo, M., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B., Generation of ESTs from Pseudomonas resistant tomato uppublished (1999)

On Dec 20, 1995 this sequence version replaced gi:1136039.

Other_ESTs: TC2277

Contact: David Frisch

Clemson University
  5 prime sequence.
Location/Qualifiers
Location/Qualifiers
l. :78
/organism="Lycopersicon esculentum"
/cultivar="R11-12 (355::Pto in Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="clRR12112"
/clone="clRR12112"
/clone="type="ty
   Lycopersicon esculentum Sukaryota, Embryophyta; Tracheophyta; bukaryota; Virigiplantee; Streptophyta; Embryophyta; Fracheophyta; euphyllophyta; Spermarcphyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
   /note-"vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLER - Tomato Pseudomonas Resistant EST Library Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoRI and 3' end with XhoI site." 139 c 133 g 137 t
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 593)
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
  B70241 593 bp DNA GSS 24-OCT-1998 CIT-HSP-2028112.TR CIT-HSP Homo sapiens genomic clone 2028112.
   Length: 11
Gaps: 0
Percent Identity: 81.818
   100 Jordan Hall, Člemson, SC 29634, USA
TE: 864 656 4566
Fax: 864 656 4293
Email: dfrisch@cLEMSON.EDU
   from: 1 to: 578
  genomic survey sequence.
B70241
B70241.1 G1:2709465
   GI:5272650
   41.00
4.556
81.818
   alignment_block:
US-08-653-294-16 x AI774609
   Align seg 1/1 to: AI774609
   seq_documentation_block:
LOCUS
  Homo sapiens
  seq_name: gb_gss3:B70241
   AI774609.1
   Percent Similarity:
   Quality:
  169
  Ratio
   comato
  human.
  alignment_scores
  DEFINITION
  SOURCE
ORGANISM
  BASE COUNT
ORIGIN
  ORGANISM
   TITLE
JOURNAL
COMMENT
  REFERENCE
AUTHORS
  ACCESSION
  VERSION
KEYWORDS
VERSION
KEYWORDS
  REFERENCE
  AUTHORS
   FEATURES
  SOURCE
```

```
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euchicotyledons; core euchpilophytes; Spermatophyta; Magnollophyta; eudicotyledons; core euchpilophyta; Asteridae; euasterida; Ensarcae; Solanaceae; Solanum; Potatoe; Lycopersicon.

El (bases 1 to 613)

El (base
  Unpublished (1997)
Other_GSSs: CIT-HSP-2028112.TFB
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Tel: 301 838 0200
Fax: 301 838 0208
Fax: 301 838 0208
Fax: deaddams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seg primer: Ml3 Reverse
Class: BAC ends.
  seq_documentation_block:

LOCUS A177548 613 bp mRNA EST 29-JUN-1999

DEFINITION EST256348 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cLERI5A13, mRNA sequence.

ACCESSION A1775248

VERSION A1775248
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building
   /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
  1 others
   Gaps: 0
Percent Identity: 72.727
  106 t
   Length:
   Location/Qualifiers
1. 593
1. 693
Acref—"GDB:704814"
Ab_xref—"GDB:704814"
Ab_xref—"CDB:704814"
Aclone—"2028112"
Aclone—11b—"CIT-HSP"
Asx—"Male"
  Align seg 1/1 to: B70241 from: 1 to: 593
  127 g
  41.00
4.100
90.909
  121 c
  "IIIbdiH
  seq_name: gb_est33:AI775248
  alignment_block:
US-08-653-294-16 x B70241
```

```
us-08-653-294-16.rst
```

Align seg 1/1 to: AI775248 from: 1 to: 613

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

February 8, 2000, 01:29:39; Search time 122.56 Seconds (without alignments) 2.319 Million cell updates/sec Run on:

US-08-653-294-17 58 1 YRLLIRRIALRY 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

188963 segs, 23686106 residues Searched:

188963 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

A\_Geneseq\_36:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|           |            | Description | 02 84- | Peptide B2702.84-7 | Immunomodulating d | HLA-B2702 CTL modu | HLA-B2702 84-75-84 | Immunomodulating d |        |              | Curvularia verrucu | Chloroperoxidase. | HLA-B2702 CTL modu | HLA-B2702 CTL modu | B2702  | B27(   | euronal |        | oţ     |        | co.    | Acetyl CoA carboxy | HLA-B2702 84-75T/7 | ซ      | Neuronal nicotinic | creted pr | ce enc | Amino acid sequenc | n pol  | Virulence gene clu | Human secreted pro | Hepatitis GB virus | T.thermophilus nit | ē   | subunit | Neuronal nicotinic |
|-----------|------------|-------------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|--------|--------------|--------------------|-------------------|--------------------|--------------------|--------|--------|---------|--------|--------|--------|--------|--------------------|--------------------|--------|--------------------|-----------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|-----|---------|--------------------|
| SUMMARIES |            | qi          |        | W33798             | W33799             | R92907             | R95428             | W33778             | W86351 | W12037       | W12042             | R82249            | R92909             | R92908             | W33791 | W33792 | W44156  | W06591 | W06590 | R71429 | R77379 | R67819             | R95430             | W61177 | W09022             | W74762    | R38889 | X10817             | R44431 | 75                 | 131                | 4                  | 754                | 889 | R73966  | 0                  |
|           |            | DB          |        |                    |                    |                    |                    |                    |        |              |                    |                   |                    |                    |        |        |         |        |        |        |        |                    |                    | Н      |                    |           |        |                    |        |                    |                    |                    |                    |     |         |                    |
|           |            | Length      | 12     | 12                 | 12                 | 20                 | 20                 | 20                 | 904    | 40           | 009                | 640               | 20                 | 20                 | 20     | 20     | 204     | 3391   | 3391   | 18     | 327    | 2240               | 20                 | 495    | 504                | 520       | 3165   | 31                 | 3567   | 4472               | 103                | 111                | 227                | 286 | 529     | 529                |
|           | *<br>Ouery | •           | 1.     | ä                  | Ξ.                 | 7                  | 7                  | ۲.                 | ä      | o.           | ö                  | ٥.                | ъ<br>ж             | ω.                 | ω.     | ω,     | ъ<br>ж  | 8      | ъ<br>Э | ė      | 。      | ė.                 | 'n.                | 55.2   | ď.                 | S.        | ω.     | ъ.                 | ω.     | ۳.                 | Ξ.                 | ή.                 | ÷                  | ij  | Ϊ.      | Ε.                 |
|           | Ö          | Score M     |        | m                  | e                  | σ                  | σ                  | 6                  | 9      | 2            | 2                  | ς.                | 4                  | 4                  | 4      | 4      | 4       | 4      | 4      | m      | m      | m                  | 7                  |        | 7                  | ~         | 0      | _                  |        | -                  | 0                  | 0                  | 0                  | 0   | 0       | 0                  |
|           | Result     | NO.         | П      | 7                  | m                  | 4                  | Ŋ                  | φ                  | 7      | <b>&amp;</b> | σ                  | 10                | 11                 | 12                 | 13     | 14     | 15      | 16     | 17     | 18     | 19     | 20                 | 21                 | 22     | 23                 | 24        | 25     | 56                 | 27     | 28                 | 29                 | 30                 | 31                 | 32  | 33      | 34                 |

| Human neuronal nic<br>Neuronal nicotinic | Alpha4 subunit of Alpha4 subunit of Tetrodotoxin-sensi | Tetrodotoxin-sensi<br>HLA-B2702 CTL modu | Immunomodulating d<br>Immunomodulatory p<br>Immunomodulatory D | Peptide #4 used in |
|------------------------------------------|--------------------------------------------------------|------------------------------------------|----------------------------------------------------------------|--------------------|
| W44155<br>W09023                         | W11824<br>W11825<br>W69361                             | W69362<br>R92911                         | W33779<br>W47264<br>W47261                                     | W33783             |
| 77                                       |                                                        |                                          |                                                                | -                  |
| 529                                      | 627<br>627<br>1978                                     | 1988                                     | 9 9 9                                                          | v                  |
| 51.7                                     | 51.7<br>51.7<br>51.7                                   | 51.7                                     | 50.0<br>0.00                                                   | 50.0               |
| 30                                       | 000                                                    | 30<br>29.5                               | 29.5<br>29<br>29                                               | 29                 |
| 35<br>36                                 | 3 3 3 4 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9                | 4 4 1 0 1 1 1 1                          | 4 4 4<br>4 3 2                                                 | 45                 |

# ALIGNMENTS

Gaps ö Score 53; DB 1; Length 12; Pred. No. 0.00035; 0; Mismatches 1; Indels 91.4%; Query Match 91.4 Best Local Similarity 91.7 Matches 11; Conservative

ö

1 YRLLIRRIALRY 12 ||| ||||||||| 1 YRLAIRRIALRY 12 ŏ ద

RESULT 2 W33798 ID W33798 standard; peptide; 12 AA. AC .W33798;

```
Fracting autoimmune diseases

Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating cerivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or crivity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or c-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise at any peptide type bond within the brackets. The compounds comprise at any peptide type bond within the brackets. The compounds comprise on mino acid sequences related to a Class I HLA-B alphal domain (positions of 9-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with amitgenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of treating autoimmune diseases, e.g. diabetes, received for decetion and diagnosis. The products can also be used for decetion and diagnosis.
  New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases.
Claim 17; Page 35; 41pp; English.
This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant is
  Gaps
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer: mmunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
  Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
   New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
  ö
  Score 53; DB 1; Length 12;
Pred. No. 0.00035;
0; Mismatches 1; Indels
   SCHOOL OUIV LELAND STANFORD JUNIOR. (SELLOW R. Clayberger C. Krensky AM; WPI; 98-086530/08.
  22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD) UNIV LELAND STANFORD JUNIOR.
BELLOW R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
  W33799 standard; peptide; 12 AA.
  91.48;
91.78;
  19-JUN-1998 (first entry)
  Best Local Similarity 91.7
Matches 11; Conservative
  24-MAY-1996; US-653294.
  1 YRLLIRRIALRY 12
   22-MAY-1997; U08689
  Homo sapiens.
WO9744351-A1.
27-NOV-1997.
  Homo sapiens
WO9744351-Al
  27-NOV-1997
  rejection.
   ection.
  Synthetic.
   Synthetic
   Query Match
   m
    ò
```

```
claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; where A, B = (R aa76-772) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84-a a represents amino acid; ab25 = R or L; aa83 = G or R; and are represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in viro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the cytocoxic used for products and response to anti-CD3. The peptide can be used for products or all abetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
   ä
   ö
   Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R82907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
  16-MAY.1996 (first entry)
16-MAY.1996 (first entry)
16-MAY.1202 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; fimunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
   Gaps
  Extension of acceptance period of transplants from MHC unmatched donor hosts – using Class I B75-84 MHC antigen of the recipient
   ö
   .
6
   91.4%; Score 53; DB 1; Length 12; 91.7%; Pred. No. 0.00035; 1.7%; Mismatches 1; Indels
   Indels
   ;
  67.2%; Score 39; DB 1;
55.0%; Pred. No. 0.25;
tive 0; Mismatches
  Krensky AM, Parham P;
   05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
   R92907 standard; peptide; 20 AA.
  1 YRLLIR-----RIALRY 12
   20
   Query Match 67.2
Best Local Similarity 55.0
Matches 11; Conservative
  Best Local Similarity 91.7
Matches 11; Conservative
  1 YRLLIRRIALRY 12
  05-APR-1995; U04349.
05-APR-1994; US-2228
  Clayberger C, Kre
WPI, 95-358582/46.
   diseaser,
The products can e
  of the patient
  Synthetic.
WO9526979-A1.
   12-OCT-1995.
   Query Match
   Sequence
  RESULT
R92907
   8888888888888888888888
  à
  셤
  à
  셤
```

```
WO9850547-A2
   Sequence
  Peptide
  Protein
   RESULT
W86351
  á
   While of the page 12, 29pp; English.

Fromposes. Comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Formula: Page 12, 29pp; English.

Reample: Page 12, 29pp; English.

R95413, and R95415-R95431 represent palindromes and fragments of human-leucocyte-associated antigens. This sequence represents the human-leucocyte-associated antigens. This sequence represents the protein associated with T-cell lysate. P74 is a T-cell surface membrane of protein associated with T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein H8c70.

Co p74 is found in a limited number of cell types, but is particularly carpressed on B and T cells. P74 can be isolated by lysis of a suitable coll with an amphoteric detergent, and then passed through an affinity expressed on B and T cells. P74 can be isolated by lysis of a suitable coll with an amphoteric detergent, and then passed through an affinity colluming containing the extracellular fragment of p74 combined with the HLA-B2702.60-84 (see R95416), induces calclum influx, and inhibits compounds can be screened for their effect on the cytolytic activity of compounds can be screened for their effect on the cytolytic activity of determining them with the extracellular portion of p74 and determining T-cells and antigen presenting cells (APCs), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete converse.
   12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
The p74; alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-Cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytocixic T lymphocyte; CTL; differentiation;
Cytolysis; antigen presenting cell.
  Gaps
   Immunomodulating dimer peptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
  Beulow'R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
New immunomodulating dimer peptide(s) - based on a Class I HLA-B
alpha-1 domain, used for preventing rejection of transplants or
  ..
80
   67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.25; Live 0; Mismatches 1; Indels
   27-NOV-1997.
22-MAX-1997, U08689.
24-MAX-1996; US-653294.
24TR ) UNIV LELAND STANFORD JUNIOR.
   18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
  W33778 standard; peptide; 20 AA.
                             R95428 standard; peptide; 20 AA.
   1 YRLLIR -----RIALRY 12
   20
   Clayberger C, Krensky AM; WPI; 95-194027/25.
   19-JUN-1998 (first entry)
  Query Match
Best Local Similarity 55.0°
Matches 11; Conservative
   WO9513288-A1.
  Homo sapiens.
WO9744351-A1.
   rejection.
   Synthetic
   Sequence
   W33778;
  ဖ
RESULT
R95428
  RESULT
  ò
   g
```

```
treating autoimmune diseases

Claim 16; Page 35; 41pp; English.

This sequence represents a specifically claimed immunomodulating
This sequence represents a specifically claimed immunomodulating
advance represents a specifically compound or variant is
claimed which has immunomodulating activity, including the N-terminal
acylated and/or C-terminal amidated or esterified forms of up to 60
acylated and/or C-terminal amidated or esterified forms of up to 60
acylated and/or C-terminal amidated or esterified forms of up to 60
acylated and/or C-terminal amidated or (as84-79) (Laa77-76R); aa76 = E or
Where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or
V; aa77 = D, Sor N; aa79 = R or G; aa80 = I or N; aa81, aa64 = a
hydrophobic or small amino acid; aa80 = I or N; aa81 aa64 = a
represents amino acid; aa80 = I or N; aa81 aa64 = a
represents amino acid; sequence in the brackets may optionally be
abbal domain (positions 79-84). They can be used to inhibit cytocoxic
T-lymphocytes (CTL) from undesirably attacking calls in a host or in
vitro. They can also be used in combination with antigenic peptides or
proteins of interest to activate CTLs. They can also inhibit the
cused for preventing rejection of transplants or for treating autoimmune
diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis.

The products
The products
The products
The products
The products
The products
The products
The products
The products
The products
The products
The products
The products
The products and also be used for detection and diagnosis.
   ä
   Immunity responses
Claim 2: Page 108-111; 171pp; English.
The present invention specifically describes human DNAX toll-like receptors 2 to 10 (DTLAZ-10). The present sequence is human DTLR3 given in the present invention. Also described are: (1) a fusion protein comprising a DTLR protein or peptide; (2) a binding compound, preferably an antibody or antibody fragment which specifically binds to a DTLR protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide; (4) an expression vector comprising the nucleic acid of (3); and (5) a host cell comprising the vector of (4). The host cell of (5) can be used to produce the DTLR proteins. The DTLR proteins can be used to alter phosphate metabolism, to modulate inflammatory function, innate
   15-MAR-1999 (first entry)
Human DNAX toll-like receptor DTLR3.

Human DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor; Interleukin 1 receptor; phosphate metabolism; innate immunity response; modulate inflammatory function; morphological effect;
   Human DNAX toll-like receptors, DTLR 2-10 - used to, e.g. alter phosphate metabolism, modulate inflammatory function or innate
   .,
  67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.25; ive 0; Mismatches 1; Indels
  12-NOV-1998.
07-MAY-1998; U08979.
07-MAY-1999; US-076947.
07-MAY-1997; US-044293.
22-JAN-1998; US-07212.
(SCHE ) SCHERING CORP.
Bazan JF, Hardiman GT, Kastelein RA, Rock FL;
WPI: 99-059670/05.
  Location/Qualifiers
   W86351 standard; Protein; 904 AA.
  l. .21
/label- signal
   22. .904
/label- DTLR3
  1 YRLAIRLNERRENLRIALRY 20
  1 YRLLIR-----RIALRY 12
   Query Match
Best Local Similarity 55.0
Matches 11, Conservative
  immunological disorder.
  Homo sapiens.
```

```
NOVO-NORDISK AS.
                  Berka RM, Cherry J,
WPI; 97-132641/12.
  Query Match
Best Local Similarity
Matches 6; Conserv
   halide; chloride.
   WETENSCHAPPEN
        (NOVO ) NC
Berka RM,
  Sequence
         qq
   셤
   ò
  ö
  ö
         of p
  Gaps
  Gaps
  haloperoxidase from Curvularia verruculosa - useful for oxidn. of halide, halogenation and, in presence of hydrogen peroxide and thiocyanate, as antimicrobial.

Claim 17: Page 38: 58pp: English.

A haloperoxidase partial peptide (W12037) corresponds to amino acids 275-314 of the Curvularia verruculosa CBS.63 anzyme. Partial peptides (W12034-41) were obtd. from the haloperoxidase by digestion with lysyl-specific protease from Achromobacter. Primers (see also 751613-14) based on the peptides were used in the PCR amplification of genomic DNA from CBS 147.63. The PCR product was used to screen a genomic library, leading to the isolation of the haloperoxidase gene (751612).
       immunity responses or morphological effects. The DTLR proteins can used in the treatment of conditions exhibiting abnormal expression the receptors of their ligands. These abnormalities are typically manifested by immunological disorders.

Sequence 904 AA;
   30-APR-1997 (first entry)
Curvularia verruculosa haloperoxidase partial peptide (aa275-314).
Haloperoxidase; halide oxidation; halogenation; antimicrobial;
  ö
  ö
  Curvularia verruculosa haloperoxidase.
Haloperoxidase; halide oxidation; halogenation; antimicrobial;
   Oxenboll KM;
   DB 1; Length 904; 44;
  DB 1; Length 40; 2.8;
  Indels
   Halkier T,
  Score 36; DB ]
Pred. No. 44;
4; Mismatches
   Mismatches
  Curvularia verruculosa strain CBS 147.63.
   Score 35; I
Pred. No. 2.
  Curvularia verruculosa strain CBS 147.63.
WO9704102-A1.
   Berka RM, Cherry J, Fuglsang C,
WPI; 97-132641/12.
   09-JUL-1996; U11458.
14-JUL-1995; US-001194.
21-FEB-1996; US-603534.
(NOVO ) NOVO NORDISK BIOTECH INC.
(NOVO ) NOVO-NORDISK AS.
   W12042 standard; Protein; 600 AA
   NOVO NORDISK BIOTECH INC
   W12037 standard; Peptide; 40 AA
  62.1%;
60.0%;
   60.3%;
50.0%;
  30-APR-1997 (first entry)
  Conservative
  Conservative
  US-001194.
  Query Match
Best Local Similarity
..... 6; Conserve
  1 YRLLIRRIALRY 12
   27 YNQIVRRIAVTY 38
  06-FEB-1997.
09-JUL-1996; U11458.
   ||::||:||:
484 REMERRVALK 493
  Query Match
Best Local Similarity
Matches 6; Conserv
   2 RLLIRRIALR 11
   WO9704102-A1.
   disinfectant.
   14-JUL-1995;
21-FEB-1996;
   Sequence
  Sequence
   ( NOVO)
   RESULT
   W12037
   g
         888888
   ò
  ò
```

```
Dekker HL, Van Schijndel JWPM, Vollenbroek EGM, Wever R;
NP1: 95-36802/46.

N-PSDB; T03875.

N-PSDB; T03875.

N-PSDB; T03875.

Tor determining the halide concn. of liquids
Fxample 3; Fig 6; 48pp; English.

Example 3; Fig 6; 48pp; English.

Example 3; Fig 6; 48pp; English.

C Achloroperoxidase (R82249) is obtd. by expression of a cDNA sequence
(T03875) isolated from curvularia inaequalis in a procaryotic host.

The apoprotein is activated by addn. of vanadate. The enzyme displays
(High thermostability (Tm 90 deg) and is stable in 40% methanol, ethanol
(Or propanol. It can is used for the analysis of halide (esp: chloride)
(Or propanomentally filendly antifouling agent in ship paint; it
(Oxidises bromide lons present in seawater to form bactericidal HOBE.
   Haloperoxidase from Curvularia verruculosa - useful for oxidn. of
Talide, halogenation and, in presence of hydrogen peroxide and
Talide, halogenation and, in presence of hydrogen peroxide and
Thiocyanate, as antimicrobial
Scilin 23; Page 346-37; Sapp; English.
The haloperoxidase of Curvularia verruculosa CBS.63 shows optimum
activity at about 60 deg C and pH 5.5, retains at least 75%
activity after incubation for 1 hr at pH 7.0 and 60 deg C in the
presence of 0.1% H202, and prefers bromide over chloride ions as
substrate. It can be obtd. from a C. verruculosa fermentation
or by expression in host cells transformed with a vector carrying
the haloperoxidase gene (see also T51612). The isolated enzyme can
be used to oxidise halide to hypohalous acid in the presence of an
CH202 source, or to halogenate cpds. It can also, in the presence
of H202 and thlocyanate, be used as an antimicrobial.
   Gaps
   Gaps
   Chloroperoxidase.
Chloroperoxidase; haloperoxidase; antifouling paint; preservative;
  ;
0
   ;
0
   Score 35; DB 1; Length 600;
Pred. No. 44;
  3; Indels
   Indels
   (SCHE-) STICHTING SCHEIKUNDIG ONDERZOEK IN NEDER (TEWE-) STICHTING TECH.
  Score 35; DB 1;
Pred. No. 47;
3; Mismatches
Halkier T,
  3; Mismatches
   R82249 standard; Protein; 640 AA R82249;
  60.3%;
50.0%;
  60.3%;
50.0%;
  25-APR-1996 (first entry)
  6; Conservative
   Conservative
  12-0CT-1995.
30-MAR-1995; NL0123.
31-MAR-1994; EP-200893.
24-JUN-1994; NL-001048.
   Curvularia inaequalis.
  301 YNQIVRRIAVIY 312
  327 YNQIVRRIAVTY 338
  1 YRLLIRRIALRY 12
   1 YRLLIRRIALRY 12
  Query Match
Best Local Similarity
'-hng 6; Conserve
```

ö

```
Homo sapiens.
WO9744351-A1.
  rejection.
  Synthetic.
   Query Match
   Sequence
   RESULT 14
W33792
ID W33792
AC W33792
DT 19-JUN
  RESULT
  g
  88888
  ð
   à
   ä
   Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (comparated to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CILS)
  R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class I MHC HLA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to
   HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)). Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
  HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84), Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
   Gaps
   the patient for a limited period of time (compared to the lifetime
   Clayberger C, Krensky Aw, rulling.

(Clayberger C, Krensky Aw, rulling.

WPI, 95-358582/46.

Extension of acceptance period of transplants from MHC unmatched former hosts - using Class I B75-84 MHC antigen of the recipient
   Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
   ٠.
ش
  DB 1; Length 20;
   2; Indels
  Score 34; DB 1
Pred. No. 2.1;
0; Mismatches
   Krensky AM, Parham P;
   (STRD ) UNIV LELAND STANFORD JUNIOR
   (STRD ) UNIV LELAND STANFORD JUNIOR
  Example 15; Page 36; 80pp; English.
                           R92909 standard; peptide; 20 AA
   R92908 standard; peptide; 20 AA
  1 YRLLIR-----RIALRY 12
  Query Match 58.6%;
Best Local Similarity 50.0%;
Matches 10; Conservative
  (first entry)
  US-222851.
   US-222851
   05-APR-1995; U04349.
05-APR-1994; US-2228
   12-OCT-1995.
05-APR-1995; U04349.
   Clayberger C, Kren
WPI; 95-358582/46.
   the patient.
  WÔ9526979-A1.
   WO9526979-A1.
   05-APR-1994;
  16-MAY-1996
  16-MAY-1996
  12-0CT-1995
   Sequence
RESULT
R92909
  RESULT
  οp
  ò
```

```
A (STR) J UNIV ELAMO STANFORD JUNIOR.

Bellow R. Clayberger C, Krensky AM;

WPI; 98-086530/08.

The munuomodulating dimer peptide(s) - based on a class I HLA-B and immunomodulating dimer peptide(s) - based on a class I HLA-B tapha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases

PT New immunomodulating dimer peptide(s) - based on a class I HLA-B tapha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases

PS Example 1; Page 19; 41pp; English.

PS Example 1; Page 19; 41pp; English.

PS Example 1; Page 19; 41pp; English.

CC ethical autoimmune diseases

CC definition activity, including the N-terminal acylated and/or activity. A peptide-type compound comprises the formula; A-B, where A, B = CC T-terminal amidated or esterified forms of Laa7-76R); aa76 = E or V; aa77 = CC (R aa76-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or V; aa77 = CC (R aa76-77L) (aa79-84) or (aa80-10 r N; aa80-10 r N; a
  Ä
  ä
administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic T lymphocytes (CTLs) of the patient.
Sequence 20 AA;
   Gaps
  Gaps
   19-JUN-1998 (first entry)
Peptide B7702.84-75745-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autofimmune disease; Class I HLA-B alpha-1 domain;
  ..
œ
  ..
œ
   Length 20;
   Score 34; DB 1; Length 20; Pred. No. 2.1; 0; Mismatches 2; Indels
  58.6%; Score 34; DB 1;
50.0%; Pred. No. 2.1;
iive 0; Mismatches
  27-NOV-1997.
22-MAY-1997; U08689.
24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
  W33791 standard; peptide; 20 AA.
   W33792 standard; peptide; 20 AA.
   1 YRLLIR-----RIALRY 12
   1 YRLATRINERRENLRIALRY 20
  20
  58.68;
  50.0%;
  W33792;
19-JUN-1998 (first entry)
  1 YRLLIR-----RIALRY
   Query Match
Best Local Similarity 50.0
Matches 10; Conservative
  1 YRLATRINERRENLRIALRY
   Conservative
  Best Local Similarity
Matches 10; Conserv
```

```
ï
   Gaps
Peptide B2702.84-75/75-84T tested for immunomodulating activity. Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
  14-WAY-1998 (first entry)
Human neuronal incotinic acetylcholine receptor alpha-3 subunit.
Human; neuronal nicotinic acetylcholine receptor; alpha-3 subunit;
brain tissue; screening; NaChR; antibody.
  .;
8
  58.6%; Score 34; DB 1; Length 20; 50.0%; Pred. No. 2.1; ive 0; Mismatches 2; Indels
   /label= TMD2
/note= "transmembrane domain"
Misc_difference 275
  240. .265
/label- TMD1
/note- "transmembrane domain"
  /label = unspecified
/note = "encoded by WWC"
  /label= unspecified
/note= "encoded by AWC"
273. .296
  27-NOV-1297; U08689.
24-MAY-1997; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
  Location/Qualifiers
   W44156 standard; Protein; 504 AA.
  used for detection and diagnosis.
  /label= signal
   1 YRLLIR-----RIALRY 12
  Query Match
Best Local Similarity 50.0
Matches 10; Conservative
   Misc_difference
  Misc_difference
   Homo sapiens.
WO9744351-Al.
  Homo sapiens.
  W44156;
14-MAY-1998
   27-NOV-1997
  Peptide
   Domain
   ò
  g
```

```
receptor (NACAR) subunit. The cells expressing the alpha and/or beta NACAR subunits may be used in a method of screening compounds to indentify any which modulate the activity of human neuronal NACAR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the identification and design of compounds that are capable of very specific interaction with of the more receptor subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells
  Human neuronal nicotinic acetylcholine receptor subunits and DNA - also transformed cells useful for screening cpds. which modulate activity of the receptor Example 2; Page 72-73; 99pp; English.

The present sequence represents a human neuronal nicotinic acetylcholine
  /label- unspecified
/note- "encoded by TWC"
459. .480
/label- TMD4
/note- "transmembrane domain"
327. .458
   note= "transmembrane domain"
  08 MARY 1993; US-028031.
(SALK ) SALK INST BIOTECHNOLOGY IND ASSOC.
(SIBI-) SIBIA NEUROSCIENCES INC.
Elliott KJ, Ellis SB, Harpold MM;
   /label= cytoplasmic_loop
/note= "encoded by IGY"
302. .326
/label= TMD3
  /label- unspecified /note- "encoded by AMC"
   /label= unspecified
/note= "encoded by WWC"
  Lhat express a variety of subtypes.
  Query Match
Best Local Similarity
7; Conserve
   Misc_difference 354
  08-MAR-1994; U02447
  Misc_difference 309
   Misc_difference 347
   Elliott KJ, Ellis (WPI; 94-303024/37. N-PSDB; V12200.
                        Domain
  Domain
  Region
```

Gaps ö 58.6%; Score 34; DB 1; Length 504; 58.3%; Pred. No. 57; tive 2; Mismatches 3; Indels Conservative

ö

1 YRLLIRRIALRY 12 ò

| | |||::| | 232 YSLXIRRLSLFY 243

8, 2000, 01:29:40 Search completed: February Job time: 1752 sec

Wed Feb

```
February 7, 2000, 11:54:27 ; Search time 117.7 Seconds
(without alignments)
4.809 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

    protein search, using sw model

  US-08-653-294-17
58
  Title:
Perfect score:
Sequence:
  OM protein
  Run on:
```

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YRLLIRRIALRY 12 Scoring table:

142080 segs, 47169319 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_62:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Description           | Na+/H+ antiporter | probable oxidoredu |        |        | probable ribosomal | hypothetical prote | oxid   |        | acyl-CoA oxidase ( | acyl-CoA oxidase ( | genome polyprotein | genome polyprotein |        | cal    |        | mem    | probable acetyl-Co | DNA-directed RNA p | hypothetical prote | TB2/DP1 protein ho | conserved hypothet | ribosomal protein | ď      |        | fimbrial assembly | nicotinic acetylch | hypothetical prote | probable membrane | ~      | nicotinic acetylch |
|-----------------------|-------------------|--------------------|--------|--------|--------------------|--------------------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------|--------|--------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------|--------|-------------------|--------------------|--------------------|-------------------|--------|--------------------|
| ID                    | JC5342            | G70882             | 569334 | C70200 | H70883             | G71167             | OXCKAX | OXCKX4 | OXCKX              | OXCKPM             | GNWV16             | GNWV26             | E69263 | S38147 | E72481 | S49844 | T07920             | F64429             | H75054             | JC4667             | D71325             | S53849            | A33489 | S36653 | D70365            | CH3                | F71307             | 7056              | S60589 | 2457               |
| DB                    | 7                 | 7                  | 7      | 7      | 7                  | ~                  | П      | Н      | П                  | П                  | П                  | П                  | Н      | 7      | 7      | ~      | ~                  | ~                  | 7                  | ~                  | 7                  | ~                 | ~      | Н      | 7                 | Н                  | 7                  | 7                 | 7      | 7                  |
| Query<br>Match Length | 313               | 309                | 609    | 88     | 8                  | 362                | 502    | 709    | 709                | 709                | 3391               | 3391               | 107    | 352    | 550    | 869    | 2304               | 78                 | 157                | 185                | 268                | 298               | 310    | 389    | 408               | 416                | 469                | 470               | 495    | 499                |
| Query                 | 63.8              | ö                  | ö      | ω.     | ω.                 | ω.                 | 58.6   | 8      | ٠.<br>ص            | ω.                 | ٠.<br>ش            | &                  | è.     | è.     | ů.     | ė.     | 9                  | 55.2               | δ.                 | ıs.                | ď.                 | 'n.               | 5.     | δ.     | ω.                | δ.                 | ъ.                 | ω.                | ک      |                    |
| Score                 | 37                |                    |        | 34     |                    | 34                 | 34     | 34     | 34                 | 34                 | 34                 | 34                 | 33     | 33     | 33     | 33     | 33                 | 32                 | 32                 | 32                 | 32                 | 32                | 32     | 32     | 32                | 32                 | 32                 |                   | 32     | 32                 |
| Result<br>No.         | п                 | 7                  | m      | 4      | S                  | ø                  | 7      | 80     | 6                  | 10                 | 11                 | 12                 | 13     | 14     | 15     | 16     | 17                 | 18                 | 19                 | 20                 | 21                 | 22                | 23     | 24     | 25                | 26                 | 27                 | 28                | 58     | 30                 |

| nicotinic acetylch | probable DNA 1198S<br>hypothetical prote | probable DNA-direc | nonstructural poly | hypothetical prote | ribosomal protein | LICA protein - Myc | transcription fact | probable cysw - My | conserved hypothet | ferrochelatase (EC | ferrochelatase - H | histocompatibility | lsu ribosomal prot |
|--------------------|------------------------------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|
| A53956             | G/2/09<br>C70031                         | D72571             | T08822             | S15010             | S74731            | 842124             | JC1496             | A70683             | F72323             | H64566             | A71860             | 829990             | A75148             |
| 010                | <b>7</b> 0                               | ~                  | ~                  | ~                  | ~                 | ď                  | ~                  | N                  | ~                  | ~                  | ~                  | ~                  | 7                  |
| 503                | 679                                      | 895                | 1998               | 3165               | 88                | 238                | 246                | 272                | 306                | 334                | 335                | 348                | 361                |
| 55.2               | 55.2                                     | 55.2               | 55.2               | 55.2               | 53.4              | 53.4               | 53.4               | 53.4               | 53.4               | 53.4               | 53.4               | 53.4               | 53.4               |
| 32                 | 32                                       | 32                 | 32                 | 32                 | 31                | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 | 31                 |
| 31                 | 7 E                                      | 34                 | 35                 | 36                 | 37                | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |

### ALIGNMENTS

| RESULT 1<br>JC5342<br>Na+7H+ antiporter cdu2 - Clostridium difficile<br>Species: Clostridium difficile<br>C:Date: 27-May-1997 #sequence_revision 18-Ju1-1997 #text_change 10-Sep-1997 | C;Accession: JC5342 R;Braun, V.; Hundsberger, T.; Leukel, P.; Sauerborn, M.; von Eichel-Streiber, C. Gene 181, 29-38, 1996 A;Title: Definition of the single integration site of the pathogenicity locus in Clos A;Reference number: JC5340; MUID:97128764 A;Accession: JC5342 A;Accession: JC5342 A;Residues: 1-313 < SRA> | A;Cross-references: EMBL:X92982; NID:g1770128; PID:e212007; PID:g1770130 A;Experimental source: strain VPI10463 C;Comment: This protein contains 11 membrane spanning domain. It functionally links t C;Genetics: A;Gene: cdu2 |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| RESULT<br>JC5342<br>Na+/H+<br>C; Spec:<br>C; Date                                                                                                                                     | C, Acce<br>R, Brau<br>Gene 1<br>A, Titl<br>A, Refe<br>A, Acce<br>A, Mole                                                                                                                                                                                                                                                    | A; Cros<br>A; Expe<br>C; Comm<br>C; Gene<br>C; Gene<br>A; Gene                                                                                                                                                                 |

Length 313; Indels Score 37; DB 2; Pred. No. 8; 6; Mismatches Query Match 63.8%; Best Local Similarity 41.7%; Matches 5; Conservative

ö 1 YRLLIRRIALRY 12 ò

ö

Gaps

259 YRVVARRLSIKY 270

g

probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Date: 17-du-11988 #sequence\_revision 17-du1-1998 #text\_change 29-Sep-1999
C;Accession: G70882
R;Cole, S:T; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Deviln, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Nature 393, 537-544, 1988
A;Authors: Krogh, A.; McLehead, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987

A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA

A;Residues: 1-309 <CCL>
A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15591.1; PID:e129
A;Experimental source: strain H37Rv

A;Gene: Rv2776c C;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; fer F;9-211/Domain: cytochrome-b5 reductase homology <CBR> F;240-297/Domain: ferredoxin [2Fe-28] homology <FER>

Gaps

ö

```
probable ribosomal protein S15 rps0 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: H70883
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atthors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atthors: Spares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Atthors: preliminary the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70800; MUID:98295987
A;Accession: H70883
A;Attus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-89 <COL>A;Accols: A108967; GB:AL123456; NID:93261491; PIDN:CAA15580.1; PID:e117
A;Experimental source: strain H37Rv
  hypothetical protein PH0539 - Pyrococcus horikoshii

(7)167

hypothetical protein PH0539 - Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

C;Species: Pyrococcus horikoshii

R;Kawarabayashi Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se

R;Kawarabayashi Y; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se

M; Obfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. S, 55-76, 1998

A;Tille: Complete sequence and gene organization of the genome of a hyper-thermophili

A;Reference number: A71000; MUID:98344137

A;Reference number: A71000; MUID:98344137

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-36 < KAM>

A;Residues: 1-36 < KAM>

A;Cross-references: GB:AP000002; NID:93236129; PID:d1030571; PID:93256945

A;Cross-references: Strain OT3

A;Cross-references: Strain OT3

A;Gene: this accession replaces an interim accession for a sequence replaced by GenBa

C;Genetics:
A;Gene: PH0539
  A;Gene: rpsO
C;Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein
F;23-89/Domain: eubacterial ribosomal protein S15 homology <ES15>
   Length 362;
  Length 89;
  Indels
  Indels
   3; Indels
                                 Length
  DB 2;
   .;
?
                              ;;
                          DB 2
8.9;
   рв
35;
   Mismatches
  Mismatches
   3; Mismatches
  Score 34; D
Pred. No. 9;
                              Score 34;
Pred. No.
   Score 34;
Pred. No.
  58.68;
63.68;
                              58.68;
   58.6%;
   Query Match 58.6
Best Local Similarity 50.0
Matches 6; Conservative
   Conservative
  Conservative
  1 YRLLIRRIALRY 12
   78 YRSLIERLGLR 88
                              Query Match
Best Local Similarity
   1 YRLLIRRIALR 11
  77 YRMLISKLGLR 87
  1 YRLLIRRIALR 11
  Query Match
Best Local Similarity
Matches 7; Conserv
   .
9
   Matches
  셤
  g
  ò
   ð
   Chloride peroxidase (EC 1.11.1.10) - Curvularia inaequalis
N.Alternate names: vanadium-containing chloroperoxidase
C.Species: Curvularia inaequalis
C.Species: Curvularia inaequalis
C.Species: U.S. Hara-1997 #sequence_revision 19-Mar-1997 #text_change 20-Sep-1999
C.Accession: S69334; S53117
R.Simons, B.H.; Barnett, P.; Vollenbroek, E.G.M.; Dekker, H.L.; Muljsers, A.O.; Messersc Eur. J. Blochem. 229, 566-574, 1995
A.Title: Primary structure and characterization of the vanadium chloroperoxidase from the A.Reference number: S69334; MUID:95265722
A.Accession: S69334
   R.; White
M.; Vugt,
tch, B.
  A; Description: catalyzes the formation of two carbon-chlorine bonds and two water molecu C; Superfamily: Curvularia inaequalis chloride peroxidase C; Keywords: blocked amino end; chloride; metalloprotein; oxidoreductase; vanadium F; 404/Active site: His #status predicted F; 404/Active site: vanadate (His) #status predicted
   C;Superfamily: Escherichia coli ribosomal protein S15; eubacterial ribosomal protein S15
F;22-88/Domain: eubacterial ribosomal protein S15 homology <ES15>
   A;Cross-references: GB:AE001179; GB:AE000783; NID:g2688738; PIDN:AAC67150.1; PID:g268874
A;Experimental source: strain B31
  RiFraser, C.M.: Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, Mature 390, 580-586, 1997
A; Authors: Smith, H.O.; Venter, J.C.
A; Tiltle: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferl.
A; Reference number: A70100; MUID:98065943
A; Recession: C70200
  submitted to the Brookhaven Protein Data Bank, September 1995
A;Reference number: A66871; PDB:1VNC
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, 3-543, 'E',545-578
A;Note: the authors believe that 544-Glu is correct from modeling evidence
  ö
   ö
   genomic DNA
   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
   ribosomal protein S15 (rpsO) - Lyme disease spirochete
C;Species: Borrella burgdorferi (Lyme disease spirochete)
C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 13-Aug-1999
C;Accession: C70200
   Gaps
   Gaps
   ŏ
   ö
   ö
  A;Molecule type: mRNA
A;Residues: 1-609 <SIM>
A;Coss-references: EMBL:X85369; NID:g732617; PID:g732618
A;Experimental source: CBS 102.42
A;Mote: part of this sequence was confirmed by sequence analysis R;Messerschmidt, A.; Wever, R.
  Score 35; DB 2; Length 609;
Pred. No. 38; 3; Indels 3; Indels
                              Length 309;
   Indels
                              ;
                          Score 35; DB
Pred. No. 19;
  1; Mismatches
  60.3%;
50.0%;
                          60.3%;
77.8%;
Ouery Match
Best Local Similarity 77.8.
  | ::||||:|
304 YNQIVRRIAVTY 315
   1 YRLLIRRIALRY 12
   Query Match
Best Local Similarity
  ||: |||||
65 YRIAIRRIA 73
   A; Molecule type: DNA
A; Residues: 1-88 <KLE>
  1 YRLLIRRIA 9
  Gene: vCPO
   Genetics
  C; Function
   Matches
  RESULT
   ò
  g
  ŏ
   g
```

ö

Gaps

ö

ö

Gaps

ö

g

```
Genome polyprotein - dengue virus type 2 (strain 16681)

N;Contains: capsid protein C; envelope protein E; membrane-associated protein M; nons twal protein Ns4s; nonstructural protein NS5
C;Species: dengue virus type 2
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 16-Jul-1999
C;Date: 31-Dec-1992 #sequence_revision and its candidate vaccine derivative: sequence A;Ttle: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence A;Residues: 1-3391 GBLOS
A;Residues: 1-3391 GBLOS
A;Residues: 1-3391 GBLOS
A;Residues: 1-3391 GBLOS
C;Superfamily: yellow fever virus genome polyprotein: DEAD/H box helicase homology C;Reywords: ATP; capsid protein: envelope protein; glycoprotein; nonstructural protein F;1-114/Product: capsid protein C #status predicted <CPC>
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 30-Sep-1993
C;Accession: A2947
E;Muraav, W.W., Rachubinski, R.A.
Gene 51, 119-128, 1987
A;Title: The primary structure of a peroxisomal fatty acyl-CoA oxidase from the yeast
A;Reference number: A29047; MUID:87248070
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Accession: A29047
A;Acce
   the peroxisomal acyl CoA oxidase from the
  A;Gene: POX4
C;Superfamily: acyl-CoA oxidase
C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
  Layer Convaires (Landida maltosa)

(Species: Candida maltosa

(Species: A244)

R.Hill, D.E.; Boullay, R.; Rogers, D.

R.Hill, D.E.; Boullay, R.; Rogers, D.

R.Hill, Complete nucleotide sequence of the peroxisomal acyl CoA oxidase francesion: A2441

A; Reference number: A29441; MUID:8812423

A; Ressidues: A2944

A; Ressidues: 1-709 <HIL>

A; Resperimental source: ATCC 20184

C; Genetics:
  acyl-CoA oxidase (EC 1.3.3.6) PXP4, peroxisomal - yeast (Candida maltosa)
  ..
7
   .;
2
  Length 709;
   Length 709
  Indels
   Indels
   Score 34; DB 1;
Pred. No. 68;
1; Mismatches
   1;
   Score 34; DB 1
Pred. No. 68;
1; Mismatches
  58.68;
  58.68;
  Query Match 58.6
Best Local Similarity 64.3
Matches 9; Conservative
   Similarity 64.3
9; Conservative
  321
   308 YRMLARVSTIALRY 321
  1 YRLLIR--RIALRY 12
   1 YRLLIR--RIALRY 12
  308 YRMLARMSTIALRY
   Query Match
Best Local S
   Matches
  GNWV16
  õ
   g
   ò
   g
  acyl-CoA oxidase (EC 1.3.3.6) POX4-2, peroxisomal - yeast (Candida tropicalis) (fragment N;Alternate names: acyl-CoA oxidase II-2 (Species: Candida tropicalis (C;Species: Candida tropicalis (C;Species: Candida tropicalis (C;Accession: A28584 R;Small, G.M.; Lazarow, P.B. R;Small, G.M.; Lazarow, P.B. J. Cell Biol. 105, 247-250, 1987 A;Title: Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a procession of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of a processi
   ъď
   gene family.
C:Comment: The peroxisomes are eukaryote subcellular organelles that generate and degrad
ic reactions as well as the enzymes involved are usually different from the mitochondria
   A:Cross-references: GB:M12160; NID:g170911; PIDN:AAA34362.1; PID:g170912
A:Cross-references: Strain party 20336
C:Comment: This enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation this enzyme, located in peroxisomes, catalyzes the oxygen-specific oxidation this enaction is the initial step of the peroxisomal beta-oxidation system. In C. trop
  C;Accession: A25123
R;Okazaki, K.; Takechi, T.; Kambara, N.; Fukui, S.; Kubota, I.; Kamiryo, T.
Proc. Natl. Acad. Sci. U.S.A. 83, 1232-1236, 1986
A;Title: Two acyl-coenzyme A oxidases in peroxisomes of the yeast Candida tropicalis: A;Reference number: A94084; MUID:86149279
A;Accession: A25123
  A;Gene: POX4
C;Superfamily: acyl-CoA oxidase
C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase; peroxisome
  peroxisome
   ï
  ä
  acyl-CoA oxidase (EC 1.3.3.6) POX4, peroxisomal - yeast (Candida tropicalis) NyAlternate annes: acyl-CoA oxidase II (Species: Candida tropicalis (C.Species: Candida tropicalis (C.Species: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 11-Jun-1999
  acyl-CoA oxidase (EC 1.3.3.6) AOx, peroxisomal - yeast (Candida tropicalis)
C;Species: Candida tropicalis
   Gaps
  Gaps
   A;Cross-references: GB:YUUb23; Nlu:gzorz; rlun.crnvvvv...; C;Genetics: A;Gene: POX4-2 C;Superfamily: acyl-CoA oxidase C;Superfamily: acyl-CoA oxidation; flavoprotein; oxidoreductase; C;Keywords: FAD; fatty acid oxidation; flavoprotein; oxidoreductase;
   A;Accession: A28584
A;Molcoule type: mrNa
A;Residues: 1-502 -SSMA>
A;Residues: 1-502 -SSMA>
A;Cross-references: GB:Y00623; NID:g2672; PIDN:CAA68660.1; PID:g2673
   2,
  ;
  Length 502;
   Length 709;
   Indels
  Indels
   ä
   ï
  Score 34; DB 1
Pred. No. 49;
1; Mismatches
  Score 34; DB ]
Pred. No. 68;
1; Mismatches
   58.6%;
   58.6%;
  Query Match 58.6
Best Local Similarity 64.3
Matches 9; Conservative
   Conservative
  [|:[ | |||||
101 YRMLARMSTIALRY 114
  321
  1 YRLLIR--RIALRY 12
   1 YRLLIR--RIALRY 12
                          296 YRFILKAIALGY 307
   Query Match
Best Local Similarity
Matches 9; Conserv
  A; Molecule type: DNA
A; Residues: 1-709 < OKA>
```

δλ g al

ä

Gaps

RESULT

ά g OXCKX

ï

Gaps

```
|:|| | :||
2728 RMLINRFTMRY 2738
   | | |:||:||
38 YVELARKIAMRY 49
  Query Match
Best Local Similarity
7; Conserv?
   12
   2 RLLIRRIALRY 12
   Query Match
Best Local Similarity
Matches 6; Conserv
   Best Local Similarity
Matches 6; Conserv
   1 YRLLIRRIALRY
  A; Molecule type: DNA
   A; Map position: 11R
  Query Match
   14
  δλ
  g
  δ
  g
  R;Blok, J.; McWilliam, S.M.; Butler, H.C.; Gibbs, A.J.; Weiller, G.; Herring, B.L.; Hems Virology 187, 573-590, 1992
A;Title: Comparison of a dengue-2 virus and its candidate vaccine derivative: sequence x Reference number: A42451; MUID:92188532
A;Accession: B42451
A;Molecule type: genomic RNA
A;Residues: 1-3391 <BLO>
  nonstru
   helicase homology
nonstructural protein;
<MPP>
  F;50-66/Domain: transmembrane #status predicted <TML)
F;107-18/Domain: transmembrane #status predicted <TML)
F;107-18/Domain: transmembrane #status predicted <TML)
F;115-280/Product: membrane-associated protein M #status predicted <SIG>F;115-206/Domain: nonterminal signal sequence #status predicted <SIG>F;206-280/Product: membrane-associated protein M #status predicted <MPM>F;208-284/Domain: transmembrane #status predicted <TMA>F;208-284/Domain: transmembrane #status predicted <TMA>F;727-743/Domain: transmembrane #status predicted <TMA>F;777-73/Domain: transmembrane #status predicted <TMF>F;776-1127/Product: nonstructural protein NS1 #status predicted <NIA>F;1128-1345/Product: nonstructural protein NS2 #status predicted <NIA>F;1128-1345/Product: nonstructural protein NS2 #status predicted <NIA>F;128-1310/Domain: transmembrane #status predicted <TMF>F;1294-1310/Domain: transmembrane #status predicted <TMP>F;1391-1367/Domain: transmembrane #status predicted <TMA>F;1371-1389/Domain: transmembrane #status predicted <TMA>F;1371-1389/Domain: transmembrane #status predicted <TMA>F;1371-1384/Domain: transmembrane #status pre
   Ξ
  ö
   N:Contains: capsid protein C; envelope protein E; membrane-associated protein tural protein NS4a; nonstructural protein NS4b; nonstructural protein NS5
   F:1759-1762/Region: DEAH motif
F:2004-2243/Product: nonstructural protein NS4a #status predicted <N4A>
F:2244-2491/Product: nonstructural protein NS4b #status predicted <N4B>
F:2249-3391/Product: nonstructural protein NS5 #status predicted <N8D>
F:2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
F:183,347,433/Binding site: carbohydrate (Asn) (covalent) #status predicted
   Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 15-May-1998
   Gaps
  Fil5-205/Domain: nonterminal signal sequence #status predicted <a href="Milo-205/Domain: nonterminal signal sequence #status predicted <AMPN-Fi206-280/Product: membrane-associated protein M *status predicted <AMPN-Fi206-280/Product: membrane #status predicted <AMI>Fi206-280/Product: envelope protein E *status predicted <EPE>Fi727-743/Domain: transmembrane #status predicted <AMI>Fi757-773/Domain: transmembrane #status predicted <AMI>Fi767-773/Domain: transmembrane #status predicted <AMI>Fi767-773/Domain: transmembrane #status predicted <AMI>Fi76-1127/Product: nonstructural protein NS2# #status predicted <NS2>Fi1846-1474/Product: nonstructural protein NS2# #status predicted <NS2>Fi166-1938/Domain: Debal/H box helicase homology <a href="Milo-2093/Product">Debal/H box helicase homology <a href="Milo-2003-Product">Debal/H   :2094-2243/Product: nonstructural protein NS4a #status predicted <N4A>
  <NS3>
   ö
   Superfamily: yellow fever virus genome polyprotein; DEAD/H box Keywords: ATP; capsid protein; envelope protein; glycoprotein; 1-114/Product: capsid protein C *status predicted <CPC>
  1475-2093/Product: nonstructural protein NS3 #status predicted 1668-1938/Domain: DEAD/H box helicase homology <DEAD>
  Length 3391;
  genome polyprotein - dengue virus type 2 (strain 16681-PDK53)
   (P-100p)
   '5/Region: nucleotide-binding motif A 0/Region: nucleotide-binding motif B
  Species: dengue virus type 2
   1759-1762/Region: DEAH motif
   Conservative
   oss-references: GB:M85259
   |:|| | :||
2728 RMLINRFTMRY 2738
   2 RLLIRRIALRY 12
   Query Match
Best Local Similarity
Matches 6; Conserv
   60/Region:
   Accession: B42451
  δ
  Dp
```

```
F;2148-2164/Domain: transmembrane #status predicted <TMC>
F;2174-2190/Domain: transmembrane #status predicted <TMD>
F;2197-2213/Domain: transmembrane #status predicted <TME>
F;227-2243/Domain: transmembrane #status predicted <TMF>
F;227-2243/Domain: transmembrane #status predicted <TMF>
F;224-2491/Product: nonstructural protein NS4b #status predicted <NAB>
F;241-2437/Domain: transmembrane #status predicted <TMG>
F;241-2427/Domain: transmembrane #status predicted <TMH>
F;241-2437/Domain: transmembrane #status predicted <NMS>
F;2492-3391/Product: nonstructural protein NS5 #status predicted <NS5>
F;183,347,433,905,982,1134,1174,1329,2301,2305,2346,2387,2457,2485,2644,2665,2704,271
   Conserved hypothetical protein AF0109 - Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: Archaeoglobus fulgidus
C; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C; Accession: E65263
R; Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
C; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, Smith, H.O.; Wosse, C.R.; Venter, J.C.
A; Aitle: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A; Accession: E69263
   Cross-references: GB:AE001099; GB:AE000782; NID:g2689422; PID:g2650539; TIGR:AF0109 Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0962
   ö
  ö
   ö
   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-107 <KLE>
  hypothetical protein YKR070w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 14-Nov-1997
C;Accession: S38147
R;Pohl, Tm., Pohl, F.M.
Submitted to the Protein Sequence Database, March 1994
A;Reference number: S37897
  Gaps
   Gaps
   Gaps
  A:Experimental source: strain $288C (; PID:9486541; MIPS:YKR070w C;Genetics:
   ö
   ö
  ö
   Length 3391;
   Length 107;
  Length 352;
   Indels
  Indels
  ;
  Score 34; DB 1; 1
Pred. No. 3.2e+02;
1; Mismatches 3;
  DB 1;
17;
  DB 2;
54;
  Score 33; DB Pred. No. 54; 3; Mismatches
  Mismatches
  Score 33;
Pred. No.
   3;
   58.6%;
54.5%;
  56.98;
  56.9%;
   Conservative
   Conservative
   Conservative
```

```
hypothetical protein APE2493 - Aeropyrum pernix (strain Kl)
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: Aeropyrum pernix
C:Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C:Accession: E72481
R:Kawarabayasi, Y:; Hino, Y:; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DN Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A:Reference number: A72450; MUID:99310339
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A; Molecule type: DNA
A:Residues: Preliminary
A; Molecule type: DNA
A; Residues: 1-550 «KAM»
A; Residues: 1-550 «KAM»
A; Cross-references: DDBJ:AP000064; NID:95105945; PIDN:BAA81509.1; PID:d1045295; PID:9510
C; Genetics:
A; Genetics:
A; Genetics:
   ö
   0; Gaps
  Query Match 56.9%; Score 33; DB 2; Length 550; Best Local Similarity 60.0%; Pred. No. 84; Matches 6; Conservative 3; Mismatches 1; Indels
1 YRLLIRRIAL 10
:||:||: ||
223 FRLLVRRLYL 232
   g
    δλ
```

Search completed: February 7, 2000, 11:54:28 Job time: 24338 sec

2 RLLIRRIALR 11 |||:||::| 405 RLLVRRVNVR 414

ò

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

Search time 63.71 Seconds February 8, 2000, 00:59:55; Run on:

(without alignments)
5.625 Million cell updates/sec

US-08-653-294-17 58 Perfect score:

1 YRLLIRRIALRY 12 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 seqs, 29864866 residues Searched:

82228 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | ,      | Description | 34162      | 49053      |            |            | 033327 mycobacteri |            | P11355 candida tro | candida    | P05335 candida mal | P29990 d genome po | P29991 d genome po | P36151 saccharomyc |                  | Q58443 methanococc | _         | ฮ          |            | bos taı    |               | rattus   |            |            | _          |            |            | macac      | homo sa    | gallu | aguife     |            | P33699 rhizobium m | O83195 treponema p | gallus | rattus   |
|-----------|--------|-------------|------------|------------|------------|------------|--------------------|------------|--------------------|------------|--------------------|--------------------|--------------------|--------------------|------------------|--------------------|-----------|------------|------------|------------|---------------|----------|------------|------------|------------|------------|------------|------------|------------|-------|------------|------------|--------------------|--------------------|--------|----------|
| SUMMARIES |        | OI .        | HEMN_ALCEU | PRXC_CURIN | RS15_BORBU | RS15_MYCLE | RS15_MYCTU         | YHS5_CAEEL | CAO3_CANTR         | CAO2_CANTR | CAO4_CANMA         | POLG_DEN26         | POLG_DEN27         | YK50_YEAST         | YD95_YEAST       | RPOH_METJA         | DP1_MOUSE | RT03_ACACA | KSS5_ECOLI | ACH3_BOVIN | ACH3_CHICK    | ACH3_RAT | ACH3_HUMAN | RS15_SYNY3 | LICA_MYCCA | MTT1_HUMAN | HEM2_HELPY | HLAF_MACMU | COXX_HUMAN |       | HEMN_AQUAE | ACH6_CAEEL | EXOT_RHIME         | SYP_TREPA          | - 1    | ACH4_RAT |
|           |        | BB:         | н          | ٦          | Н          | -          | Н                  | Н          | Н                  | Н          | Н                  | Н                  | Н                  | Н                  | <del>, - 1</del> | ~                  | Н         | H          | -          | ~          | <del></del> 1 | щ        | Н          | -          | Н          | Н          | Н          |            |            | Н     | Н          | -4         | П                  | П                  | П      | 7        |
|           | Query  | Length      | 491        | 609        | 88         | 83         | 83                 | 411        | 502                | 708        | 708                | 3391               |                    | 352                | 869              | 78                 | 185       | 298        | 389        | 495        | 496           | 499      | 203        | 68         | 238        | 246        | 334        | 348        | 443        | 454   | 456        | 487        | 464                | 617                | 622    | 633      |
| d         | Query  | Match       | 61.2       | 0          | œ          | æ          | æ                  | œ          | œ                  | 28.6       | ω                  | æ                  | œ                  | 9                  | 9                | S                  | S         | S          | 2          | S          | S             | S        | S          | 3          | m          | 3          | m          | 3          |            | m     |            | m          | 'n                 | 53.4               | m.     | 53.4     |
|           |        | Score       |            |            |            |            |                    |            |                    | 34         |                    |                    |                    | 33                 |                  | 32                 |           |            |            |            |               |          |            |            |            |            |            |            |            |       |            |            |                    | 31                 |        |          |
|           | Result | o<br>Q      | 1          | ~          | m          | 4          | S                  | ø          | 7                  | 80         | თ                  | 10                 | 11                 | 12                 | 13               | 14                 | 15        | 16         | 17         | 18         | 19            | 20       | 21         | 22         | 23         | 24         | 25         | 56         | 27         | 28    | 59         | 30         | 31                 | 32                 | 33     | 34       |

ä

Gaps

3;

Query Match 61.2%; Score 35.5; DB 1; Length 491; Best Local Similarity 57.1%; Pred. No. 11; Matches 8; Conservative 3; Mismatches 0; Indels 3

454

a a

à

2 RLLIRRIAL --- RY 12 |||:||:||: || 441 RLLVRRVAMVEDRY 609 AA.

PRT;

PRXC\_CURIN STANDARD; F P49053; 01-FEB-1996 (Rel. 33, Created)

RESULT 2 PRXC\_CURIN

| P24814 saccharomyc 041174 p genome po 003132 saccharopol 073672 carassius a P24495 xenopus lae P40301 drosophila P33178 saccharomyc P38717 saccharomyc P21473 bacillus su P80378 thermus aqu P48229 zymomonas m |            | AA.                          | date)<br>update)<br>uli Oxibase (EC 1)                                                                                                             | n; Burkholderia group;             |                               | JAHN D., KYLEDRICH B.,<br>ecocding the Oxygen independent<br>equired for heme biosynthesis                                                                            | F COPROPORPHYRINOGEN-III INTO D NAD (OR NADP) FOR ACTIVITY.  Y SIMILARITY). COPROPORPHYRINOGEN III                                                                                                                                                       | OXIDASE FAMILY.  S WISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation be European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch). | Magnesium; NAD.<br>CRC32;                                                            |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------|------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------|-------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|
| GRR1_YEAST<br>POLG_PEY9U<br>ERY2_SACER<br>PRG3_CARAU<br>PRC3_XENLA<br>PRC3_DROME<br>YD87_YEAST<br>SIP3_YEAST<br>SIP3_YEAST<br>SIP3_REAST<br>RS15_BACSU<br>CR15_THETH                                            | ALIGNMENTS | PRT; 491 A                   | 36, Last sequence update) 36, Last sequence update) 39, Last annotation update) ENASE) (COPROGEN ILI OXI                                           | beta subdivision;                  | ¢                             | gene<br>is r                                                                                                                                                          | FUNCTION: ANAEROBIC TRANSFORMATION OF COPI<br>PROTOPORPHYRINGEN-IX.<br>COFACTOR: REGUIRES MAGNESIUM, ATP AND NAD<br>PATHWAY: PORPHYRING: CYTOPLASMIC (BY SIM.<br>SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIM.<br>SIMILARITY: BELONGS TO THE ANAEROBIC COPR | MMLY.  Off entry is copyright. It is swiss institute of Bioinforma Bioinformatics Institute. The profit institutions as long this statement is not removed ires a license agreement (See Mail to license@isb-sib.ch).                                                                                                                                                                                                                                                               | 42; AAB66374.1;<br>biosynthesis; Oxidoreductase; Ma<br>491 AA; 54216 MW; 3EE82375 CF |
| 1151<br>2168<br>2168<br>2367<br>2333<br>2334<br>1228<br>1229<br>188                                                                                                                                             |            | STANDARD;                    | reat<br>ast<br>ast<br>OPOF                                                                                                                         | ria;                               |                               | x.A., High<br>sutrophus ]<br>III oxida<br>growth.";                                                                                                                   | OBIC TRAI<br>GEN-IX.<br>RES MAGNI<br>RIN BIOS<br>ATION: C                                                                                                                                                                                                | MMILY.  COT entry is copyright Swiss Institute of Bi Bioinformatics Institutions Profil institutions This statement is not this statement is not the a license agreem ail to license@isb.si                                                                                                                                                                                                                                                                                         | 374.1; sis; Oxic<br>54216 M                                                          |
| 50 50 50 50 50 50 50 50 50 50 50 50 50 5                                                                                                                                                                        |            | STAN                         | (Rel. 3<br>(Rel. 3<br>(Rel. 3<br>(Rel. 3<br>PENDENT                                                                                                | s eutrophus.<br>Proteobacteria;    | FROM N.A.<br>16;<br>98060717. | purgui k<br>genes eu<br>rinogen<br>robic gr                                                                                                                           | FUNCTION: ANAEROBIC TR<br>PROTOPORPHYRINGEN-IX.<br>COFACTOR: REQUIRES MAG<br>PATHWAY: PORPHYRIN BIO<br>SUBCELLUTAR LOCATION:<br>SIMILARITY: BELONGS TO                                                                                                   | OXIDASE FAMILY. SWISS-PROT etc. SWISS-PROT etc. European Bioinfe by non-profit fied and this st ties requires a end an email to                                                                                                                                                                                                                                                                                                                                                     | 42; AAB66374.1;<br>biosynthesis; 0<br>491 AA; 54216                                  |
| 8 8 9 11 1 8 8 8 9 1 8 8 9 9 9 9 9 9 9 9                                                                                                                                                                        |            | LT 1<br>ALCEU<br>HEMN_ALCEU  | 0.34102, 15<br>15-JUL-1998 (Rel. 36, L<br>15-JUL-1998 (Rel. 36, L<br>15-DEC-1999 (Rel. 39, L<br>0XYGEN-INDEPENDENT COPR<br>(COPROPORPHYRINGGENASE) | n.<br>aligene<br>teria;<br>stonia. | DENCE<br>AIN=H.               | Lits C., SIDJIQU K.A., HIPPLEK<br>"The Alcaligenes eutrophus hemN<br>coproporphyrinogen III oxidase,<br>during anaeroblo growth.";<br>Arch. Microbiol. 169:52-60(1998 | - FUNCTION: AN<br>PROTOPORPHYF<br>- COFACTOR: RE<br>- PATHWAY: POH<br>- SUBCELLULAR<br>- SIMILARITY:                                                                                                                                                     | OXIDASE FAMILY.  This SWISS-PROT entry is copyright, between the Swiss Institute of Bloi the European Bioinformatics Institutuse by non-profit institutions as modified and this statement is not entities requires a license agreement or send an email to license@ilsb-sib.                                                                                                                                                                                                       | EMBL; U9474;<br>Porphyrin b;<br>SEQUENCE                                             |
| 00000044444444444444444444444444444444                                                                                                                                                                          |            | · RESULT<br>HEMN_AL<br>ID HE |                                                                                                                                                    | OC Ba                              |                               |                                                                                                                                                                       |                                                                                                                                                                                                                                                          | CC Third CC Third CC CC The CC CC The CC CC CC CC CC CC CC CC CC CC CC CC CC                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                      |

```
11
   ||:|| :: ||
77 YRMLISKLGLR 87
  Query Match
Best Local Similarity
Matches 6; Conserv
  RPSO OR MLCB22.28C
  1 YRLLIRRIALR
  RESULT 4

15.4WCLE

AC 032967;
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15-7UL-1998
DT 15
   burgdorfer
    ద
  ò
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  ö
   STRAIN-ATCC 35210 / B31;
MEDLINE: 98065943.
FRASER C.M., CASJENS S., HUANG W.M., SUTTON G.G., CLAYTON R.A.,
LATHGRA R., WAITE O., KETCHUM K.A., DODSON R., HICKEY E.K., GWINN M.,
DOUGHERTY B., TOMB J.FF., FLEISCHMANN R.D., RICHARDSON D.,
  Gaps
   MESSERSCHMIDT A., WEVER R.;
"X-ray structure of a vanadium-containing enzyme: chloroperoxidase
"Income the fungus Curvularia inaequalis.";
Proc. Natl. Acad. Sci. U.S.A. 93:392-396(1996).
-i- CATALYTIC ACTIVITY: 2 RH + 2 CHLORIDE + H(2)O(2) = 2 RCL + 2
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
VANADIUM CHLOROPEROXIDASE (EC 1.11.1.10) (VCPO) (VANADIUM CHLORIDE
  Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; Curvularia
   Curvularia inaequalis.
Eukaryota; Fungi; Ascomycota; Euascomycetes; Loculoascomycetes;
  ö
   SIMONS B. H., BARNETT P., VOLLENBROEK E.G.M., DEKKER H.L., MUIJSERS A.O., MESSERSCHWIDT A., WEVER R.; "Primary structure and characterization of the vanadium chloropercoxidase from the fungus Curvularia inaequalis."; Eur. J. Biochem. 229:566-574(1995).
  DB 1; Length 609;
17;
  3; Indels
  -> S (IN AA SEQUENCE).
19112E80 CRC32;
  Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
   Oxidoreductase; Peroxidase; Vanadium; 3D-structure.
ACT_SITE 404 404
METAL 496 496 VANADIUM.
  Borrelia burgdorferi (Lyme disease spirochete)
   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
SAS RIBOSOWAL PROTEIN S15.
  88 AA.
  Score 35; DB 1
Pred. No. 17;
3; Mismatches
   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
   -!- SUBCELLULAR LOCATION: SECRETED.
-!- PTM: THE N-TERMINUS IS BLOCKED.
  PRT;
   67530 MW;
  EMBL; X85369; CAA59686.1; -.
   60.3%;
50.0%;
  Query Match 60.3
Best Local Similarity 50.0
Matches 6; Conservative
  STANDARD;
  H(2)O.
   454
  304 YNQIVRRIAVTY 315
   1 YRLLIRRIALRY 12
  454
609 AA;
  MEDLINE; 96133943.
   95262722
   SEQUENCE FROM
  PEROXIDASE)
   RS15_BORBU
ID RS15_BORBU
AC 051744;
  CONFLICT
    ò
  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  ö
  SEQUENCE FROM N.A.

DEVILIN K., CHORCHER C.M., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
SUDMILLEd (AUG-1997) to the EMBL/GenBank/DDBJ databases.
1- FUNCTION: THIS PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING
PROTEINS (BY SIMILARITY).
1- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
  Gaps
PETERSON J., KERLAVAGE A.R., QUACKENBUSH J., SALZBERG S., HANSON M., VAN VUGT R., PALMER N., ADAMS M.D., GOCAYNE J.D., WEIDMAN J., UTTERBACK T., WATTHEY L., MCDONALD L., ARTIACH P., BOWMAN C., GARLAND S., FUJII C., COTTON M.D., HORST K., ROBERTS K., HATCH B., SMITH H.O., VENTER J.C.;
  Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium
   Nature 390:580-586(1997).
--- FUNCTION: THE PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING PROPEINS (BY SIMILARITY).
---- SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
  ó
   'Genomic sequence of a Lyme disease spirochaete, Borrelia
  Length 88;
  Indels
  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
  Score 34; DB 1;
Pred. No. 3.4;
3; Mismatches
   Ribosomal protein; rRNA-binding.
SEQUENCE 89 AA; 10348 MW; 0E24D709 CRC32;
  Last sequence update)
Last annotation update)
   Ą.
   PROSITE; PS00362; RIBOSOMAL_S15; 1. PFAM; PF00312; Ribosomal_S15; 1.
   PRT;
   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last seq
15-JUL-1998 (Rel. 36, Last anno
30S RIBOSOWAL PROTEIN 515.
   EMBL; AE001179; AAC67150.1; -.
  58.68;
   EMBL; 298741; CAB11393.1; -. HSSP; P05766; 1A32.
  Conservative
   STANDARD;
   Mycobacterium leprae.
```

```
Conservative
   128 LLIRRTIIRY 137
   502 AA;
   Query Match
Best Local Similarity
Matches 9; Conserv
  SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
KERSHAW J.;
  3 LLIRRIALRY 12
  Multigene family.
   CAO3_CANTR
  NON_TER
SEQUENCE
  RESULT 7
                      à
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  ö
  ö
  COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GORDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKALA F., DAVIEN S.V., EASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R., DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMLIN N., HOLROYD S., HORNSEY T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPHY L., OLIVER S., OSBORNE J., QUAIL M., RAJANDREAM M.A., ROGERS J., RAYLOR K., WHITEHEAD S., BARRELL B.G., TAXLOR K., WHITEHEAD S., BARRELL B.G., COMPLES S., SQARES R., SULSTON J.E., TAXLOR K., WHITEHEAD S., BARRELL B.G., COMPLES S., SQARES R., SULSTON J.E., TAXLOR K., WHITEHEAD S., BARRELL B.G., BARRELL B.
  Gaps
   Gaps
   Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  FUNCTION: THIS PROTEIN IS ONE OF THE 16S RIBOSOMAL RNA BINDING
  -! - SIMILARITY: BELONGS TO THE S15P FAMILY OF RIBOSOMAL PROTEINS.
  ö
  ö
                    Length 89;

    Length 89;

  3; Indels
  Indels
  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
HYPOTHETICAL 48.2 KD PROTEIN ZK849.5 IN CHROMOSOME I.
                  Score 34; DB 1;
Pred. No. 3.5;
  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
30S RIBOSOWAL PROTEIN S15.
RPSO OR RV2785C OR MIY002.50C.
   89 AA; 10475 MW; 374C7EB8 CRC32;
   Ouery Match 58.6%; Score 34; DB 1
Best Local Similarity 63.6%; Pred. No. 3.5;
Matches 7; Conservative 1; Mismatches
  Mismatches
  83
  PROSITE; PS00362; RIBOSOMAL_S15; 1. PFAM; PF00312; Ribosomal_S15; 1.
   EMBL; AL008967; CAA15580.1; -.
                    58.68;
   PROTEINS (BY SIMILARITY)
Ouery Match
Best Local Similarity 63.0،
مرح 7; Conservative
  STANDARD;
   STANDARD;
   1 YRLLIRRIALR 11
  1A32.
   78 YRSLIERLGLR 88
  78 YRSLIERLGLR 88
  1 YRLLIRRIALR 11
  Ribosomal protein.
  SEQUENCE FROM N.A.
  MEDLINE; 98295987.
   STRAIN=H37RV;
  YHSS_CAEEL
ID YHSS_CAEEL
AC 018304;
  RS15_MYCTU 033327;
   SEQUENCE
   RS15_MYCTU
  g
  DE PT PE
  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   ö
  ä
  SEQUENCE FROM N.A.

MEDLINE, 87280361.

SMALL G.M., LAZAROW P.B.;

"Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of Candida tropicalis.";

J. Cell Biol. 105:247-250(1987).

-!- CATALYTIC ACTIVITY: ACYL-COA + O(2) - TRANS-2,3-DEHYDROACYL-COA + H(2)0(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FROM 8 TO 18).
  -!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
  Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
   Gaps
  Gaps
ZK849.5.
Caenorhabditis elegans.
Eukaryota: Metazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.
   Candida tropicalis (Yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
   ö
  ;;
  01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-NUV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE POX4-2 (EC 1.3.3.6) (ACYL-COA OXIDASE)
(FRAGMENT).
  Score 34; DB 1; Length 411;
Pred. No. 18;
1; Mismatches 2; Indels
   58.6%; Score 34; DB 1; Length 502; 64.3%; Pred. No. 22; 1ve 1; Mismatches 2; Indels
   Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
  411 AA; 48236 MW; B5736F70 CRC32;
   55528 MW; EACE80C4 CRC32;
  502 AA
   -!- SUBCELLULAR LOCATION: PEROXISOMAL.
PIR; A28584; OXCKAX.
  WORMPEP, ZK849.5; CE16750.
PFAM; PF01062; Worm_family_8; 1.
Pypothetical protein.
SEQUENCE 411 AA; 48236 MW; B5
   58.6%;
   EMBL; 282095; CAB05028.1;
   Query Match
Best Local Similarity 70.0
Matches 7; Conservative
   STANDARD;
  -1- SUBUNIT: HOMOOCTAMER.
```

```
||:| | ||||||
307 YRMLARVSTIALRY 320
   1 YRLLIR--RIALRY 12
  1 YRLLIR--RIALRY 12
435
462
495
576
697
708 AA;
   PIR; A29441; OXCKPM
  708 AA;
  Best Local Similarity
Matches 9; Conserv
   STRAIN-ATCC 20184;
   Multigene family.
  SEQUENCE FROM N.A
   CAO4_CANMA
P05335;
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
   Query Match
   RESULT 10
POLG_DEN26
   CAO4_CANMA
   SHHHH
  음
  DDHT DD DDHT DD DDHT DD DDHT DD DDHT
  셤
  à
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  SMALL G.M., LAZAROW P.B.;
Import of the carboxy-terminal portion of acyl-CoA oxidase into peroxisomes of Candida tropicalis.";
J. Cell Biol. 105:27-250(197).
-:- CATALYTIC ACTIVITY: ACYL-COA + H(2)0(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FOOD BY TO BE ACTIVITY. ACYL-COA + H(2)0(2) (ACTS ON COA DERIVATIVES OF FATTY ACIDS WITH CHAIN LENGTH FORMS TO 18).
  -!- COFACTOR: FAD.-!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
  Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
  SEQUENCE FROM N.A.
STRAIN=ATCC 20336 / PK233;
MEDLINE: 87248070.
MURRAY W.W., RACHUBINSKI R.A.;
"The primary structure of a peroxisomal fatty acyl-CoA oxidase from the yeast Candida tropicalis pK233.";
Gene 51:119-128(1987).
  STRAIN=ATCC 20336 / PK233;
MEDLINE; 86149279.
OKAZAKI K., TAKECHI T., KAMBARA N., FUKUI S., KUBOTA I., KAMIRYO T.;
TWO acyl-coenzyme A oxidases in peroxisomes of the yeast Candida tropicalis: primary structures deduced from genomic DNA sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:1232-1236(1986).
  01-JAN-1988 (Rel. 06, Created)
Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
ACYL-COENZYME A OXIDASE II (EC 1.3.3.6) (ACYL-COA OXIDASE) (PXP-4).
  Candida tropicalis (Yeast).
Eukaryota, Fundi, Ascomycota, Hemiascomycetes, Saccharomycetales,
Candidaceae, Candida.
  REF. 3).
REF. 2 AND 3).
REF. 2).
ERROR (IN REF. 2 AND 3).
  708 AA
  Q -> E (IN F
P -> A (IN F
N -> K (IN F
FRAMESHIFT E
  SUBUNIT: HOMOOCTAMER.
SUBCELLULAR LOCATION: PEROXISOMAL.
   EMBL; M16193; AAA34322.1; --.
EMBL; M12160; AAA34362.1; --.
EMBL; Y00623; CAA68660.1; --.
EMBL; Y00623; CAA68661.1; ALT_INIT.
EMBL; Y00623; CAA68662.1; ALT_INIT.
PIR; A25123; OXCKX4.
  PRT;
  SEQUENCE OF 208-709 FROM N.A.
   [2]
SEQUENCE FROM N.A.
STRAIN-ATCC 20336 / PK233;
VENTINE; 86149279.
  STANDARD;
   101 YRMLARMSTIALRY 114
   216
216
245
335
393
                               1 YRLLIR--RIALRY 12
   OXCKX
  STRAIN-RR1;
MEDLINE; 87280361.
   Multigene family.
  01-JAN-1988
01-NOV-1988
01-NOV-1997
   OR POX-4.
   PIR; A29047;
   CAO2_CANTR
P06598;
  CAO2_CANTR
  <u>:</u>.
                               ó
   g
   HE LEE THE LEE TO COULD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profilt institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  ï
  -!- PATHWAY: INITIAL STEP OF THE PEROXISOMAL FATTY ACID BETA-OXIDATION
   Gaps
   Oxidoreductase; Fatty acid metabolism; Peroxisome; Flavoprotein; FAD;
  Gaps
   01-NOV-1988 (Rel. 09, Created)
01-NAY-1992 (Rel. 22, Last sequence update)
01-NAY-1992 (Rel. 22, Last annotation update)
ACYL-COENZYME A OXIDASE POX4 (EC 1.3.3.6) (ACYL-COA OXIDASE) (AOX).
   Candida maltosa (Yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Candidaceae; Candida.
   ;
;
  ;
;
  58.6%; Score 34; DB 1; Length 708; 64.3%; Pred. No. 33; 2; Indels :ive 1; Mismatches 2; Indels
   Length 708
   Indels
H -> Y (IN REF. 2).
G -> A (IN REF. 2).
E -> S (IN REF. 2).
ELA -> DLV (IN REF. 2).
Q -> E (IN REF. 2 AND 3).
   Score 34; DB 1;
Pred. No. 33;
1; Mismatches 2
   D97A4EC8 CRC32;
  BY SIMILARITY.
D5E344D2 CRC32;
  -!- SUBCELLULAR LOCATION: PEROXISOMAL.
  PRT;
435
462
6 495
578
697
79041 MW;
  0 E
78242 MW;
   58.6%;
   EMBL; X06721; CAA29901.1;
   Query Match
Best Local Similarity 64.3
Matches 9; Conservative
  SUBUNIT: HOMOOCTAMER
  Conservative
```

```
ŏ
  셤
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isp-sib.ch/announce/or send an email to license@isb-sib.ch).
   PFAM; PF00869; Flavi_alycoprot; 1.

R PFAM; PF00948; Flavi_NS1; 1.

R PFAM; PF00949; Flavi_NS1; 1.

R PFAM; PF00942; Flavi_NS5; 1.

R PFAM; PF01002; Flavi_NS5; 1.

R PFAM; PF01004; Flavi_NS2; 1.

R PFAM; PF01004; Flavi_NS2; 1.

R PFAM; PF01004; Flavi_NS2; 1.

R PFAM; PF01369; Flavi_NS4; 1.

R PFAM; PF01369; Flavi_NS4; 1.

R PFAM; PF01370; Flavi_NS4; 1.

R PFAM; PF01370; Flavi_propep; 1.

R PFAM; PF01370; Flavi_propep; 1.

W Polyprotein; Glycoprocein; Transferase; RNA-directed RNA polymerase;

W Core protein; Goat protein; Envelope protein; Helicase; ATP-binding;
                  01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (COWTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E;
NONSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3);
RNA-DIRECTED RNA POLYMERASE (EC 2, 77, 48) (NS5)].
Dengue virus type 2 (strain 1668).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
  BLOK J., MCWILLIAM S.M., BUTLER H.C., GIBBS A.J., WEILLER G.,
HERRING B.L., HEMSLEY A.C., AASKOV J.G., YOKSAN S.,
HERRING B.L., HEMSLEY A.C., AASKOV J.G., YOKSAN S.,
BHAMARAPRAVATI N.;
"Comparison of a dengue-2 virus and its candidate vaccine derivative:
sequence relationships with the flaviviruses and other viruses.";
Virology 187:537 590 (1992).
-! FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
-! SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
PROTEIN C AND MRNA.
  NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
HELLGASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
   ENVELOPE GLYCOPROTEIN M. ENVELOPE PROTEIN E.
   CAPSID PROTEIN C.
3391 AA.
   (POTENTIAL)
   POTENTIAL. POTENTIAL.
  POTENTIAL.
POTENTIAL.
POTENTIAL.
  DEAH BOX.
POTENTIAL.
  protein.
   Nonstructural
   EMBL; M84727; AAA73185.1; -.
STANDARD;
   1127
1345
1474
2093
2243
2491
3391
1675
1762
  : GNWV16.
  HSSP; P14336; 1SVB
   SEQUENCE FROM N.A. MEDLINE; 92188532.
   206
281
1128
11346
11346
11346
1138
1159
102
102
102
103
1158
  Transmembrane;
   PIR; A42451
POLG_DEN26
   CHAIN
NP_BIND
SITE
TRANSMEM
   TRANSMEM
TRANSMEM
   TRANSMEM
TRANSMEM
TRANSMEM
   CHAIN
   CHAIN
   CHAIN
  CHAIN
  CHAIN
   CHAIN
```

```
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
GENOME POLYPROTEIN (CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E;
PROTEIN (ENVELOPE GLYCOPROTEIN M); MAJOR ENVELOPE PROTEIN E;
PROSTRUCTURAL PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3);
RNA-DIRECTED FRAM POLYMERASE (EC 2.7.7.48) (NS5)].
Dengue virus type 2 (strain 16681-pDK53).
Viruses; SSRNA positive-strand viruses, no DNA stage; Flaviviridae;
  BHAMARAPRAPATI N.;

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Comparison of a dengue-2 virus and its candidate vaccine derivative:

"Virology 187:573-590(1992).

"I FUNCTION: THE SMALL PROTEINS NS2A, NS2A, NS4A AND NS4B ARE

HYDROPHORIAC. SUGGESTING A POSSIELE MEMBRANE-RELICATION.

"SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A LIPOPROFIEN BYNELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:

PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF PROTEIN C AND MENA.
  Gaps
  ö
   G.
  Score 34; DB 1; Length 3391;
Pred. No. 1.8e+02;
2; Mismatches 3; Indels
  BLOK J., MCWILLIAM S.M., BUTLER H.C., GIBBS A.J., WEILLER HERRING B.L., HEMSLEY A.C., AASKOV J.G., YOKSAN S.,
  67D1695A CRC32;
   POTENTIAL.
POTENTIAL.
BY SIMILARITY.
POTENTIAL.
  PRT; 3391 AA.
  POTENTIAL. POTENTIAL.
   POTENTIAL.
  POTENTIAL.
POTENTIAL.
   POTENTIAL
  POTENTIAL
   POTENTIAL
                                POTENTIAL
  POTENTIAL
   POTENTIAL
  POTENTIAL
  POTENTIAL
   POTENTIAL
   POTENTIAL
   POTENTIAL
  POTENTIAL
   POTENTIAL
   379540 MW;
  58.6%;
54.5%;
  Conservative
   STANDARD;
  1389
1464
2164
2190
2213
   2728 RMLINRFIMRY 2738
   2 RLLIRRIALRY 12
   Best Local Similarity
Matches 6: Conserv
   SEQUENCE FROM N.A. MEDLINE; 92188532.
  2305
2457
2485
2665
2704
3173
3391
  Flavivirus.
  POLG_DEN27
P29991;
  TRANSMEM
TRANSMEM
TRANSMEM
  DISULFID
DISULFID
DISULFID
  TRANSMEM
DISULFID
TRANSMEM
TRANSMEM
   CARBOHYD
  CARBOHYD
  CARBOHYD
  CARBOHYD
  SEQUENCE
  Query Match
  TRANSMEM
  DISULFID
   DISULFID
  CARBOHYD
  CARBOHYD
   CARBOHYD
   CARBOHYD
   CARBOHYD
  CARBOHYD
   CARBOHYD
   CARBOHYD
  CARBOHYD
   CARBOHYD
   TRANSMEM
                                TRANSMEN
  POLG_DEN27
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@lsb-sib.ch).
  PFAM; PF00948; Flavi_NSI; I.
PFAM; PF00949; Flavi_NBI; I.
PFAM; PF01002; Flavi_NBS; 1.
PFAM; PF01003; Flavi_NBS; 1.
PFAM; PF01004; Flavi_NBS; 1.
PFAM; PF01005; Flavi_NBS; 1.
PFAM; PF01005; Flavi_NBS; 1.
PFAM; PF01349; Flavi_NBS; 1.
PFAM; PF01570; Flavi_NBS; 1.
PFAM; PF01570; Flavi_Dropep; 1.
PF017PF01610; Coat protein; Envelope protein; Helicase; ATP-binding;
   HELICASE (NS3).
NONSTRUCTURAL PROTEIN NS4A.
NONSTRUCTURAL PROTEIN NS4B.
RNA-DIRECTED RNA POLYMERASE (NS5).
  ENVELOPE GLYCOPROTEIN M.
ENVELOPE PROTEIN E.
NONSTRUCTURAL PROTEIN NS1.
NONSTRUCTURAL PROTEIN NS2A.
NONSTRUCTURAL PROTEIN NS2B.
   protein.
CAPSID PROTEIN C.
   (POTENTIAL).
   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
   POTENTIAL.
POTENTIAL.
POTENTIAL.
   POTENTIAL. POTENTIAL.
   POTENTIAL. POTENTIAL.
  POTENTIAL. POTENTIAL.
  POTENTIAL
POTENTIAL
  POTENTIAL
   EMBL; M84728; AAA73186.1; -.
EMBL; M84727; -; NOT_ANNOTATED_CDS.
   EMBL; M84727; -; NOT_ANNOTATED_CDS
BIR 8424541; GNW726.
HSSP; P14336; LSVB.
PFAM; PF00869; Flavi_glycoprot; 1.
   Nonstructural
   1345
1474
2093
2243
22491
3391
1675
1762
66
  Fransmembrane;
   294
  DISULFID
   CARBOHYD
CARBOHYD
CARBOHYD
   TRANSMEM
TRANSMEM
  TRANSMEM
TRANSMEM
  TRANSMEM
TRANSMEM
   TRANSMEM
TRANSMEM
   TRANSMEM
TRANSMEM
   DISULFID
  CARBOHYD
CARBOHYD
   NP_BIND
SITE
   CARBOHYD
  CARBOHYD
  TRANSMEM
  TRANSMEM
  TRANSMEM
   TRANSMEM
   TRANSMEM
  DISULFID
   DISULFID
   CARBOHYD
   CARBOHYD
   TRANSMEN
  PROPEP
CHAIN
CHAIN
   CHAIN
CHAIN
CHAIN
   CHAIN
   CHAIN
   CHAIN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   ö
   ö
   Gaps
  Gaps
  01-FEB-1995 (Rel. 31, Created)
1-FEB-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
HYPOTHETICAL 98.7 KD PROTEIN IN SLU7-BMH2 INTERGENIC REGION.
HYPOTHETICAL 98.7 KD PROTEIN IN SLU7-BMH2 INTERGENIC REGION.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Pungl; Ascomycota; Hemiascomycetes; Saccharomycetales;
   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
  RESULT 12
YK50_YEAST
ID YK50_YEAST
AC D36151;
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 29, Last sequence update)
DT 01-NOV-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 39.4 KD PROTEIN IN MET1-SIS2 INTERGENIC REGION.
GN Saccharomycetaceae; Saccharomyces:
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomyces.
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetales
CN Saccharomycetaceae; Saccharomycetales
CN Saccharomycetales
CN Saccharomycetales
CN Saccharomycetales
CN Saccharomycetales
CN Saccharomycetales
CN Saccharomycetales
CN Saccharomycetales
CN S
   ö
   .;
0
  Length 3391;
  Length 352;
   1; Indels
   Indels
  SEQUENCE OF 1-161 FROM N.A.
STRAIN=S288C / FY1679;
COSTER F., JONNIAUX J.-L., GOFFEAU A.;
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
   58.6%; Score 34; DB 1; Le 54.5%; Pred. No. 1.8e+02; Live 2; Mismatches 3;
  POTENTIAL.
MW; 70570314 CRC32;
  56.9%; Score 33; DB 1; 60.0%; Pred. No. 24; 1ive 3; Mismatches
  869 AA.
   POTENTIAL. POTENTIAL.
   PRT;
   Saccharomycetaceae; Saccharomyces.
2665 2665
2704 2704
2714 2714
3391 AA; 379878 M
   Query Match 56.9
Best Local Similarity 60.0
Matches 6; Conservative
  Ouery Match 58.6
Best Local Similarity 54.5
Matches 6; Conservative
  STANDARD;
  |:|| | :||
2728 RMLINRFTMRY 2738
   2 RLLIRRIALRY 12
  :|||:||:|
223 FRLLVRRLYL 232
   1 YRLLIRRIAL 10
  RESULT 13
YD95_YEAST
ID YD95_YEAST
AC P38966;
   CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
   Best Loca
Matches
   셤
  a
  FFF8
  ò
  à
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EmBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   SEQUENCE FROM N.A.
MEDLINE; 96194804.
MEDLINE; 96194804.
MEDLINE; 96194804.

THE ESCHL E.E., PERDL G.G., HARRER N.E., BAUMRUKER T.;

The murine homolog of TB2/DP1, a gene of the familial adenomatous polyposis (FAP) locus.";

Gene 168:215-218 (1996).

-1 - SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-1 - SUMILARITY: TO C.ELEGANS T19C3.4.
   PROSITE; PS01110; RNA_POL_H_23KD; 1.
PFAM; PF01191; RNA_POL_H; 1.
Transferase; Transcription; DNA-directed RNA polymerase; 3D-structure.
SEQUENCE 78 AA; 9001 MM; 9F10C0F3 CRC32;
-i- SIMILARITY: TO OTHER ARCHAEBACTERIAL RPOH AND TO THE C-TERMINAL OF EUKARYOTIC SUBUNIT ABC27 (RPB5).
  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 35, Last annotation update)
POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (TB2 PROTEIN HOMOLOG) (GP106).
   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  Length 185;
  Length 78;
   Indels
  Indels
  3;
   .
0
   55.2%; Score 32; DB 1; 75.0%; Pred. No. 7.6;
  POTENTIAL.
FC5BA4A2 CRC32;
  1;
   185 AA
  Score 32; DB
Pred. No. 19;
  2; Mismatches
  2; Mismatches
   POTENTIAL.
  51 PO
106 PO
21050 MW;
  EMBL; U67546; AAB99042.1; -. PDB; 1HMJ; 05-APR-99.
  55.2%;
58.3%;
  EMBL; U28168; AAB07994.1; -. MGD; MGI:1270152; DP1.
   Query Match
Best Local Similarity 56.3.,
7; Conservative
   Conservative
   STANDARD;
   YRLLIRRIALRY 12
  31
86
185 AA;
   Query Match
Best Local Similarity
Matches 6; Conserv
   |||:|:||
70 YRLVIKRI 77
  1 YRLLIRRI 8
  TIGR; MJ1039;
  Transmembrane
  DP1_MOUSE
Q60870;
  TRANSMEM
SEQUENCE
   TRANSMEM
   RESULT 15
DP1_MOUSE
  용
  à
  ò
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@licenselent.).
  ö
   fold that is present in archaea and eukaryotes.";
J. Mol. Biol. 287:753-760(1999).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
  BULT C.3., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D., SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLATTON R.A., GOCAYNE J.D., KERLAVAGE A.R., DOUGHERTY B.A., TOMB J.-F., ADAMS M.D., REICH C.I., OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., WERRICK J.M., GLODEK A., SCOTT J.L., GEOGHAGEN N.S.M., WEIDBAN J.E., FUHRMANN J.L., NGTYEN D., UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C., COTTON M.D., ROBERTS K.M., HURST M.A., KAINE B.P., BORODOVSKY M., KLENK H.-P., FRASER C.M., SMITH H.O., WOESE C.R., VENTER J.C.; Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.
  'RNA polymerase subunit H features a beta-ribbon motif within a novel
  Gaps
   CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE
  THIRU A., HODACH M., ELORANTA J.J., KOSTOUROU V., WEINZIERL R.O., MATTHEWS S.;
   B.G., RAJANDREAM M.A., WALSH S.V.;
  ö
   Length 869;
  Methanococcus jannaschii.
Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
SEQUENCE OF 1-260 FROM N.A. RICHARDS C., HARRIS D.E., BARRELL B.G., RAJANDREAM M.A.; Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
   SEQUENCE OF 248-869 FROM N.A. OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WAL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNA DIRECTED RNA POLYMERASE SUBUNIT H (EC 2.7.7.5).
RPOH ON MJ1039.
  DB 1;
64;
  .l protein.
869 AA; 98711 MW; F8ED2ABB CRC32;
   78 AA
   Pred. No. 64;
2; Mismatches
   Score 33;
   SEQUENCE FROM N.A.
STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
MEDLINE; 96337999.
   PRT;
   EMBL; 246795; CAA86811.1;
EMBL; 274385; CAA98910.1;
PIR; 248778; S48778.
Hypothetical protein.
SEQUENCE 869 AA: 98711 MW:
  56.9%;
  EMBL; X82086; CAA57618.1; -.
   Science 273:1058-1073(1996).
  Query Match 56.9
Best Local Similarity 77.8
Matches 7; Conservative
   STANDARD;
  |:|:|||||
126 LIIQRIALR 134
   MEDLINE; 99208760
  3 LLIRRIALR 11
  STRUCTURE BY NMR
   SUBSTRATES.
  Methanococcus
   RPOH_METJA
  RNA(N)
  ò
  I I D D T T D T D
```

Gaps

ö

ö

ó

Search completed: February 8, 2000, 00:59:56 Job time: 3785 sec

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database :

```
032384 synechococc 08583 sphingomona 083438 treponema p 017713 caenorhabd1 04740 secherichia 05551 aquifex aeo 066951 aquifex aeo 066951 aquifex aeo 066951 aquifex aeo 066917 mycobacteri 059954 klebsiella 08280 arachia hyp 097211 leishmania progogo arachia progogo aeropyrum p 06966 bacillus su 099418 aeropyrum p 06966 bacillus su 099418 aeropyrum p 06966 bacillus su 099410 aeropyrum p 06966 bacillus su 099410 aeropyrum p
  Q9ytu2 cryphonectr
Q04350 cryphonectr
Q9z50 streptomyce
Q31072 synechococc
P71746 mycobacteri
   Gaps
  022063 PRELIMINARY: PRT; 795 AA.
022063; Q93489;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10.
101C3.10
   ö
   Query Match 65.5%; Score 38; DB 5; Length 795; Best Local Similarity 58.3%; Pred. No. 31; Matches 7; Conservative 2; Mismatches 3; Indels
   WILD A.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; 281061; CAB016939.1; -.
EMBL; 278413; CAB01667.1; -.
EMBL; 281061; CAB01667.1; -.
EMBL; 281061; CAB01667.1; -.
EMBL; P19491; 1GR2.
PFAM; PF00060; 11g-chan; 1.
SEQUENCE 795 AA; 89703 MW; DD722166 CRC32;
  Created)
Last sequence update)
Last annotation update)
  ALIGNMENTS
 032384
085853
085853
08138
017713
047402
09X5N8
06951
069477
059958
083593
083593
083593
  097211
P79087
098018
006966
09YAU1
016779
  10
   222
   00X378 PRELIMINARY;
09X378;
01-NOV-1999 (TEMBLEE1, 12
01-NOV-1999 (TEMBLEE1, 12
01-NOV-1999 (TEMBLEE1, 12
PX01-117,
Bacillus anthracis.
  2274
2966
4066
4066
4452
4452
4452
4452
613
613
895
11355
31164
31164
  1 YRLLIRRIALRY 12
   || :||:| ||
YRTSLRRLATRY 17
   SEQUENCE FROM N.A.
 RESULT
Q9X378
  RESULT
Q22063
     a
   SEPPER
  Q22063 caenorhabdi
Q9x378 bacillus an
P97213 clostriddium
Q9487 homo sapien
Q9xD05 myxococcus
O15455 homo sapien
O86547 mycobacteri
O07074 porphyromon
O87630 arabidopsis
   O58274 pyrococcus
O9yw77 melanoplus
O11875 dengue viru
O09234 unidentifie
O30127 archaeoglob
Q9yw17 melanoplus
O9y821 aeropyrum p
Q93329 caenorhabdi
O5389 streptomyce
Q9y483 homo sapien
Q42617 brassica na
  Search time 209.03 Seconds
(without alignments)
3.980 Million cell updates/sec
  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  Description
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
  Total number of hits satisfying chosen parameters:
  225878 segs, 69334122 residues
  8, 2000, 13:17:44;
  SUMMARIES
  summaries
   OM protein - protein search, using sw model
   Q22063
Q9X378
P972378
P972378
O94887
Q9X805
Q95374
Q97074
Q97077
Q97077
Q9707
Q9230
Q9230
  BLOSUM62
Gapop 10.0 , Gapext 0.5
  09YW71
09Y8Z1
093329
053839
09Y483
   sp_vertebrate:*
sp_unclassified:*
  sp_human:*
sp_invertebrate:*
sp_mammal:*
  sp_organelle:*
sp_phage:*
   1 YRLLIRRIALRY 12
   sp_archea:*
sp_bacteria:*
sp_fungi:*
   Post-processing: Minimum Match 0%
Listing first 45
  US-08-653-294-17
58
   sp_plant:*
sp_rodent:*
sp_virus:*
   2
   Minimum DB seq length: 0
Maximum DB seq length: 1000000
   SPTREMBL_12:*
  sp_mhc:*
  Length
  February
   Query
   6:
7:
8:
9:
```

Score

Result No.

 $\begin{smallmatrix} \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G} & \mathbf{G}$ 

20001111111000074

ö

```
MIGAGE T. SINTAWA K., SUYAMA M., KIKUNO R., MIYAJIMA N., TANAKA A., KOTANI H., NOWURA N., OHARA O.;

"Prediction of the coding sequences of unidentified human genes. XI. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 5:277-286(1998).

SEQUENCE OF 1-754 FROM N.A.

MEDLINE; 99063792.

SULSTON J.E., WATERSTON R.;

Genome Res. 8:1097-1108(1998).
   SEQUENCE OF 1-754 FROM N.A.
SEQUENCE OF 1-754 FROM N.A.
SUN H., STONEKING T., LANGSTON Y., LAPLANT Y.;
"The sequence of Homo sapiens BAC clone RG442F18.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
  Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO1835; BAA4513.1; -.
EMBL; ACO05104; AAD12224.1; -.
HSSP; POB567; 1PLS.
SEQUENCE 1054 AA; 119888 MW; 3BA89171 CRC32;
   WATERSTON R.H.; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases
   Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
   325 AA; 35985 MW;
   63.8%;
58.3%;
  SEQUENCE OF 1-754 FROM N.A.
  SEQUENCE OF 1-754 FROM N.A.
  [6]
SEQUENCE OF 1-754 FROM N.A.
   Conservative
  PRELIMINARY;
  ||||:||: |
688 YRLLLRRLCGHY 699
   1 YRLLIRRIALRY 12
   1 YRLLIRRIALRY 12
   Query Match
Best Local Similarity
Matches 7; Conserv
   Myxococcus xanthus
  SEQUENCE FROM N.A.
   Query Match
Best Local Similarity
   STRAIN-ER-15;
   WATERSTON R.
   WATERSTON
  SEOUENCE
  09XB05
  O9XB05;
   Ŋ
   Matches
   RESULT
Q9XB05
RRARRER RRARRE
  õ
  g
   ò
   ö
   ö
   OKINARA R.T., CLOUD K., HAMTON O., HOFFWASTER A., HILL K.K., KEIM P., KOEHLER T., LAMKE G., KUMANO S., MAHILLON J., MANTER D., MARTINEZ Y., RICKE D.O., SVENSSON R., JACKSON P.J.;

"The sequence and organization of pXO1, the large Bacillus anthracis plasmid harboring the Anthrax toxin genes.";

Bacteriol. 0:0-0(1999).

EMBL; AF065404; AAD32421.1; -.
   Gaps
  Gaps
  X-1997 (TrEMBLrel. 03, Created)
X-1997 (TrEMBLrel. 03, Last sequence update)
X-1997 (TrEMBLrel. 03, Last annotation update)
X-1097 (TrEMBLrel. 03, Last annotation update)
   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Clostridium.
   ö
   ö
   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
  63.8%; Score 37; DB 2; Length 132; 63.6%; Pred. No. 8.2; 2; Indels Live 2; Indels
  63.8%; Score 37; DB 2; Length 313;
41.7%; Pred. No. 19;
iive 6; Mismatches 1; Indels
   SEQUENCE FROM N.A.
STRAIN-VPI10463;
VON EICHEL-STREIBER C.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; X92982; CAA635591; -.
EMBL; X92982; CAA635581; -.
SEQUENCE 313 AA; 33380 MW; 4F20347A CRC32;
   Last sequence update)
Last annotation update)
                         Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
  132 AA; 15748 MW; 097E4E16 CRC32;
  313 AA.
   PRT; 1054 AA
  Created)
  PRT;
   Plasmid virulence plasmid PX01
   01-MAY.1999 (TrEMBLrel. 10, C. 01-MAY-1999 (TrEMBLrel. 10, LA 01-NOV-1999) (TrEMBLrel. 12, LA KIAA0793 PROTEIN.
  01-MAY 1997 (TrEMBLrel. 0
01-MAY-1997 (TrEMBLrel. 0
01-MAY-1997 (TrEMBLrel. 0
CDUZ, CDUI, TCDD, TCDB, TW.
GENES.
  Query Match 63.8
Best Local Similarity 63.6
Matches 7; Conservative
   Best Local Similarity 41.7
Matches 5; Conservative
  PRELIMINARY;
  PRELIMINARY;
  Clostridium difficile.
   14:: 11::::1
259 YRVVARRLSIKY 270
  1 YRLLIRRIALRY 12
   2 RLLIRRIALRY 12
  87 RILLRRAALNY 97
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   TISSUE-BRAIN
  SEQUENCE
  Query Match
  094887
   P97213
   4
  m
  RESULT P97213 P9
  RESULT
094887
   ò
   ò
```

```
ö
  ö
   PAITMA E. 17 ORR E., RON E.Z., ROSENBERG E.;
"Genetic and functional analysis of genes required for the post-
modification of the polyketide antiblotic TA of Myxococcus xanthus.";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ132503; CAR46503.1;
  Gaps
  Gaps
  ö
  ö
4; Length 1054;
   Bacteria; Proteobacteria; delta subdivision; Myxobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcaceae
  Length 325;
  Indels
  01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
MEMBRANE ASSOCIATED PROTEIN.
  62.1%; Score 36; DB 2;
ilarity 58.3%; Pred. No. 31;
Conservative 1; Mismatches
  4CC64E85 CRC32;
  Score 37; DB 4
Pred. No. 63;
2; Mismatches
  325 AA
   PRT;
```

Gaps

0

Indels

```
SERAIN—CV. LANDSBERG ERECTA;
STRAIN—CV. LANDSBERG ERECTA;
STRAIN—CV. LANDSBERG ERECTA;
STRAIN—CV. LANDSBERG ERECTA;
SEDITION—FOR THE STRAIN STRAIN—CV. LACOMBE B., BOUCHEZ D., BRUNEAU D.,
BOUCHEREZ J., MICHAUX-FERRIERE N., THIBAUD J.B., SENTENAC H.;
BOUCHEREZ J., MICHAUX-FERRIERE N., THIBAUD J.B., SENTENAC H.;
Involved in R+ release into the xylem sap.";
Cell 94:647-655(1998).
EMEL; AJ223358; CAA11281.1; -.
FSCP, 200421: LAWC.
PFAM; PF00033; auk; 3.
PFAM; PF00031; CNG_membrane; 1.
PFAM; PF00027; CNNP_Dinding; 1.
  HONGO H.;
"Nucleotide sequence upstream from the fimbrilin gene (fimA) of the oral anaelobe Porphyromonas gingivalis.";
Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AB004560; BAA330661; -.
SEQUENCE 490 AA; 55272 MW; 385AD4FF CRC32;
   Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; eudiochyledons; core eudiocts; Rosidae; eurosids II; Brassicales; Brassicaceae;
   60.3%; Score 35; DB 2; Length 490; 70.0%; Pred. No. 72; 1; Indels 1; Indels
   2; Length 309
   Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Cytophagales; Bacteroidaceae; Porphyromonas
  01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
STELAR K+ OUTWARD RECTIFIING CHANNEL.
  01-JUL-1997 (TrEMBLrel. 04, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
PFAM; PF00175; oxidored_fad; 1.
Hypothetical protein; 1ron-sulfur.
SQCBNCE 309 AA; 33517 WW; B152B590 CRC32;
  828 AA
  DB 46;
   490 AA
   Mismatches
   Score 35;
Pred. No.
  PRT;
   Query Match 60.3%;
Best Local Similarity 77.8%;
Matches 7; Conservative
  Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
   PRELIMINARY;
  PRELIMINARY;
  92 YRIIDRRIAL 101
  1 YRLLIRRIAL 10
  SEQUENCE FROM N.A.
  65 YRIAIRRIA 73
   1 YRLLIRRIA 9
   Arabidopsis.
   STRAIN-381;
  FIMBRILIN.
   007074
   082630
   σ
  FIMA
   RESULT
082630
  RESULT
007074
 SWR
  ô
  g
  á
  셤
  ö
   STRAIN-H37RV;
MEDLINE; 9829597.
COLE S.T., BROSCH R., PARKHILL J., GARNIER T., CHURCHER C., HARRIS D., GONDON S.V., EIGAMEIER K., GAS S., BARRY III C.E., TEKAIA F.,
BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
DAVIES R., DEVLIN K., FELTWELL T., GENTLES S., HAMIIN N., HOLROYD S.,
HORNESP T., JAGELS K., KROGH A., MCLEAN J., MOULE S., MURPY L.,
CLIVER S., OSBORNE J., QUAIL M.A., RAJANDREAM M.A., ROGERS J.,
RUTTER S., SEEGER K., SKELTON S., SQUARES S., SQARES R., SULSTON J.E.,
TAYLOR K., WHITEHEAD S., BARRELL B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
Nature 393:537-544(1998).
  Gaps
  Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMILLED (FED.), HARDIMAN G., TIMANS J.C., KASTELEIN R.A., BAZAN J.F.,
SUBMILLED (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: 408899; AAG341341; -
PFAM; PF00560; LRR; 15.
PFAM; PF001463; LRRCT; 1.
PFAM; PF01582; TIR. 1.
PRINTS; PR00019; LEURICHRPT.
   ;
0
   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Length 904;
  Indels
  Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases. EMBL, ALO08967; CAA15591.1; -. HSSP, P33164; 2PTA. PROSITE: PSO1977; ZFESS_FERREDOXIN; 1. PROSITE: PSO1977; ZFESS_FERREDOXIN; 1.
  Last sequence update)
Last annotation update)
   01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
HYPOTHETICAL 33.5 KD PROTEIN.
  904 AA; 103828 MW; F857CE1C CRC32;
   Score 35; DB 4;
Pred. No. 85;
   904 AA
  Mismatches
   Created)
   PRT;
   62.1%;
60.0%;
  05,
12,
   Mycobacterium tuberculosis.
  6; Conservative
   PRELIMINARY;
   PRELIMINARY;
  01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
 TOLL-LIKE RECEPTOR 3.
  ||::||:||:
484 RLMLRRVALK 493
   Query Match
Best Local Similarity
Matches 6; Conserv
  2 RLLIRRIALR 11
  SEQUENCE FROM N.A.
   SEQUENCE FROM N.A.
  STRAIN-H37RV;
  PARKHILL J.;
  SEQUENCE
  086347
086347;
   015455
   RESULT
086347
   g
  g
  õ
```

ö

Gaps

; 0

Gaps

; 0

g

qq

ò

```
Dengue virus type 2.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
   KINNEY R.M., BUTRAPET S., CHANG G.J., TSUCHIYA K.R., ROEHRIG J.T., BHAMARAPRAVAI N., GUBLER D.J.;
"Construction of Infectious cDNA clones for dengue 2 virus: strain 1661 and its attenuated vaccine derivative, strain PDK-53.";
Virology 230:300-308(1997).
EMBL: URALS, AMBS8783.1;
   Score 34; DB 12; Length 3391;
Pred. No. 7.5e+02;
2; Mismatches 3; Indels
   Length 530;
   Score 34; DB 12; Length 53
Pred. No. 1.2e+02;
3; Mismatches 3; Indels
   Last sequence update)
Last annotation update)
  Created)
Last sequence update)
Last annotation update)
   5F56B205 CRC32;
EMBL; AF063866; AAC97756.1; -.
SEQUENCE 530 AA; 65062 MW; D29ED6FE CRC32;
   PRT; 3391 AA.
   PRT; 3391 AA
  Created)
   PF00869; Flavi_glycoprot; 1. PF00949; Flavi_helicase; 1. PF01004; Flavi_M; 1.
   379861 MW;
   PFAM; PF01349; Flavi_NS4B; 1.
PFAM; PF00972; Flavi_NS5; 1.
PFAM; PF01570; Flavi_propep; 1.
PFAM; PF01003; Flavi_capsid; 1.
   58.6%;
54.5%;
  Flavi_NS2A; 1
Flavi_NS2B; 1
   58.6%;
50.0%;
  01-JUL-1997 (TIEMBLEEL. 04, 01-JUL-1997 (TIEMBLEEL. 04, 01-NOV-1999 (TIEMBLEEL. 12,
   Flavi_NS1; 1.
  04,
12,
   Flavi_NS4A;
  Ouery Match
Best Local Similarity 50.0°
   Query Match 58.6
Best Local Similarity 54.5
Matches 6; Conservative
   PRELIMINARY;
  01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-NOV-1999 (TrEMBLrel.
   PRELIMINARY;
  1:|| | :||
2728 RMLINRFIMRY 2738
  :|| :| | :||
139 HRLYLREIPIRY 150
   1 YRLLIRRIALRY 12
   3391 AA;
   2 RLLIRRIALRY 12
  [1]
SEQUENCE FROM N.A.
STRAIN-16681;
MEDLINE; 97288308.
  SEQUENCE FROM N.A.
  STRAIN-PDK-53;
MEDLINE; 97288308
  EMBL; U87412;
HSSP; P14336;
  unidentified unclassified
   Polyprotein
SEQUENCE
  POLYPROTEIN
   Flavivirus
  009234;
   011875
   009234
  PFAM;
PFAM;
PFAM;
  PFAM;
   RESULT 13
  RESULT 12
  011875
ID 01
   009234
   δ
  SOR
   ö
  MEDLINE; 98344137.
KAWARABAYASI Y., SAWADA M., HORIKAWA H., HAIKAWA Y., HINO Y.,
YAMAMOTO S., SEKINE M., BABA S., KOSUGI H., HOSOYAWA A., NAGAI Y.,
SAKAI M., OGURA K., OTUKA R., NAKAZAWA H., TAKAMIYA M., OHFUKU Y.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI J., KUSHIDA N., OGUCHI A.,
AOKI K., NAKAMURA Y., ROBB T.F., HORIKOSHI K., MASUCHI Y., SHIZUYA H.,
KIKUCHI H.;
  Gaps
  Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
  Melanoplus sanguinipes entomopoxvirus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirinae;
Entomopoxvirus B.
  "Complete sequence and gene organization of the genome of a hyper-thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DANA Res. 5:55-76(1998).
EMBL; AROUGO02: BAA228.1; -. SEQUENCE 362 AA; 41831 MW; EB8D18CF CRC32;
  STRAIN=TUCSON;
AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
   ö
  5;
  Length 828;
  Length 362;
   1; Indels
   3; Indels
   MEDILINE; 99102612.
AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., RU"The genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73:533-552(1999).
   01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-AN-1999 (TrEMBLrel. 09, Last annotation update)
362AA LONG HYPOTHETICAL PROTEIN.
   01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
0RF MSV205 TRYPTOPHAN REPEAT GENE FAMILY PROTEIN.
  Score 35; DB 10;
Pred. No. 1.2e+02;
  DB 1;
83;
 93898 MW; AA41E3DD CRC32;
  530 AA.
   362 AA.
  3; Mismatches
   3; Mismatches
  Score 34;
Pred. No.
   PRT;
  58.6%;
  60.3%;
ilarity 57.1%;
Conservative
  Query Match 58.6
Best Local Similarity 50.0
Matches 6; Conservative
  PRELIMINARY;
  PRELIMINARY;
  ||:::| |||||
|143 YRMIYKRSSIALRY 156
   1 YRLLIRR--IALRY 12
  Pyrococcus horikoshii
  || ::: ||| |
296 YRFILKAIALGY 307
  1 YRLLIRRIALRY 12
828 AA;
  Query Match
Best Local Similarity
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
  SEQUENCE FROM N.A.
   STRAIN=TUCSON;
   ∞
   SEQUENCE
   Q9YVN7;
   058274
  Q9YVN7
  RESULT 10
058274
   RESULT 11
  Matches
```

g

õ

ö

Gaps

; 0

```
38 YVELARKIAMRY 49
  09YW71;
  RESULT 15
Q9YW71
  Q9YW71
    g
G
   ò
   ö
   ö
   SEQUENCE FROM N.A.

STRAIN-VC-16 / DSM 4304 / ATCC 49558;

MEDLINE; 98049343.

KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,

KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,

KICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,

FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,

KIKKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,

PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,

OVERBEEK R., GOGCAYNE J.D., WEIDMAN J.F., MCHONALD L., UTTERBACK T.,

COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,

SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,

MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
   Gaps
  Gaps
KINNEY R.M., BUTRAPET S., CHANG G.J., TSUCHIYA K.R., ROEHRIG J.T., BHAMMRAPRAVATI N., GUBLER D.J.;
ECONSTRUCTION Of infectious cDNA clones for dengue 2 virus: strain 16681 and its attenuated vaccine derivative, strain PDK-53.";
Virology 230:300-308(1997).
EMBL; U87411, AAB58782.1; -.
HSSP; P14336; LBV.
FFRAM; PF00869; Flavi_glycoprot; 1.
PFAM; PF00949; Flavi_helicase; 1.
   "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997).
EMBL: AE01099; AAB91122.1; -.
   ö
   ;
0
  Score 34; DB 12; Length 3391;
Pred. No. 7.5e+02;
2; Mismatches 3; Indels
  Archaea; Buryarchaeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
  Length 107;
   Indels
  01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
CONSERVED HYPOTHETICAL PROTEIN.
  3391 AA; 379800 MW; A839A51C CRC32;
   Score 33; DB 1;
Pred. No. 39;
2; Mismatches
  11 protein.
107 AA; 13307 MW; F23652A7 CRC32;
   107 AA
   2; Mismatches
  PRT;
  PF01005; Flavi_NS2A; 1.
PF01002; Flavi_NS2B; 1.
PF01350; Flavi_NS4A; 1.
PF01349; Flavi_NS4B; 1.
PF00972; Flavi_NS5; 1.
   PF01570; Flavi_propep; 1 PF01003; Flavi_capsid; 1
   54.5%;
  56.9%;
58.3%;
  PF01004; Flavi_M; 1.
PF00948; Flavi_NS1; 1.
   6; Conservative
  Query Match 56.9
Best Local Similarity 58.3
Matches 7; Conservative
   PRELIMINARY;
  Archaeoglobus fulgidus
   |:|| | :||
2728 RMLINRFTMRY 2738
  2 RLLIRRIALRY 12
   Query Match
Best Local Similarity
Matches 6; Conserv
  Hypothetical
SEQUENCE 1(
   VENTER J.C.;
   Polyprotein
SEQUENCE
   030127
  PFAM;
PFAM;
   PFAM;
  PFAM;
   PFAM;
  PFAM;
  PFAM;
  PFAM;
  RESULT 14
    g
  δ
```

1 YRLLIRRIALRY 12

ò

```
Gaps
   MSV021.
Melanoplus sanguinipes entomopoxvirus.
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Entomopoxvirus B.
  STRAIN-TUCSON;
AFONSO C.L., TULMAN E.R., LU Z., OMA E., KUTISH G.F., ROCK D.L.;
SUDmitted (MAT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF063866; AA697850.1; -
SEQUENCE 260 AA; 31180 MW; AB880E14 CRC32;
  OMA E., KUTISH G.F., ROCK D.L.;
   ö
  Length 260;
   4; Indels
   STRAIN-TUCSON;
MEDLINE; 99102612.
AFONSO C.L., TULAAN E.R., LU Z., OMA E., KUTISH G.F., RC "The genome of Melanoplus sanguinipes entomopoxvirus.";
J. Virol. 73:533-552(1999).
   01-MAY-1999 (TrEMBLrel. 10, Created)
1-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
ORF MSV021 MTG MOTIF GENE FAMILY PROTEIN.
   Query Match 56.9%; Score 33; DB 12;
Best Local Similarity 58.3%; Pred. No. 93;
Matches 7; Conservative 1; Mismatches 4.
260 AA
  Search completed: February 8, 2000, 13:17:45 Job time: 32494 sec
PRT;
PRELIMINARY;
  234 YYLLIEKILLNY 245
   1 YRLLIRRIALRY 12
  SEQUENCE FROM N.A.
```

ô

THIS PAGE BLANK (USPTO)

```
AC014422 Drosophila melano
AC018284 Drosophila melano
295124 Human DNA sequence
   DNA HTG 09-DEC-1999
*** SEQUENCING IN PROGRESS ***, in ordered
  DMRNA3 1050 bp DNA INV 31-MAR-1992
Three Drosophila melanogaster genes for transfer RNAs (Glu
specific).
  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea;
Drosophilidae; Drosophila.

( (bases 1 to 1050)
Hosbach, H.A., Silberklang, M. and McCarthy, B.J.
Evolution of a D. melanogaster glutamate tRNA gene cluster
81001852
  ...yun: 12
Gaps: 0
Percent Identity: 66.667
  59865
67392
74562
   Location/Qualifiers
1. 1050
/organism="Drosophila melanogaster"
(db.xref="taxon:7227"
1. 1050
  /gene="tRNA:E4:62Aa"
/note="transfer RNA:glu4:62Aa"
/allele=""
  25. .96
/gene-"tRNA E4:62Aa"
/note-"tRNA Glu"
/db_xref="FlyBase:FBgn0011851"
262. .333
   /db_xref-"FlyBase:FBgn0011851"
190 c 213 g 323 t
  262. .333
/gene="tRNA:E4:62Aa"
/note="tRNA Glu"
/db_xref="FlyBase:FBgn0011851"
  /db_xref-"FlyBase:FBgn0011851"
  922 TACAGAATGTCGATGCAACGCATTGCTTTACGTTAT 957
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
8.3e+03
9.5e+03
1.1e+04
  from: 1 to: 1050
   v60238 Júli46
V00238 l GI:8458
transfer RNA: transfer RNA-Glu.
fruit fly.
   /gene="tRNA:E4:62Aa"
/note="tRNA Glu"
86.71
85.64
84.74
  seq_documentation_block:
LOCUS AC017966 8849 bp D
DEFINITION Drosophila melanogaster,
  Drosophila melanogaster
   AC017966
AC017966.1 GI:6553224
HTG; HTGS_PHASE2.
fruit fly.
38.00
38.00
  43.00
3.909
91.667
  Align seg 1/1 to: DMRNA3
   alignment_block:
US-08-653-294-17 x DMRNA3
  seq_name: gb_htg7:AC017966
   seg_documentation_block:
   seq_name: gb_in1:DMRNA3
  Quality:
Ratio:
Percent Similarity:
   324
  pieces.
gb_htg5:AC014422
gb_htg7:AC018284
gb_pr2:HS225D2
  alignment_scores:
   VERSION
KEYWORDS
SOURCE
ORGANISM
  source
   ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  DEFINITION
   REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
   BASE COUNT
  ACCESSION
  gene
   trna
  LRNA
   trna
  FEATURES
   ORIGIN
  Len | Documentation | .. |
1050 | V00238 Three Drosophila melanogast |
14394 | AC017966 Drosophila melanogast |
14394 | AC010564 Drosophila melanogast |
14391 | AC010564 Drosophila melanogast |
168369 | AC005847 Drosophila melanoga |
100389 | Y08256 S.solfataricus | 100 kh |
100389 | Y08256 S.solfataricus | 100 kh |
10042 | AL132800 Homo sapiens chromc |
19142 | AL132800 Homo sapiens chromc |
1948 | J096137 Anabaena PCC7120 apcEAF |
19283 | Z81502 Cenorhabditis elegans |
107672 | AC005834 Drosophila melanoga |
107672 | AC005834 Drosophila melanoga |
107672 | AL03310 Mycobacterium leprae |
10745 | AL03310 Mycobacterium leprae |
10745 | AL03310 Mycobacterium leprae |
10745 | AC017368 Homo sapiens chromc |
10767 | AC017368 Homo sapiens chromc |
107768 | AC005805 Homo sapiens chromc |
187560 | AC016031 Homo sapiens chromc |
187560 | AC016031 Homo sapiens chromc |
187560 | AC016031 Homo sapiens chromc |
187560 | AC016031 Homo sapiens chromc |
187560 | AC016031 Homo sapiens chromc |
187560 | AC016031 Homo sapiens chromc |
187560 | AC0160307 Homo sapiens chromc |
187560 | AC0160307 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
187560 | AC017003 Homo sapiens chromc |
1875750 | AC017003 Homo sapiens chromc |
187580 | AL121956 Homo sapiens chromc |
187580 | AL121956 Homo sapiens chromc |
187580 | AC017003 Homo sapiens chromc |
187580 | AC017003 Homo sapiens chromc |
187580 | AL121956 Homo sapiens chromc |
187580 | AL121956 Homo sapiens chromc |
187580 | AL121956 Homo sapiens chromc |
187580 | AL121956 Homo sapiens chromc |
187590 | AL121956 Homo sapiens chromc |
18750 | AC0
  AJ131275 uncultured euryarchaed
AF142982 Uncultured archaeon BU
AF015992 Uncultured archaeon 2
AF015979 Uncultured archaeon 2
AF015979 Uncultured archaeon 2
AF015978 Uncultured archaeon 2
AF015978 Uncultured archaeon 2
AF015978 Uncultured archaeon 2
AF015978 Uncultured archaeon 2
AF015078 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 2
AF015071 Uncultured archaeon 
  Continuation (4 of 4) of CEY1
   AL031853 S.pombe chromosome
   299165 S.pombe chromosome
  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format : pfs
  1046
  510
365
910
   3.7e+03
650.63
2.0e+03
1.1e+03
6.9e+03
7.67
  3e+03
.2e+03
.1e+04
  EScore
   .3e+03
.3e+04
.4e+04
.9e+04
  1.9e+04
1.9e+04
2.0e+04
3.3e+04
  26.22
526.23
3.2e+03
3.3e+03
  42.41
63.38
63.38
78.87
78.96
78.96
78.96
1109.77
1144.02
2265.78
2265.78
3.0e+03
3.2e+03
  25,007e
142,27
194,27
196,37
197,88
198,113
1112,73
1112,73
1112,73
1112,73
1113,16
1114,113
1114,113
1114,113
1114,113
1114,113
1114,113
1114,12
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
1114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
114,13
11
OM of: US-08-653-294-17 to: GenEmbl:*
  Database sequences: 821193
Database length: -1518192014
Search time (sec): 11370.480000
   Strd Orig
  Search information block:
Query: US-08-653-294-17
Query length: 12
   Command line parameters:
   4:41
  Database: GenEmbl:*
  9b_vi.AF055731
9b_vi.AF055732
9b_ini.CEK03D3
9b_ini.SPBC25B2
9b_pi2:SPAC2F3
9b_htg1:CEY113B8_3
  9b_htg3:AC009613
9b_htg2:AC009613
9b_htg2:HSD468N3
9b_htg2:HSD468SC5
9b_bal:HSD4655C5
9b_bal:AF00959
9b_bal:AF015971
9b_bal:AF015971
9b_bal:AF015978
9b_hal:AF015978
9b_hal:AF015978
  Date: Feb 8, 2000
   9b_htg7:AC017966
9b_htg7:AC017966
9b_htg4:AC010564
9b_btg4:AC010564
9b_btg1:AC005687
9b_btg1:CNS01DTM
9b_htg1:CNS01DTM
9b_htg1:CNS01DTM
9b_htg1:CNS01DTM
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
9b_htg1:CNS01BT
  gb_htg6:AC016384
gb_htg7:AC017368
gb_htg3:AC009341
gb_p12:F10A2
gb_htg2:AC005805
  Sequence
```

```
68045:
68873:
  39939
41158
42006
   47499
49101
50372
   51977
54051
550028
550028
550028
60133
61361
63495
64635
68035
68035
  43466
   8404
   5927
TITLE
JOURNAL
  COMMENT
   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 143914)

8 Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhac, C.,
Burtows, J., Carter, M., Chacko, J., Chen, Z., Cox, C.,
Burtora, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Horashid, N.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Hodgeson, A., Hogues, M.,
Forly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lu, J., Luder, R.,
Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S.,
Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M., Morris, S.,
Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S., Shah, E.,
Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgangy, R., Tabor, P.,
Taylor, T., Vasquez, L., Vinson, R., Wolliamson, A., Worles, M., Watlington, S.,
Mrensford, G., Yu, W., Zhou, X., Nelson, D. and Gibbs, R.,
Unpublished
Unpublished
Unpublished
States I to 143914)
          ACO10564 143914 bp DNA HTG 16-OCT-1999
Prosophila melanogaster chromosome 3L/62Al clone RPC198-2701, ***
SEQUENCING IN PROGRESS ***, 89 unordered pleces.
ACO10564 GI:5917942
HTG. HTGS_PHASE1.
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
1735 c 1884 g 2626 t
   Length: 12
Gaps: 0
Percent Identity: 66.667
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
  from: 1 to: 8849
   Drosophila melanogaster
   43.00
3.909
91.667
   AC017966
  alignment_block:
US-08-653-294-17 x AC017966
  seq_name: gb_htg4:AC010564
   seq_documentation_block:
LOCUS AC010564 14
  Worley, K.C.
   Quality:
Ratio:
Percent Similarity:
   2604 a
   fruit fly
  Align seg 1/1 to:
  alignment_scores:
   VERSION
KEYWORDS
SOURCE
ORGANISM
  source
   DEFINITION
   BASE COUNT
  TITLE
JOURNAL
REFERENCE
AUTHORS
  REFERENCE
AUTHORS
   TITLE
JOURNAL
   REFERENCE
AUTHORS
  ACCESSION
  FEATURES
   COMMENT
  ORIGIN
```

```
Submitted (16-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Sep 22, 1999 this sequence version replaced gi:5916428.

* NOTE: This is a "working draft' sequence. It currently
* Consists of 89 configs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N. but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
             Department
   1260 bp in length
815 bp in length
815 bp in length
1220 bp in length
613 bp in length
814 bp in length
819 bp in length
819 bp in length
819 bp in length
819 bp in length
819 bp in length
811 bp in length
718 bp in length
1155 bp in length
1155 bp in length
1155 bp in length
1155 bp in length
1155 bp in length
1150 bp in length
1172 bp in length
1142 bp in length
1142 bp in length
1152 bp in length
1152 bp in length
1152 bp in length
1152 bp in length
1153 bp in length
1153 bp in length
1153 bp in length
1154 bp in length
1155 bp in length
1156 bp in length
1157 bp in length
1158 bp in length
1159 bp in length
1159 bp in length
  831 bp in length
814 bp in length
831 bp in length
835 bp in length
856 bp in length
844 bp in length
848 bp in length
860 bp in length
860 bp in length
878 bp in length
878 bp in length
878 bp in length
878 bp in length
   bp in length
bp in length
bp in length
  ength
  length
   in lens
' length
   무
   in
in
  44444444444
  of of of
  of
of
  of
of
  ŏ
  contig
contig
contig
contig
contig
  contig
contig
contig
  contig
contig
   contig
   contig
   contig
  contig
contig
  contig
   contig
contig
   contig
contig
  contig
   contig
  contig
  contig
  contig
   contig
  contig
   conti
  conti
conti
   conti
  conti
   conti
   conti
  conti
  1645:
2519:
3350:
4206:
5469:
6313:
7273:
8101:
8941:
10144:
   13937:
14752:
15972:
  24541:
25726:
  11825:
   60132:
61360:
  21252:
   27681:
   63494:
   64634:
  66834:
  30391:
  30635:
   18403:
   58815:
  17184:
18018:
   26570:
   2005:
   7498:
   13085
  8837
   33026
   12899
   34092
   14928
   9100
   1976
   54050
   57411
  16571
   21970
   36891
```

```
Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Maxda, P., Moshrefi, A.R., Moshrefi, M., Mixon, K., Pacleb, J.M., Park, S., Pfelifer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M. Sequencing of Drosophila chromosome 3L, region 61F3-62A2

Unpublished (1997)

E. (Dases i to 268369)

E. Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfelifer, B., Punch, E., Snir, E., Twomey, B., Pacleb, J.M., Park, S., Pfelifer, B., Punch, E., Snir, E., Twomey, B., Pacleb, J.M., Park, S., Pfelifer, B., Punch, E., Direct Submission
  For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.orgkeiv.com.
Library locations: 11.34, 21-67, 44-36, 73-50, 92-76.
  Submitted (12-021-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, US Sequence submitted by:

Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720
   1. .268369
/organism="Drosophila melanogaster"
/db.xref="taxon,7227"
/chromosome="31."
  /map="61F3-62A2"
   alignment_block:
US-08-653-294-17 x AC005847/rev
  seq_documentation_block:
LOCUS MTCY427 38110 bp
   43.00
3.909
91.667
  seq_name: gb_bal:MTCY427
  Ratio:
Percent Similarity:
   Quality:
   71701
  alignment_scores:
  DEFINITION
  SOURCE
ORGANISM
   BASE COUNT
   ACCESSION
VERSION
KEYWORDS
  TITLE
   TITLE
   REFERENCE
AUTHORS
  FEATURES
  COMMENT
  ORIGIN
  Drosophila melanogaster (Subclones in tet from P1 clones DS03179 (D226), DS06357 (D230), DS03404 (D231), DS06962 (D232); and DS07291 (D240)) DNA.
   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 268369)
Celniker, S. E., George, R. A., Galle, R. F., Hoskins, R. A.,
Svirskas, R. R., Harris, N. L., Agbayani, A., Arcaina, T. T., Baxter, E.,
  DNA 22-OCT-1998
DNA sequence (Pls DS03179 (D226), DS06357
DS06962 (D232), and DS07291 (D240)),
   complete sequence.
AC005847 AC004331 AC004436 AC004334 AC004488 AC004489
AC005847.1 GI:3779012
  557 others
  length
length
length
ength
ength
  ength
                      ength
  ength
  ength
   ength
  ength
ength
ength
   ength
  ength
   length
Length
   ength
  ength
  ength
  Dercent Identity: 66.667
  /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
       i i i
 contig of 1146 bp in contig of 12304 bp in contig of 2304 bp in contig of 2555 bp in contig of 1271 bp in contig of 1378 bp in contig of 1378 bp in contig of 1378 bp in contig of 1378 bp in contig of 1378 bp in contig of 1378 bp in contig of 1378 bp in contig of 1378 bp in contig of 1389 bp in contig of 298 bp in contig of 298 bp in contig of 2090 bp in contig of 2789 bp in contig of 2789 bp in contig of 2789 bp in contig of 2789 bp in contig of 2789 bp in contig of 2789 bp in contig of 33113 bp in contig of 3113 bp in contig of 3388 bp in contig of 3388 bp in contig of 3388 bp in contig of 3388 bp in contig of 3388 bp in contig of 3388 bp in contig of 4117 bp in
  58362 TACAGAATGTCGATGCAACGCATTGCTTTACGTTAT 58397
   'clone="RPCI98-2701"
33523 c 32072 g 39042 t
  to: 143914
  132811: contig of 3473
137892: contig of 5081
143914: contig of 6022
  /chromosome="3L/62Al"
   Location/Qualifiers
  Align seg 1/1 to: AC010564 from: 1
   seq_documentation_block:
LOCUS AG005847 268369 bp
DEFINITION Drosophila melanogaster
(D230), DS03404 (D231),
   78389:
80840:
82111:
  97095:
100091:
102072:
  104497:
107508:
  109598:
  84052:
   87488:
89108:
   91457:
92907:
  115204:
   121885:
  125221:
   129338:
   95337
  118317
   3.909
   US-08-653-294-17 x AC010564
  seq_name: gb_in2:AC005847
  129339
132812
137893
   68874
70020
73760
73760
75835
78390
82112
84053
86111
86111
86111
86111
86111
86111
87489
89109
92508
92508
   104498
107509
109599
1112406
115205
118318
  .02073
  38720 a
  Percent Similarity:
  Quality:
   Ratio:
   alignment_scores:
  alignment_block:
   source
  BASE COUNT
   ORGANISM
  ACCESSION
   VERSION
KEYWORDS
SOURCE
  REFERENCE
   AUTHORS
   FEATURES
   ORIGIN
```

```
Mycobacterium tuberculosis H37Rv complete genome; segment 99/162. 270692 AL123456 Z70692.1 GI:3261567
/clone="P15" 2523179 (D226), DS06357 (D230), DS03404 (D231), DS06962 (D232), and DS07291 (D240)" / Coordinates are the P15 were completed as a project. The coordinates are the lends for each P1. DS03404 (D231)extends from bp 1 to bp 80.732. DS03179 (D226) extends from bp 32,734 to bp 117,954. DS06357 (D230) extends from bp 88,745 to bp 169,482. DS06652 (D232) extends from bp 127,117 to bp 209,427. DS07291 (D240) extends from bp 194,759 to bp 268,369."
   Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
   to: 268369
  Length: 12
Gaps: 0
Percent Identity: 66.667
  Align seg 1/1 to reverse of: AC005847 from: 1
```

TITLE

COMMENT

```
misc_feature
  misc_feature
  source
  gene
   gene
   CDS
  Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 ISA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhillésanger.ac.uk on Jun 27, 1998 this sequence version replaced gi:1261921.
  YVEDDGLAFOGSSIRGFOSIHESDMLLLPDPFTARIDPFRAAKTLNINFFVHDPFTLE
PYSRDPRNIARKAENYLISTGIADTAYFGAEAEFYIFDSVSFDSRANGSFYEVDAISG
WWNTGAATEADGSPNRGYKVRHKGGYFPVAPNDQYVDLRDKMLTNLINSGFILLEKGHH
  /note="Ry2220, (MTCY190.31-MTCY427.01), len: 478.glnAl, Probable glutamine synthetase, glnA, similar to many eg SW:GLMA_STRCO P15106 (71.4% identity in 475 aa overlap); contains PS00180 Glutamine synthetase signature 1, PS00181 Glutamine synthetase putative ATP-binding region signature, PS00182 Glutamine synthetase class-I
  /db_xref="swiss-proT:010377"
/translation="MTEKTPDDVFKLAKDEKVEYVDVRFCDLPGIMQHFTIPASAFDK
"(Dases 1 to 38110)

Cole.S.T. Brosch.R., Parkhill, J., Garnier, T., Churcher, C.,
Harris, D., Gordon, S.V., Eiglmeier, K., Gas, S., Barry III, C.E.,
Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,
Connor, R., Davies, R., Devlin, K., Feltwell, T., Genles, S.,
Hamilin, W., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A.,
Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,
Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
Barrell, B.G.

Barrell, B.G.

Deciphering the biology of Mycobacterium tuberculosis from the
  (URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers. Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is an increase in the observed/expected third position G + C.
  CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
  Details of M. tuberculosis sequencing at the Sanger Centre are available on the World Wide Web.
   Erratum:[[published erratum appears in Nature 1998 Nov
12;396(6707):190]]
   1. .38110
/organism="Mycobacterium tuberculosis"
/strain="H37Rv"
   /organism="Mycobacterium tuberculosis"
/strain="H37Rv"
  /protein_id="CAA94665.1"
/db_xref="GI:3261568"
   complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
  /db_xref-"taxon:1773"
  /db_xref="taxon:1773"
/clone="Y190"
  Location/Qualifiers
  adenylation site"
  /transl_table=11
   /product-"glnA1"
   /gene="glnA1"
163. .1599
  /codon_start=1
  /gene="glnA1"
   2 (bases 1 to 38110)
Parkhill, J.
   .1599
   <1. .5460
  Parkhill,J.
Direct Submission
  source
          REFERENCE
AUTHORS
   MEDLINE
REMARK
   AUTHORS
TITLE
JOURNAL
  gene
  JOURNAL
  REFERENCE
```

CDS

FEATURES

```
ginE_Probable ginE, similar to SW:GLNE_ECOLI P30870
glutamate-ammonia-ligase adenylyltransferase (24.4%
identity in 721 aaoverlap) and SW:GLNE_HAEIN P44419 (28.1%
identity in 199 aa overlap); initiation codon uncertain
unless at 39346 or 39247"
   'translation="MVVTKLATORPKLPSVGRLGLVDPPAGERLAQLGWDRHEDOAHV
DLLWSLSRAPDADAALRALINESPDTGWDELMAALINESTSLRGRLSTSALG
DHLWALBAPDADAALRALINESPDTGWDELMAALINESTSLRGRLSTSALG
DHLVAHPOSKKLLGROYTLPSHDQLORSFVECVEESEGMPGSLVHRLRTOYRDYULM
AALDLAATVEDEPVLPFTVVAARLADAADAALAAALRVAEASVCGEHPPPRLAVIAMG
KCGARELNYYSDYDVIFVABREDPRINRRVASEMRWASAAFEFUVDAALREBGRNGELV
RTLGSHIAYYORWATWEFQALLKARPVYGDAELGERYLTALMPMWRACEREDFVVA
VQAMRRRVEQLVPADVRGRELKIGSGGLRDVEFAVQLLQLVHARSDESLRVAAL
  /db_xref="SWISS-PROT:010378"
//db_xref="SWISS-PROT:010378"
//translation="WDRQKEFVLRTLEERDIRFVRLWFTDVLGFLKSVAIAPAELEGA
FEGIGFDGSSIEGFRAVSSDTVAHPDPSTFQVLPWATSSGHHHSARWFCDITMPDG
SPSRADPRHYLRRQLICFSCYVHPEIEFFLLKPGPEDGSVPPVDNAGFFDQA
VHDSALNFRRHAIDALEFMGISVEFSHHEGAPGQEIDLRFADALSMADNVMIFRYVI
                           CHOSLWKDGAPLMYDETGYAGLSDTARHYIGGLLHHAPSLLAFTNPTVNSYKRLVPGY
EAPINLYYSQRNRSACVRIPITGSNPKAKRLEFRSPDSSGNPYLAFSAMLMAGLDGIK
NKIEPQAPVDKDLYELPEEAASIPQTPTQLSDVIDRLEADHEYLTEGGVFTNDLIET
   aalgeggy igredaanwtasy efirilehriqlorikrthilpdpedeeavrw<mark>iaraa</mark>
hirpdgrndaagvlreelkkonvrvskihtklfyqpillesigptgleiahgw<u>tleaag</u>
rrlaalgyegpqtaikhwsalvnqsgrrgryosvlpprildhwsyapdpdggliayrr
  LSEALATESWY.LATLRDKPAVARRLMHVLGTSAYVPDLLMRAPRVIQOYEDGPAGPRL
LETEPAVARALIASARSKYPDPERAIAGARTLERRELARIGSADLLGLEVTEVRAL
TSWWYAYLQAALDWYRTASLEDDRAPAAIAYUGMGRLGGAELGYGSDADWMYCEPA
TGVDDARAVKWSTSIAERVRALLGTPSVDPPLELDANLRPEGRNGPLVRTLGSYAAYY
  EQWAQPWEIQALLRAHAVAGDAELGQRFLRMVDKTRYPPDGVSADSVREIRRIKARIE
SERLPRGADPNTHTKLGRGGLADIEWTVQLLOLQHAHQVPALHNTSTLQSLDVIAAAD
EVGSGGQAEINYQFNSLLHAADDMQLYKYIIKNTAWQNGKTVTFMPKPLFGDNGSGMH
  /note-"Rv2222c, (MTCY427.03c), len: 446. glnA2, probable allo, (overlaps MTCY190.33c partials sequence) probable classII glutamine synthetase, similar to MTCY190.31 (and partiallorf MTCY427.01) (34.3% identity in 300 aa overlap)"
   KEVALEEGARASFMPKPFGQHPGSAMHTHMSLFEGDVNAFHSADDPLQLSEVGKSFIA
GILEHACEISAVTNQWVNSYKRLVQGGEAPTAASWGAANRSALVRVPMYTPHKTSSRR
  VEVRSPDSACNPYLTFAVLLAAGLRGVEKGYVLGPQAEDNVWDLTPEERRAMGYRELP
   LVPAADVELLRQAWLTATRARNALVLVRGKPTDQLPGPGRQLNAVAVAAGWRNDDGGE
  Glutamine synthetase putative ATP-binding
  'note-"PS00182 Glutamine synthetase class-I adenylation
   (MTCY190.32c-MTCY427.02c), len: 994
   382. .>38110
/organism="Mycobacterium tuberculosis"
  WISFKRENEIEPVNIRPHPYEFALYYDV"
  /protein_id="CAA94664.1"
/db_xref="GI:1261923"
/db_xref="SWISS-PROT:Q10379"
   /protein_id="CAA94645.1"
/db_xref="GI:1261924"
   complement(1917. .4901)
/gene="glnE"
  /db_xref="taxon:1773"
/clone="Y427"
955. .1002
/gene="glnA1"
  complement(1917. .4901)
  complement(4950. .6290)
   complement(4950. .6290)
  FLDNYLRVTRRAKAVVRKVFGS
  /note-"PS00181 Gluregion signature"
   /transl_table=11
  /codon_start=1
/transl_table=11
   /product-"glnA2"
   /note="Rv2221c,
  /strain="H37Rv"
   /product-"glnE
  /codon_start=1
  ginAl"
   /gene="glnA2'
  /gene="glnA2'
  _eueb/
   site
```

us-08-653-294-17.rge

```
solfataricus
   TYKSE"
  Mol. Micr
97055432
  source
            ORGANISM
   AUTHORS
TITLE
JOURNAL
  JOURNAL
MEDLINE
REFERENCE
   gene
  REFERENCE
   AUTHORS
   COMMENT
FEATURES
  TITLE
  complement(2385. .7947)

complement(2385. .7947)

/gene="Rv2233"
/note="Rv2233"
/note="Rv2233"
/note="Rv2233"
/note="Rv2233"
/note="Rv2233"
/note="Rv2233"
/note="Rv2233"
/note="Rv2233"
/note="Rv223"
   RFGALLVNPGGPGASAVDMVAAMAPATADTDIIRHFDIVĞFDPRĞVGHSTPALRCRTD
ABFDAYRRDPMADYSPAGYTHVEQYYRQLAQDCVDRMGFSFLANIGTASVARDMDMVR
QALGDDQINYLGYSYGTELGTAYLERFGTHVRAMYLDGATDPAYSPIEBSISQMAĞRĞ
TAFNDYAADCAFACPLGTDSAQWYRYHALVDPLVQKPGKTSDPRGLSYADATTGT
INALYSPQRWXYLTSGLLGLQRGSDAGOLLYLADDYDGRBDADGHYSNDQDAFNANRCY
DAPTPADDAAWVAADQRIRQVAPFLSYGQFTGSAPRDLCALMPVPATSTPHPAAPAGA
  /translation="MAAMMRRRPLSSALLSFGLLLGGLPLAAPPLAGATEEPGAGGTP
GAPVVAPQQSWNSCREFIADTSEIRTARCATVSVPVDYDQPGGTQAKLAVIRVPATGQ
   GKVVVVSTTHDPATPYQSGVDLARQLGAPLITFDGTQHTAVFDGNQCVDSAVMHYFLD
                            6349. .6366
/note="inverted repeat between 3' end of MTCY427.04c and 5' end of MTCY427.03c"
complement(6385. .7947)
/gene="Rv2223c"
   acylamino-acid-releasing enzyme; alpha-amylase; amidase; aminopeptidase; daunorubicin resistance protein; glycerol kinase; glycogen operon protein GlgX; HIT protein; IS element; L-lactate permease; oxidoreductase; pyruvate-ferredoxin oxidorecuctase; riboflavin blosynthesis protein; sugar transporter. Sulfolobus solfataricus.
SSLDSALRAMEASELVAEALGEHVFDFFLRNKRTEWANYRSHVTPYELRTYLSL"
6349. .6366
   /note="GGTGA, possible ribosome binding site upstream
  29-APR-1997
   /note="PS00120 Lipases, serine active site" complement(7952. .7956)
   /transl_table=11
/product="hypothetical protein Rv2223c"
/protein_id="CaA94646.1"
/db_xref="G1:1.261925"
/db_xref="SWISS-PROT:Q10508"
   to: 38110
  Length: 12
Gaps: 0
Percent Identity: 75.000
  BCI
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
  seq_documentation_block:
LOCUS SSIOOKBER 100389 bp DNA
DEFINITION S.SOLITATICUS 100 kbp DNA fragment.
ACCESSION Y08256
VERSION Y08256.1 GI:1707679
   to reverse of: MTCY427 from: 1
   /gene="Rv2224c"
complement(8009. .9571)
  complement(7243. .7272)
  complement(8009. .9571)
  /gene="Rv2223c"
   /gene="Rv2224c"
  GTLPPTSLRCAP'
  alignment_block:
US-08-653-294-17 x MTCY427/rev
  42.00
4.200
83.333
   seq_name: gb_bal:SS100KBFR
  Quality:
Ratio:
   Percent Similarity:
  misc_feature
  misc_feature
  alignment_scores
   Align seg 1/1.
   gene
  gene
  CDS
   RBS
   KEYWORDS
```

SOURCE

```
Sensen, C.W., Klenk, H.P., Singh, R.K., Allard, G., Chan, C.C.,
Liu, O.Y., Penny, S.L., Young, F., Schenk, M.E., Gaasterland, T.,
Doollittle, W.F., Ragan, M.A. and Charlebois, K.L.

Organizational characteristics and information content of an
archaeal genome: 156 kb of sequence from Sulfolobus solfatarious P2

Mol. Microbiol. 22 (1), 175-191 (1996)
   /protein_id="cha69511.1"
/db_xref="G1:1707682"
/db_xref="STREMBL:P95851"
/translation="WATVYMLIERKKGTEINATNOPITSTLFLPKSSESFPAMKLNAP
FTNPKDTKGNNRLNIEMFICFSNTGIIILRVPRYNPVKKTNIVNKINCLFIISTKI"
   QKYYEVYKSLEDKGLVRVIEGRPKKVKLIDPSISLKYYRDKIVSELDYAIGNVISYWS
EKGKGEADRSLHIKGKTIVWRMIRELVDKSNKIKVVWDILPEWLIKIIKKYKGNLTVI
TSSNNLSLNAEVKYVKNIKSKFIIFDDSVLVTFNDQDEIVVDSCRGCVLQAEEHFDLL
   /translation="manrofiletilveftglylgtlriipveekoinisimlslll
plvsrgfvkgafnflagklsddlgrkrvlvigwlvalisvplflsibli
ainqaltwittvtsqidisgklragfatginemsgylgvsfgslfasylfklssifig
  /db_xref="SPTREMBL:P95849"
/translation="MMIFRQIISKSGGCATYVFGCTQAGELFVVDPKYEMVDEIIELA
RDLGDMKIAYIIDTHTHADHLSGAKKLASLTNANVYYHELSQVKFKVERVKNGEEIKA
  EENLYYSLAKLKELPDYVEIYPAHTAGSVCGIGISGKPSSTIGFEKRFNSLFRINNKD
EFVNRIREVKMPKFVEFDDYIRKNLEGVI"
  GNVKIKVLHTPGHTPDSISVLIYDRRRDESWNEPWAILITGDTLFVGGLGRIDI<b>GGENA
   Submitted (19-SEP-1996) C.W. Sensen, Institute for Marine Biosciences, National Research Council of Canada, 1411 Oxford Street, Halifax, N.S., Canada, B3H 3Z1, CANADA Related sequence: Y08257.
Location/Qualifiers
1. .100389
/organism="Sulfolobus solfataricus"
Sulfolobales; Sulfolobus.
   /db_xref="G1:1707683"
/db_xref="SPTREMBL:P95852"
  db_xref-"SPTREMBL:P95850"
   /gene="orf c06003"
/gene="orf c06003"
complement(2360. .2665)
/gene="orf c06003"
/codon e+a-t
  /protein_id="CAA69509.1"
/db_xref="GI:1707680"
   /protein_id="CAA69510.1"
/db_xref="GI:1707681"
   'protein_id="CAA69512.1"
   complement(889 .1632)
/gene="orf c06001"
complement(889 .1632)
/gene="orf c06001"
  complement(1664. .2335)
/gene="orf c06002"
  /db_xref="taxon:2287"
   2376. .3476
/gene="orf c06004"
2376. .3476
/gene="orf c06004"
  /gene="orf c06002"
  complement (1664.
   transl_table=11
  /transl_table=11
   /transl_table=11
  /transl_table=11
Crenarchaeota;
  (bases 1 to 100389)
  /strain="P2"
   Sensen, C.W.
Direct Submission
```

gene

CDS

gene

CDS

```
/transl_table=11
/protein_id="CaA69494.1"
/brotein_id="CaA69494.1"
/db_xref="GI:1707690"
/db_xref="SpTREMBL"
/translation="WDKKFKLVFIFYCLLPLPLRNSTKPTNSTITPIIARKKPRPVYN
ATFINEDANSWLKTYFTEMGVVRLFTIIASYLGLNNANIYPFSAICGTDWFVPFTSCN
   /translation-"maigktvilvgalilivgialffiggylassglikivntlstas
pttlopgssgdlgvpsklsillyntssgovlkiloevngtngsvpolaekgyilalls
pkydalmvnnlttpisvkyvlsoefasslinvalytglgfflaligvivllvglyff
   /db_xref="SPTREMBL:P95857"
/translation="MVKLVATLGTSPGGVIESFLYLVKKGENIDEVRVVTTSNAEVKK
AWRIVRLMFVCCIQEKFPKVEISEHPLDIEDIYSEDDLRKVREFVEKQLGEGDYLDIT
  GGRKSMSVAAALAÄKNKGVKIITSIIPQDDYNKISKKVRELKEIPEIRNRGECRQEMK
ETYCSLIVQDARSIEFEI"
7797. .8135
/gene="orf c06011"
/997. .8135
/gene="orf c06011"
  HTG 02-OCT-1999
clone L2259 strain Friedlin, ***
unordered pieces.
  Leishmania major.
Leishmania major
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
  to: 100389
  Length: 11
Gaps: 0
Percent Identity: 81.818
  from: 1
  39542 IACTTACTCCTAATTCGGCGTTTGGCTTTAAGA 39510
  /db_xref="SPTREMBL:P95859"
  /protein_id="CAA69493.1"
/db_xref="G1:1707689"
  /protein_id="CAA69495.1"
   1 TyrArgLeuLeulleArgArglleAlaLeuArg 11
   complement(8375, .9304)
/gene="orf co6013"
complement(8375, .9304)
/gene="orf co6013"
complement(7257, .7793)
/gene="orf c06010"
complement(7257, .7793)
/gene="orf c06010"
   complement(7829. .8332)
/gene="orf c06012"
complement(7829. .8332)
/gene="orf c06012"
  seg_documentation_block:
LOCUS AC009602 40000 bp DNA
DEFINITION Leishmania major chromosome 35
SEQUENCING IN PROGRESS ***, 6 u
  to reverse of: SS100KBFR
   /db_xref="GI:170769
   /codon_start=1
/transl_table=11
  /transl_table=11
  /codon_start=1/trans1_table=11
  /codon_start-1
  AC009602
AC009602.2 GI:6006095
HTG; HTGS_PHASE1.
   codon_start-
  alignment_block:
US-08-653-294-17 x SS100KBFR/rev
  Leishmania.
1 (bases 1 to 40000)
   IFNTCPELVL"
  42.00
4.200
90.909
   RGRGKRO
   seq_name: gb_htg3:AC009602
   Ouality:
Ratio:
  Percent Similarity:
   alignment_scores
  Align seg 1/1
   ORGANISM
   gene
  gene
              gene
   gene
  ACCESSION
  REFERENCE
  VERSION
KEYWORDS
  CDS
   CDS
   IICLIALISSFNVIETKTLIPNATLSKKENNHINYFSITKISIAGLLEKFVDSAFFIL
IPFELLOHYTELIGITVSSYTFYBOSLSQPLEGXLADTYNKRELILVGFLLENGVGF
INYSELPILFSIIGGIGGGMYIYPNLAFVNNKINESVRGKALGYYRLYRDSGYGVAGL
LLPLLXSFYGYETTLIVGILQVVALLLVVRS"
   /transl_table=11
/protein_id="CAA69513.1"
/db_xref="GI:1707687"
/db_xref="SPTREME.: 995853"
/translation="MRRVGSKNCSRGCENRKVLLEALGKNNYKNSVKVYIIESIPAIL
IVSLMLGKYSSIINFALTLLSLSPVVIAIPAVLVGILISNKRIMGKYAYTKTRLLAYF
  VITERIAGE AND THE TRANSPORT OF THE TRANS
   /db_xxef="SPTEMBL:P95854"
/translation="WRIRDSAKLFGPAWIALLADADAASILGGLSTGEEYGYKLIWFV
/translation="WRIRDSAKLFGPEINEBHYSTRISILESTEPIELVOFFTYLSEYA
GLASLPIFITIOPASGREGATGKGGGEELTREHYSTRISILESTEPIELVOFFTYLSEYA
GIAIGCYLIGWNPLFCLIYPFILHVLYVLTRYYETTERYLVYTSYLILLISALINVGPK
LSFTGGDDVFYFSTSKNFLFFTANNVGAVYTPPCMLVYGSSATAIRYSKIGIDNSKKTS
   /transl_table=11
/db_xref="da-"CaA69491.1"
/db_xref="G1:1707687"
/db_xref="SPIRMBL:P95855"
/translation="MOEKPOGPKVVGYEILEKSGLDIKKLVDKLVKATAAEFTTYYYY
TIRMHLTGMEGEGLKEIREDARLEDRIHFELMTQRIYELGGGLPRDIRQLADISACS
DAYLDENWKDPKEILEKVLLEAEQCA.RTWKEVCDMTYGKDPRTYDLAQRILGEEIEHE
AWFLELLYGRESGHFRRSSPGNAPYSKK"
   /protein_id="cAA69492.1"
/db_xref="G1:1707688"
/db_xref="STREMBL:P95856"
/translation="WAURYSSLSDLEEKKPRKFSINGIEVVIVRVGDKVFAIEAYCPH
KGRNLEYGEVEGYKIRCDLHGYEYSLEDGELIFNPYGKTSGWYFSPNLRIYKVEIKGK
  /transl_table=11
/protein_id="CAA69514.1"
/protein_id="CAA69514.1"
/db_xxfe="sprakel:055275"
/db_xref="sprakel:055275"
/translation="MTKELTREEYYRALEKAVNEVILSMTGTRKDVAKRLLLGAVVGR
  WIGIETLLGAIITELIIVLSEMIGTSIGNIDPIDPAQLLYNLGSVHYIFGITLISAGF
LTLIVVSLSSAWGLLE"
  complement(3975, .5039)
/gene="orf c06006"
/note="IS element ISC1217"
  /transl_table=11
/protein_id="CAA69490.1"
/db_xref="G1:1707686"
  complement(3665. 4024)
/gene="orf c06005"
  LIVAMIVAGGLVGILHL"
complement(3975. 5039)
/gene="orf c06006"
  complement(5112. .5990)
/gene="orf c06007"
  complement(5112. 5990)
/gene="orf c06007"
/codon_start=1
  complement(3665, .4024)
/gene="orf c06005"
  /gene="orf c06008"
6315. .6881
  6315. .6881
/gene="orf c06008"
  /gene="orf c06009"
6934. .7260
/gene="orf c06009"
   _table=11
  /codon_start-1
  /codon_start=1
  /codon_start=1
   /codon_start=1
   5315. .6881
  /gene="orf
   /trans]
```

gene

CDS

gene

gene

CDS

```
contaminated with foreign sequence from E.coli, yeast, vector,
   software (G. 133712, .133
  to: CNS01DTM
  41.00
3.727
91.667
   alignment_block:
US-08-653-294-17 x CNS01DTM
  seq_name: gb_sts:G18985
   ಥ
  Quality:
Ratio:
  Percent Similarity:
  53877
                   phage,
contig
  alignment_scores:
  Align seg 1/1
   source
  BASE COUNT
ORIGIN
   STS
  SIS
   STS
   STS
  STS
   SIS
  STS
  SIS
   FEATURES
        Direct Submission
Submitted (28-Aug-1999) Seattle Biomedical Research Institution, 4
Nickerson Street, Seattle, MA 98109-1651, USA
Noct 1, 1999 this sequence version replaced gi:5801666.
NOTE: This is a 'working draft' sequence. It currently
consists of 6 contigs. The true order of the pleces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
* as soon as it is available and the accession number will
   - Web : www.genoscope.cns.fr)
IMPORTANT: This sequence is unfinished and does not necessarly
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continue. The sequence may be
Myler,P.J., Sisk,E., Hixson,G., Kiser,P., Rickel,E., Hassebrock,M.,
Cawthra,J., Marsolini,F., Sunkin,S. and Stuart,K.D.
  Direct Submission
Submitted (04-NOV-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 191442)
  1441 others
   g of 2595 bp in length f unknown length g of 1486 bp in length f unknown length
  in length
  of 5678 bp in length
unknown length
of 7691 bp in length
  of 3892 bp in length
unknown length
  to: 40000
   Length: 12
Gaps: 0
Percent Identity: 66.667
   unknown length
   gap of unknown leng
contig of 17259 bp
   28900 IAICGTCGCCCATTCGTCGTCGTCTTTT 28865
   1. .40000
/organism="Leishmania major"
  ų
  from: 1
  1 TyrArgLeuLeulleArgArglleAlaLeuArgTyr 12
  8195
   /db_xref="taxon:5664"
/chromosome="35"
   contig c
gap of c
contig c
  Location/Qualifiers
  Align seg 1/1 to reverse of: AC009602
  contig
gap of
  10082 c 10936 g
   contig
  contig
   gap of
   /strain-"Friedlin
  clone-"L2259"
  AL132800
AL132800.1 GI:6272127
   4361:
  22741:
40000:
   US-08-653-294-17 x AC009602/rev
   4491:
   2462:
  .40000
  41.00
3.727
91.667
  HTG; HTGS_PHASE2
  seq_name: gb_htgl:CNS01DTM
   Homo sapiens
   2596
2876
4362
4642
8534
   8814
   14492
14772
22463
22742
   ø
  Ratio:
Percent Similarity:
  enoscobe
  Ouality:
  9346
   human.
  alignment_scores
   alignment_block:
   source
  BASE COUNT
ORIGIN
   ORGANISM
  REFERENCE
AUTHORS
   TITLE
JOURNAL
                                 TITLE
JOURNAL
  ACCESSION
 AUTHORS
  KEYWORDS
  FEATURES
  COMMENT
  COMMENT
```

```
/standard_name="AA194835"
/note="matching EMBL:AA194835; Identified using the e-PCR
software (G. Schuler)"
  /note="matching EMBL:M69137; Identified using the e-PCR
ooftware (G. Schuler)"
132481. .13268
  /note="matching EMBL: Z41390; Identified using the e-PCR software (G. Schuler)" 133741. .133892
  e-PCR
   /standard_name="T15974"
/note="matching EMBL:T15974; Identified using the e-PCR
   e-PCR
: 13 10 12 11 14 15 9, 1000 N's separate segments
   /note="matching EMBL:R39150; Identified using the
software (G. Schuler)"
  /standard_name="R37382"
/note="matching EMBL:R37382; Identified using the software (G. Schuler)"
146875. 146986
  /standard_name="R52665"
/note="matching EMBL:R52665; Identified using the software (G. Schuler)"
154585. .154748
   the
  This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
  using
  6098 others
   /standard_name="T31019"
/note="matching EMBL:T31019; Identified
software (G. Schuler)"
   Length: 12
Gaps: 0
Percent Identity: 58.333
                Contig 13: length 15976 bp
Contig 10: length 5980 bp
Contig 12: length 5980 bp
Contig 11: length 8121 bp
Contig 14: length 67723 bp
Contig 15: length 81177 bp
Contig 9: length 4117 bp.
* NOTE: This is a 'working draft' sequence.
   software (G. Schuler)"
41528 c 39774 g 50165 t
   to: 191442
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
  /organism-"Homo sapiens"
   67422. .67594
/standard_name="M69137"
   /standard_name="241390"
  /standard_name="R39150"
  /clone_11b="RPCI-11"
/clone="R-80A15"
67422, .67594
   /db_xref="taxon:9606"
   Location/Qualiflers
  from: 1
  .146899
  133909
```

```
/protein_1d="AAC97585.1"
/db_xref="G1:2072511"
/translation="MKHQLFCNIFEPRYYQWRLQEAQKEYESGFERLSQMNSYSVRTA
   456. 459

/note-"for orfA and orfAB"

join(466. .. 816,816. .1421)

/note-"orfAB; -1 frame shift in the frame-shift window

during translation produces the full-length fusion protein

orfAB, presumably the active protein"
  VDRMLORIEISLKKKTLHASEKETERVOLLRVOFWLOLOGILAENLVFLDEAGANLSL
IRHSARSKKGKRAYGCRPQKRHQNVSIIGAIALKGVISQYSILGTSDGLFFEAYISQK
LVPRLWEAACVIMDNCSIHKGGDIEKLIESAGAKLIYLPPYSPDFSPIENCWSKIKNF
   /translation="mkaySLDFRQKIFDTYKTGGISQRQLANKFCVSLGFIEKLLKQY
RETASIAPKVRTKQTPPKLNEEQMKILEEIVEAKNDLTLSEIRFILKEKTGITIGIST
Cai,Y.A., 'Lantoine,F.L. and Glazer,A.N.
Characterization of Anabaena sp. PCC 7120 mutants defective in the
large core-membrane linker protein of the light-harvesting
   Direct Submission
Submitted (02-APR-1997) Department of Molecular and Cell Biology,
University of California, Berkeley, CA 94720-3206, USA
Location/Qualifiers
   383. ...393
/note="inverted repeat B, copy 2; transposable element
ISAn1"
   398. .413
/note="ISAn1 terminal inverted repeat, copy 1 (IRL)"
  i.Aalorisopposoiirivkuseiolreekupekureekailor"
271. 293
770-direct repeat A, copy 1"
771. 283
770-direct repeat A, copy 1"
771. 283
772. 297
772. 297
772. 297
776. 297
776. 297
776. 297
776. 297
776. 297
   LRSIEARSYPDLAKAIESAFNQVSLNDIYNWFTHSCYCTSPD 466. .861
  <u>-</u>-
  copy 1"
  5
   5
  copy
  copy
  294. .314
//note="direct repeat A, copy 2"
/rpt_type=direct
369. .379
/note="inverted repeat B, copy
//rpt_type=inverted
   /organism="Anabaena PCC7120"
/strain="PCC7120"
   /organism="Anabaena PCC7120"
   .23. .434 note-"inverted repeat C,
  /transl_table=11
/protein_id="AAC97588.1"
/db_xref="G1:2072514"
   /note="hypothetical"
/codon_start=1
/transl_table=11
/brate4
  /1solate="mutant SB12"
  /db_xref="taxon:1174"
complement(<1. .268)
  /db_xref="taxon:1174"
/transposon="ISAn1"
  /rpt_type=inverted
  /rpt_type_inverted
   'rpt_type=inverted
  /rpt_type=inverted 437, 448
   Unpublished
4 (bases 1 to 7948)
   phycobilisomes
  Cai, Y.A.
  repeat_region
  repeat_region
   repeat_region
  repeat_region
  repeat_region
   repeat_region
   repeat_region
  repeat_region
   repeat_region
   source
   source
   JOURNAL
REFERENCE
  AUTHORS
   JOURNAL
  FEATURES
   RBS
   CDS
  CDS
  <u>L</u>
  Cai.Y.A., Lantoine,F.L. and Glazer,A.N.
Characterization of the Anabaena transposable element ISAn1 that
belongs to the phylogenetically wide-spread Tc1/mariner superfamily
unpublished
3 (bases 1500 to 7948)
  seq_documentation_block:

LOCUS APU96137 7948 bp DNA BCT 22-DEC-1998

DEFINITION Anabaena PCC7120 apcEABC gene cluster, phycobilisome core-membrane
linker protein (apcE), allophycocyanin alpha subunit (apcA),
allophycocyanin beta subunit (apcB) and phycobilisome core linker
protein LC7.8 (apcC) genes, complete cds.
                    13-MAR-1996
  Cal. Y.A., Schwarts, S.H. and Glazer, A.N.
Transposon insertion in genes coding for the biosynthesis of structural components of the Anabaena sp. phycobilisome Photosyn. Res. (1997) in press
2 (bases 1 to 1560)
  Anabaena PCC7120.
Anabaena PCC7120
Bacteria: Cyanobacteria; Nostocales; Nostocaceae; Anabaena
1 (bases 5592 to 7391)
  U.S. Meat Animal Research Center
U.S. Dept. of Agriculture - Agricultural Research Service
P.O. Box 166, Clay Center, NE 68933
Tel: (402) 762-4166
Fax: (402) 762-4173
   1 others
   Quality: 40.00 Length: 12
Ratio: 3.333 Caps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
                      SIS
  to: 333
  sequence tagged site
  111111:::||||:::||||:::|||||||||:::
   ų
   1 TyrArgLeuLeulleArgArglleAlaLeuArgTyr 12
   83
  from: 1

    .333
    /organism="Bos taurus"

   .326)
   Primer A: AGGAACCCATAGGCAGACAC
Primer B: GCTGGCAAAGAGAAATTC
STS size:
Location/Qualifiers
   88
  Align seg 1/1 to reverse of: G18985
  104. .326
104. .123
complement(307.
a 64 c 88
  STS sequence; primer;
                    333 bp
   G18985.1 GI:1223442
   096137
096137.1 GI:2072510
  Contact: Roger Stone
  (bases 1 to 333)
   Cow Markers
Unpublished (1996)
   alignment_block:
US-08-653-294-17 x G18985/rev
                                    cow STS BMS2840.
   seq_name: gb_ba2:APU96137
seq_documentation_block:
LOCUS G18985
  taurus.
   Bos taurus
  Stone, R.T
   91
   G18985
   primer_bind
   alignment_scores
  primer_bind
   KEYWORDS
SOURCE
ORGANISM
                                      DEFINITION
   ORGANISM
   BASE COUNT
   ACCESSION
VERSION
KEYWORDS
  TITLE
JOURNAL
   JOURNAL
REFERENCE
AUTHORS
TITLE
   ACCESSION
VERSION
  AUTHORS
TITLE
   JOURNAL
REFERENCE
  AUTHORS
  REFERENCE
   REFERENCE
  STS
  FEATURES
   COMMENT
  SOURCE
   ORIGIN
```

CDS

```
repeat_region
   DEFINITION
ACCESSION
VERSION
KEYWORDS
  ORGANISM
  REFERENCE
   AUTHORS
  TITLE
  SOURCE
   /41 . 855
'note-"inverted repeat D, copy 2; stem-loop formation from
.nverted repeat D facilitates the -1 frame shift during
   /translation-"MKAYSLDFRQKIFDTYKTGGISQRQLANKFCVSLGFIEKLLKQY
RETASIAPKVRTKQTPPKLNEEQMKILEEIVEAKNDLTLSEIRFILKEKTGITIGIST
VDRMLQRIEISLKKKHCTPQKKRLKEFNY"
   DVRESMKLGTVTYVETRGGFLENLRSIFNTSPSGPTPPGFRPINIARYGPSNMAKSLR
DDLSWFLRYARTAIVAGDFNITVONTERASLSSTFR
DPDABATYAIVALGENTRAASLSSTFR
DPDABATYAIVALGENTRAASLSSTFR
DPDABATIVALGETRAASLSSTFR
TGLSATEKNEVIKAAYRGIFFRAPTPSKKLRQRESGDQGGLQLPQIYFSBABRREKFVMR
TGLSATEKNEVIKAAYRQIFFRDITRAYSLSISDLESKVKNGDISMKEFVRRLAKSPL
YQCPYQPPTFT INSRVIELAFRHILGREPSREEVOKTSGIISMGGLPALVDALVDSBEY
SDYRGEETVPYLRGLGGGAQGCRNMQPQODLENYSAEPRRVPGFITTPAAYDRLDD
HPYGSGNDPLEIQFGAIFPKETRNFSTSPAPFGKDTRILLHQGFGINNQVSNPSAG
   LAPGSLGPRVFKLDOLPGTIGKKAAKGASVKFSESSTOAVIKATYLOVFGRDYYEGOR
LKVQEIKLENGEISVRDFVRALAKSDLFRKLYWTPFYVCKAIEYIHRRLLGRPTYGRQ
ENNKYFDIASKKGLYAVVDAILDSLEYTETFGEDTVPYERYLTPAGVALRQLRVGTIR
   DLAAQAKQMIKSKPLFIELGRSYNDGRGGSVEVGVGTTRRKPARITRLINGIGGAEKO
LVINAIYRQVLDVFSGQVPDXYRRTELDSKLRNGEISVREFVREIASSEIYRKRFYTP
YPNTKVIEFLFRHLLGRAPATQGEIRQYNKLLADNGLRAAVEAIVDSPEYSRYFGEDV
  /translation="MSVKASGGSSVARPQLYQTLAVATITQAEQQDRFLGRGELDELA
SYFASGAKRLEIAQLLTENSEIIVSRAANRIFVGGSPMAFLEKPREPELAMAAVGGGG
   EDVANVEKQETPRFVELGTVKENRTQPDIDFRINQGVTKQREQTKVFKRVAGIKDKAA
   TPYPNTKVIELGTKHFLGRAPIDQAEIRKYNQILATQGIRAFINALVNSQEYNEVFGE
   DIVPYRREPILPAANFPNIQKLYNQLIKQNNDVVIPSFKPVQARIQSDKIPILAKAIA
   <810. .1421
/note="orfB of ISAn1; follows translation frame-shift</pre>
   'product="phycobilisome core-membrane linker protein"
'protein_id="AAC97589.1"
'db_xref="GI:2072515"
  /rpt_type=inverted
1417. 1432
/note="ISAn1 terminal inverted repeat, copy 2 (IRR)"
   VPYPRFPSLPAGNYLGSVQAAADLVKQSWSSLSPSTLTGRPGDR
   818. .831
/note="inverted repeat D, copy 1"
/rpt_type=inverted
   591. 1602
note="inverted repeat E, copy 1"
  1609. 1620
note="inverted repeat E, copy 2"
'rpt_type=inverted
1624. 1637
  // rept_type=inverted
1606. 1619
/note="direct repeat B, copy 1"
// rept_type=direct
  624. [1637
hote="direct repeat B, copy 2"
  /protein_id="AAC97586.1"
/db_xref="G1:2072512"
  'rpt_type=inverted
   /transl_table=11
   /rpt_type=direct
908. 1911
   codon_start=1
transl_table=11
   1908. .5323
/gene="apcE"
   gene="apcE"
   925. .5323
gene="apcE"
   translation
   repeat_region
  repeat_region
  repeat_region
  repeat_region
  repeat_region
   repeat_region
  repeat_region
```

gene

RBS

```
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I (bases 1 to 29283)
I
   02-SEP-1999
   Caenorhabditis elegans cosmid F14B6, complete sequence 281502
281502.1 GI:2814053
   to: 7948
  Length: 12
Gaps: 0
Percent Identity: 58.333
  note="inverted repeat F, copy 1"
   /note="inverted repeat F, copy 2"
   /rpt_type=direct
5356. .5382
/note="direct repeat D, copy 1"
   /rpt_type=direct
5388. 5401
/note="direct repeat E, copy 1"
   3
  5
   repeat C, copy 3"
  4
   5
  "mote-"direct repeat D, copy 2"
'n
   /note="direct repeat C, copy /rpt_type=direct 5352 5358 /note="direct repeat C, copy
      copy
  repeat E, copy
  Align seg 1/1 to reverse of: APU96137 from: 1
  ບັ
   ы́
   repeat C,
   /rpt_type=direct
5402. .5415
/note="direct repeat
   repeat
  'rpt_type=inverted
   DNA
   5416. .5429
/note="direct repower
/rpt_type=direct
5425. .5450
         /rpt_type=direct 5338. .534.
   /rpt_type=direct
5345. .5351
  rpt_type-direct
  'rpt_type=direct
  338. .5344
/note="direct
   Caenorhabditis elegans.
Caenorhabditis elegans
   alignment_block:
US-08-653-294-17 x APU96137/rev
   29283 bp
  40.00
3.636
91.667
   seq_name: gb_in1:CEF14B6
   seq_documentation_block:
LOCUS CEF14B6
  alignment_scores:
Quality:
Ratio:
   Percent Similarity:
   elegans
  repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
   repeat_region
```

```
trna
   gene
  trna
  gene
  gene
   gene
   CDS
   CDS
   bin/displaydb-wormaceclass-Sequence tobject=F14B6
Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

IMPORTANT: This sequence is not the entire insert of clone F14B6. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left and of clone F41B3 is at 29177 in this sequence. The
  The end of this sequence (29177. .29283) overlaps with the start of
   /translation-"MFSVFEWILIFFGILNWFKFTQPSTPEPASRFFTRVCQQLRETV LIEIDSSGYVOPFVSIVEEGEKPYFSPHYGCAECMQWMDVYGEQPHYVEETEDODTDE GVEESEIEDSDFDDQTTFPAPLSPETENFIEDKMKFHFQATDIINEYLGKGT DWGIVSNLIRISQYFXQVOLKQVSSKSSMKEIEGILKSLQKEFEQEIEGLNGEISEAE ENNESDIDESFEFVENLELDSDFE"
   /protein_id="CAB54218.1"

\[ Jab_xref="03:5824443" \]

\translation="WGICVPRWEFFLFUVVGFVTSLTIAIMSSIMYFLID

EMTSDSLFEFLLVAFYIDIVLILYAIVVGIAYRCCGRLVDNSIKETSINYSVSSNGEA
   true right end of clone C15C6 is at 19321 in this sequence. The start of this sequence (1. .109) overlaps with the end of sequence
  /note="cDNA EST yk242e8.5 comes from this gene; cDNA EST yk442e8.3 comes from this gene; cDNA EST yk47b10.5 comes from this gene; cDNA EST yk47b2.3 comes from this gene; cDNA EST yk47b2.5 comes from this gene; cDNA EST yk608e9.3 comes from this gene;
   Submitted (06-NOV-1996) Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu on Jan 28, 1998 this sequence version replaced gi:1665918. Coding sequences below are predicted from computer analysis, usin predictions from Genefinder (P. Green, U. Washington), and other
   For a graphical representation of this sequence and its analysis
   complement(join(2938. .3065,3115. .3212,3260. .3345))
/gene="F14B6.7"
  complement(join(947. .1390,1835. .2063,2114. .2169))
/gene="F1486.1"
  complement(join(4016. .4423,4517. .5309,5485. .5820,
6093. .6275,6563. .6657))
/gene="F14B6.2"
   /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
  /db_xref="SPTREMBL:062161"
   /protein_id="CAB04105.1"
//db_xref="G1:3875879"
  complement(2938. .3345)
/gene="F14B6.7"
  complement(4016. .6657)
   /clone="F1486"
complement(947. .2169)
/gene="F1486.1"
   Nature 368 (6466), 32-38 (1994)
  http://webace.sanger.ac.uk/cgi-
   Location/Qualifiers
  /chromosome="I
   /codon_start=]
   /codon_start=1
  available information.
  (bases 1 to 29283)
   Direct Submission
  281537
  sednence
   White, S.
  281034
  source
JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
JOURNAL
   gene
   gene
   gene
   CDS
   CDS
  CDS
  FEATURES
  COMMENT
```

```
join(17155. 17218,17267. 17455,17898. 18232,18389. 18591,
19031. 19178,19319. 19537)
/gene="F1486.6"
  comes from this gene; DNA EST EMBL: 088102 comes from this gene; CDNA EST EMBL: 09873 comes from this gene; CDNA EST EMBL: 09873 comes from this gene; CDNA EST yk198f11.5 comes from this gene; CDNA EST yk328e12.3 comes from this gene; CDNA EST yk338a7.3 comes from this gene; CDNA EST yk338a7.3 comes from this gene; CDNA EST yk40463.5 comes from this gene; CDNA EST yk40463.5 comes from this gene; CDNA EST yk40465.5 comes from this gene; CDNA EST yk415a6.3 comes from this gene; CDNA EST yk415a6.3 comes from this gene; CDNA EST yk415a6.3 comes from this gene; CDNA EST yk415a6.3 comes from this gene; CDNA EST yk43010.3 comes from this gene; CDNA EST yk43010.3 comes from this gene; CDNA EST yk50953.3 comes from this gene; CDNA EST yk50312.3 comes from this gene;
   DSNNIITSPEYFDESSEEPEFANGESECHRWINRYGENIA ENGLEDENTYTY
SETSDSELGQDSPNYBLEEPEFANGESECHRWINRYGENIA ENGEEDSEDETDYE
SETSDSELGQDSPNYBLSEALNYCIENFOQLYDEYVRHKDFHERSQLLRYLEECLGNY
NSFLQNEENLYDDDISTGACALLNETAEKLKOMFSSSGISGRKESSEGTNKDLIKFGEL
ERGDBEEDDDDDESYYGGEEDSSDEDLDEOGGESSIEPRLSETFKKSEARRSLSS
KEAPYKDLYTYGKFRDEHEDLEESENBPRMSDEAEKLYEDKIIEESDESFDIIGRDE
ELDDDSNGKEEBELELDYTQEDSEDBOFFSL"
17155 . 19537
   /protein_id="CAB04109.2"
/bc_xref="G1:5824444"
/db_xref="STREMBL.562165"
/translation="WRARKILITYAILASTLAYRYYSORTMEFLIEEDQMCLQREWYE
SEFFCQHSEILNVFNKFKFSLKFFKKSNJFNNIIYSKFTISSOINSTADJGNSYQISF
  /translation="MSTSSSVLPTTPIGKQQVIDLKAGAILRENARKSVLFFGCPLSV
VLVLIVLIKCLCISFWIIREHETFDFRCAAWNGGQPTDYMYRAKRSIAFEKSDPRKFS
KIPDDDDDDNSKTDVINKKDKKKRPLYGRSTSPANDIISDAPKIDPRLDFGPLPPNFQ
   RKIDSNHIPAVPPYEPDDDLPMTMVTLTNTQIVQLSGEETGVVKMKTIRNRVEKVGS
DEEQFIEIDIANAPRIYVSKIKSRHGGEBEBHFDLLKELKKDEBEKEKKKEKKKGKG
LKKAKKLTEAEKLLNNSTSTSVIPDTAVSRKPKGKGLKKSKKLNQKPKSDEEVTKQPR
  ANMOGKIKEVVMAEAKLFGDIVVTSMEDRYSKLSFKTLTLLLFGVSKVPSAQLIGKID
  GDVLFFPNLFLSTIKNENSMINVTSASVYGKIAEAGVPIVSNCCKRFLKYNFRRNSLI
SFGCTRYAFYLAGPFYLYTRSAALRLLEASKHRNFHKIEDTLITGVLADDTDVSRVQL
HRINLGQEKGTDLVFAWHSPLNDPEYKDLXYKTMSSQQFKEKLRLQEINVT"
   HLVGKSSSLSPTTPRPKSSWANGVLDPODPNFSNOGOIRGYPMOKASRRPSATTASPS
EKDEDEEKLKLSESTRAMMDMDELKYTTFLAPKTTEGTKQVEEGVKEVIQEAHERSQK
PMLKETFEEATTSTEKPLPGGMSKDQWEKKKEAFEAYTPPISLSDLQPSHSSHSGPAQ
   APQHIHFESASSTPSTPPAFHFIPPSSEAPYYVEINDADTETYVSSYTPMYRPVFEN
MGHLESTTKSYDPLHEVSFESFFCCVGQLLCHFVFDP"
complement (9869. .9940)
/gene="F1486.t2"
   /db_xref="GI:3875878"
/db_xref="SPTREMBL:062160"
/translation="MLSFLQSFFKSLGYEDYFKPIAPSSPRFFTKYCNETQKKITIVI
  SDVOSTFKWIHIPKISGSPEILLIVLSRPDDFSRRNVIRHTWMSQENEIKYLFLIGLG
   preliminary predicted using tRNAscan-SE-1.11; preliminary prediction; similar to tRNA-Met" 13752. 13823 /gene="F1486.t1" 15024
  /note="CAT Met M-tRNA; predicted using tRNAscan-SE-1.11;
prelliminary prediction; similar to tRNA-Met"
complement(9869. .9940)
/gene="F1486.t2"
  /note="predicted using Genefinder; cDNA EST yk329e12.5
  Join(15024, .15079,15134. .15329,15847. .16695)
/gene="F14B6.3"
   'note="cDNA EST yk549c2.3 comes from this gene"
  /db_xref-"SPTREMBL:062162"
'protein_id="CAB04106.1"
'db xref="GI:3875880"
   Id-"CAB04104.1"
  5024. .16695
gene="F14B6.3"
   17155. .19537
/gene="F14B6.6"
   /codon_start=1
  /codon_start=1
  13752. .13823
/gene="F14B6.
```

```
Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Blazel, R.G., Chew, M., Doyle, C.M., Farfan, D.E., Flangan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Kim, S. H., Lee, B., Lomottan, M.A., Mak, J., Madda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacheb, J. M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M. Direct Submission

10. Submitted (20-0CT-1998) Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley Drosophila Genome Project, MS 64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road, Berkeley, CA 94720, Wational Laboratory, MS 64-121

Berkeley Drosophila Genome Project
Lawrence Submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121

Berkeley, CA 94720

For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu.

Library locations: 53-17, 90-16, 5-27.
   Direct Submission
Submitted (03-NoV-1999) Wellcome Trust Genome Campus, Hinxton,
Cambridgeshire, CB10 18A, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 4, 1999 this sequence version replaced 9i:6065938.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the
  /note-"These three pls were completed as a project. The coordinates are Pl end to Pl end. DS02501 (D281) extends from bp 1 to bp 85,627. DS01529 (D280) extends from bp 74,691 to bp 155,821. DS01589 (D279) extends from bp 126,132 to bp 207,672. " 42102 c 41711 g 62161 t
   /clone="Pls DS01589 (D279), DS01529 (D280), and DS02501
  23-NOV-1999
*** SEQUENCING IN
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 229644)
   Homo sapiens chromosome X clone RP13-348B13, PROGRESS ***, in unordered pieces.

    .207672
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

   Length: 12
Gaps: 0
Percent Identity: 41.667
   39804 ITTCGAATCATAATTAAAAGGGTTGCAATTCAATAT 39839
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   from: 1
  /chromosome="2L"
  /map="28B1-28B4
   AL121872
AL121872.2 GI:6249374
HTG; HTGS_PHASE1.
   seq_documentation_block:
LOCUS HSB348B13 229644 bp
   to: AC005834
  Ratio: 3.333
Percent Similarity: 100.000
  US-08-653-294-17 x AC005834
   40.00
   seq_name: gb_htg1:HSB348B13
   Homo sapiens
   Quality:
  Pavitt, R.
  61698
  human.
   alignment_scores:
  alignment_block
   Align seg 1/1
  BASE COUNT
ORIGIN
  DEFINITION
   ACCESSION
VERSION
KEYWORDS
  TITLE
   ORGANISM
  REFERENCE.
AUTHORS
  TITLE
JOURNAL
  FEATURES
  COMMENT
  COMMENT
  Drosophila melanogaster (Subclones in sac from P1 clones DS01589 (D279), DS01529 (D280), and DS02501 (D281)) DNA.

SM Drosophila melanogaster Arthropoda; Tracheata; Hexapoda; Insecta; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

E (Celniker, S.E., George, R.A., Galle, R.F., Hoskins, R.A., Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.F., Baxter, E., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Karra, K
   join[23603...23727,23784. .24048,24104. .24209,24287. .24373,
24425. .24635,24799. .24965,25030. .25343,25388. .25514,
25566. .25580,25729. .25933,25988. .26251)
join(20434. .20524,21137. .21250,21298. .21659,21969. .22168,
22218. .22344,22393. .22482,22538. .22684)
/gene="F14B6.4"
  /db_xref="SPTREMBL:062164"
/translation="MSVAAKPKRLDLQGIRGLAILSVLGFHFYPALFPNGYLGVDQFF
VLSGFLMCMLLKRAENEPTCTLITLFYSKRFKRILPLYLLIILLSMISLYTIFPDTSI
  AIKLSGLLSYAFFFFTPSNTSFNSVFARIWOFLIGMIVFLLSSHSKKSPEAEKNIEEC
KRIEDDEBNYOKAOKPSIHLISYFPLISILILCIIPYQUNDFVYPPLYLAFGALM
LISSSMLILSKNILTYYIGDISYSLYLIHWPIYAYWKLAFDGDVNLILLSLLSSIILAI
IVFEFFEKWYLKLSSTSIGLLIVFLFFLNVILINKDELIPDREENNNHNSSMNTDDAI
  ETNQKSAMRALLFVSNAPKSVQDDYFTMLARAVDIFTHTWSLSVEVQFYFLVPFIFLF
   21-OCT-1998
(D279), DS01529
   2 (bases 1 to 207672)
Celniker,S.E., George,R.A., Galle,R.F., Hoskins,R.A.,
  AC005834 207672 bp DNA INV Drosophila melanogaster DNA sequence (P1s DS01589 (D280), and DS02501 (D281)), complete sequence. AC005834 AC004777 AC005733 AC004717 AC004718 AC005834.1 GI:3776556
   Percent Identity: 58.333
  3030 TACCGACTACTATCGCGTAGAGTATTAATACAATAT 3065
   1 TyrArgLeuLleArgArgIleAlaLeuArgTyr 12
  to: 29283
   /protein_id="CAB04108.1"
/db_xref="G1:3875882"
  from: 1
  23603. .26251
/gene="F14B6.5"
   Unpublished (1997)
  40.00
   83,333
  Align seg 1/1 to: CEF14B6
   US-08-653-294-17 x CEF14B6
  seq_name: gb_in2:AC005834
  seq_documentation_block:
Locus AC005834 2
   Percent Similarity:
   alignment_block:
  DEFINITION
   ACCESSION
VERSION
  ORGANISM
   gene
   JOURNAL
REFERENCE
   KEYWORDS
SOURCE
   REFERENCE
  AUTHORS
  AUTHORS
   CDS
                               CDS
   TITLE
```

contence may change as work continues. The sequence may change a continue of the continues of the continues of the continues. The sequence may change a continue of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of the continues of th

```
Submitted (07-5EP-1999) Nematode Sequencing Project, Sanger Centre, Submitted (07-5EP-1999) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RO, UK and Department of Genetics, Washington University, St. Louis, Wo 63110, USA. E-mail: hes@sanger.ac.uk or re@ematode.wustl.edu
On Aug 10, 1999 this sequence version replaced gi:4938508.
Order of segments is not known; 800 n's separate segments.
INPORTANT: This sequence is unfaished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
  CEY47HI0 296589 bp DNA HTG 07-SEP-1999
Caenorhabditis elegans chromosome I clone Y47H10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.
  Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
1 (bases 1 to 296589)
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
  NOTE: This is a 'working draft' sequence. This record will be updated with the finished sequence as soon as it is available and the accession number will
  1. .229644
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP13.348B13"
/clone="RP13.348B13"
/s1906 c 32427 g 57543 t 47255 others
   2401 others
   0 13
   Percent Identity: 70.000
   Location/Qualifiers
1. 296589
/organism="Caenorhabditis elegans"
  to: 229644
   Length:
Gaps:
   92582 t
  Gabs:
  3 LeuLeuIleArgArgIleAlaLeuArgTyr 12
  /db_xref="taxon:6239"
/chromosome="1"
   /clone="Y47H10"
55009 c 53606 g
  Location/Qualifiers
   from: 1
  HTG; HTGS_PHASE1.
Caenorhabditis elegans.
Caenorhabditis elegans
   Z95311.10 GI:5725202
   to: HSB348B13
   alignment_block:
US-08-653-294-17 x_HSB348B13
  Quality: 40.00
Ratio: 4.000
Percent Similarity: 100.000
   Direct Submission
   40.00
   seq_name: gb_htg1:CEY47H10
   preserved
  seq_documentation_block:
  60513 a
  phage etc
   alignment_scores:
Quality:
Ratio:
   92991
  McLay, K
   alignment_scores:
   as
be
   Align seg 1/1
   source
   source
  BASE COUNT
  DEFINITION
  ORGANISM
   BASE COUNT
   TITLE
JOURNAL
   REFERENCE
AUTHORS
   ACCESSION
  VERSION
KEYWORDS
SOURCE
  FEATURES
  FEATURES
  COMMENT
  ORIGIN
  ORIGIN
```

```
/codon_start=1
/bpotein_id="CaA02953.1"
/db_xref="G1:2300907"
/translation="ATFEIVNRCSYTWWAAASKGDAALDAGGRQLNSGESWTINVEPG
/translation="ATFEIVNBCOSYLTWRCKRGRPPTTADFSTMQYGKDYIDI
SNIKGENWARTDCYPDDSGSGICKTGGODGALKKRGRPPTTADFSTMQYGKDYIDI
SNIKGENWARTSPTRGCRGVRCAADIVGQCPAKLKAPGGGCNDACTVFQTSEYCCT
TGKCGPTEXSRFFKRLCPDAFSYVLDKPTTVTCPGSSNYRVIFCPTA"
   Cyanelle Thaumatococcus daniellii
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida;
Zingiberales; Marantaceae; Thaumatococcus.
1 (bases 1 to 624)
Uriach Maraal, J., Rubio-Susan, V., Patino-Martin, C., Iossif, R.E.,
Blade-Pique, J.
  /note="unnamed protein product; Protein sequence is in conflict with the conceptual translation"
  07-MAR-1997
  Preparation process of a natural protein sweetener Patent: EP 0684312-A 7 29-NOV-1995; UROUIMA S A (ES)
UROUIMA S A (ES)
Other publication ES 2080689 96020
Other publication FI 951868 951022
Other publication FI 951868 951022
Other publication CA 2147541 951022.

Cocation/Qualifiers

ce 1. .624
//organism="Thaumatococcus daniellii"
  PAT
Percent Identity: 58.333
   Length: 12
Gaps: 0
Percent Identity: 58.333
  /tissue_type="ARILS"
/cell_type="POLLEN MOTHER CELL"
1..621
  Align seg 1/1 to: CEY47H10 from: 1 to: 296589
  A46810 624 bp DNA
Sequence 7 from Patent EP0684312.
A46810.1 GI:2300906
   Align seg 1/1 to: A46810 from: 1 to: 624
   /cyanelle
/db_xref="taxon:4621"
/dev_stage="ADULT"
  147 g
   39.00
3.545
91.667
Percent Similarity: 83.333
                                     alignment_block:
US-08-653-294-17 x CEY47H10
  alignment_block:
US-08-653-294-17 x A46810
  miracle fruit.
   seq_documentation_block:
LOCUS A46810
   seq_name: gb_pat:A46810
   Quality:
Ratio:
Percent Similarity:
  103
  alignment_scores
  DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  FEATURES
SOURCE
  BASE COUNT
ORIGIN
   REFERENCE
AUTHORS
  TITLE
JOURNAL
   CDS
   COMMENT
```

THIS PAGE BLANK (USPTO)

```
Polynucleotide sequence fro TIM gene. Nuclear transloca
               TIM gene. Nuclear transloca
Timeless gene. New protein
Enterococcus faecalis genom
   Claim 1: Page 1853-1855; 2084pp; English.

Claim 1: Page 1853-1855; 2084pp; English.

A computer readable medium has been developed which has recorded on it.

A computer readable medium has been developed which has recorded on it.

X12938 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importence. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring progression of disease, and for identifying agents which can be used to modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the collypeptides encoded by the Enterococcus faecalis nucleotide sequences can be used in vaccines to prevent or attenuate an Enterococcal
   12-FEB-1999 (first entry)
EST clone DT478.
EST clone DT478.
EST clone protein; haematopoiesis regulator;
EST clone provent, activin; inhibin; tumour invasion suppressor; EST; human;
chemotaxis; chemokinesis; haemostasis; gene therapy; thrombolysis;
Homo sapiens.
W09845437-A2.
  WPI: 99-045171/04.
New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
   19-MAR-1999 (first entry) Enterococcus facealis genome contig SEQ ID NO:603. Enterococcus facealis contig; detection; Enterococcus recals; contig; detection; Enterococcus infection; vaccine; attenuation; computer readable medium; ds.
  738 T;
  2469
   Length: 12
Gaps: 0
Percent Identity: 50.000
 4444
5198
5198
6835
  483 G;
  Align seg 1/1 to reverse of: X13540 from: 1 to:
   1322 TICCAGCITCITCIAACGCGGGITTCGCTTCGGTAI 1287
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
1.8e+03
2.2e+03
2.2e+03
2.9e+03
  471 C;
   12 NOV-1998.
04-MAY-1998; U08985.
14-NOV-1997; US-066009.
06-MAY-1997; US-044031.
16-MAY-1997; US-046655.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Dillon PJ, Kunsch CA;
90.99
89.63
89.63
87.25
   X13540 standard; DNA; 2469 BP. X13540;
   BP.
  771 A;
  seq_documentation_block:
ID V88170 standard; cDNA; 321
34.00
34.00
34.00
   alignment_block:
US-08-653-294-17 x X13540/rev
  seq_name: N_Geneseq_36:X13540
   38.00
3.455
91.667
  seq_name: N_Geneseq_36:V88170
   Enterococcus faecalis. W09850555-A2.
  2469 BP;
   seq_documentation_block
   Quality:
Ratio:
   Percent Similarity:
N_Geneseq_36:X20635
N_Geneseq_36:T60333
N_Geneseq_36:X27127
N_Geneseq_36:X13141
   alignment_scores
   Sequence
   Chloroperoxidase gene. Enzymat Chloroperoxidase cpan. Use of Enterococus factalis genome of S. cerevisiae scauring genome of S. cerevisiae scauring genome of S. cerevisiae scauring genome of S. cerevisiae scauring genome of S. cerevisiae scauring genome of S. cerevisiae scauring genome of Aureobasidin resistance gene of Aureobasidin resistance gene of Polynucleotide sequence from to present mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant beta-toxin expression mutant expression from the man gene signature HUMGS08571 Polynucleotide sequence from the man gene signature HUMGS08571 Polynucleotide sequence from the man neuronal nicotinic acety Haemophilus adhesion protein HIMA encophilus adhesion protein enco
  Lucilia cuprina ecdysteroid re
TIM coding sequence. Nuclear t
Drosophila Timeless gene prote
Drosophila semaphorin I cDNA.
Lung cancer associated gene. N
Lung cancer associated gene. N
Lung cancer associated gene. N
   Lung cancer associated gene. N
Enterococcus facealis genome of
TIM splice variant coding sequ
Drosophila Timeless gene prote
  About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
   out_format :
   1176
3382
3382
11314
11314
1202
2225
3336
3356
3356
44114
44114
4110
  428.18
552.84
552.84
552.84
552.84
552.84
552.84
1.46+03
1.46+03
1.46+03
1.66+03
2.86+04
3.56+03
1.36+04
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
1.36-09
  ESCOTE 1
151.66
39.11
420.45
1.7e+03
16.50
24.93
   .3e+03
.4e+03
.4e+03
.5e+03
OM of: US-08-653-294-17 to: N_Geneseq_36:*
   69.47
85.76
  ZSCOTE
110.34
120.91
102.39
91.54
124.42
102.25
100.20
100.21
   93.14
93.14
92.06
  1111.18
105.08
101.5.08
991.56
997.75
993.39
92.91
92.82
92.91
92.82
   Search time (sec): 590.520000
  Database: N_Geneseq_36:*
Database sequences: 311585
Database length: 125096042
  Search information block:
Query: US-08-653-294-17
Query length: 12
   Command line parameters:
   Strd
                                 Date: Feb 8, 2000 1:28
   N_Geneseq_36:X07550
N_Geneseq_36:Y04441
N_Geneseq_36:Y18840_5 +
N_Geneseq_36:T19288
N_Geneseq_36:T19288 +
N_Geneseq_36:T19288 +
N_Geneseq_36:T19288 +
   N_Geneseq_36:V88170
N_Geneseq_36:V80665
N_Geneseq_36:Q79140
N_Geneseq_36:Q81920
N_Geneseq_36:T38465
  N_Geneseq_36:T09350
N_Geneseq_36:T09355
N_Geneseq_36:T5612
N_Geneseq_36:T51612
N_Geneseq_36:X07549
N_Geneseq_36:X07549
   N_Geneseq_36:V53425
N_Geneseq_36:X13210
N_Geneseq_36:V12200
   N_Geneseq_36:T00803
   N_Geneseq_36:X13540
  6: X21079
  :T84032
  N_Geneseq_36:T41477
  _Geneseq_36:V60302
_Geneseq_36:T60335
   _Geneseq_36:X27128
  Geneseq_36:X40189
  N_Geneseq_36:T60334
N_Geneseq_36:X27129
   N_Geneseq_36:X40190
   N_Geneseq_36:
N_Geneseq_36:
N_Geneseq_36:
N_Geneseq_36:
N_Geneseq_36:
  N_Geneseq_36
  Genesed_36
  .Genesed_36
  N_Geneseq_3
N_Geneseq_3
  -THREADS=1
```

```
phosphate metabolism, modulate inflammatory function or innate
  alignment_scores:
 ovary, pitulitary, retina and colon cDNA libraries

"Towary, pitulitary, retina and colon cDNA libraries

"Towary, pitulitary, retina and colon cDNA libraries

"Towary, pitulitary, retina and colon cDNA libraries

"The present sequence represents an expressed sequence tag (EST), and is

"The present sequence represents an expressed sequence tag (EST), and is

"The present sequences and protains encoded by them are predicted to

"The serverted EST sequences lacitated from a variety of human tissue

"Sources. The EST sequences and protains encoded by them are predicted to

have useful biological activities which would make them suitable for

treating, preventing or ameliorating medical conditions in humans and

animals, although no supporting data is given. Suggested activities

include nutritional activity, immune stimulating or suppressing activity,

haematopoiesis regulating activity, tissue growth activity,

activity, acadherin/tumour invasion suppressor activity, tumour inhibition

activity, The EST sequences are also stated to be useful for gene
   Human DNAX toll-like receptor DTLR3 encoding cDNA.

DNAX toll-like receptor; DTLR; Drosophila toll receptor; IL-1 receptor; interleukin 1 receptor; phosphate metabolism; innate immunity response; modulate inflammatory function; morphological effect; immunological disorder; ss.
  Agostino MJ, Jacobs K, Lavallie ER, McCoy JM, Merberg D, Racie LA, Spaulding V, Treacy M; WPI; 99-070078/06.
New polynucleotides encoding human secreted proteins - derived from
   e.g. alter
  DNAX toll-like receptors, DTLR 2-10 - used to,
  Quality: 36.00 Length: 12
Ratio: 3.273 Gaps: 0
Percent Similarity: 91.667 Percent Identity: 50.000
  51 G;
  Bazan JF, Hardiman GT, Kastelein RA, Rock FL;
WPI; 99-059670/05.
P-PSDB; W86351.
Human DNAX toll-like receptors, DTLR 2-10 - u
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   to: 321
   80 C;
   Location/Qualifiers
1. .2715
   /*tag= a
/product= "DTLR3"
   from: 1
  seq_documentation_block:
ID V80665 standard; cDNA; 2715 BP.
   79 A;
   /*tag= b
64. .2712
/*tag= c
  15-MAR-1999 (first entry)
                                      (GEMY ) GENETICS INST INC.
  seq_name: N_Geneseq_36:V80665
   12-NOV-1998.
07-MAY-1998; U08979.
05-MAY-1998; US-076947.
07-MAY-1997; US-044293.
22-JAN-1998; US-072212.
(SCHE ) SCHERING CORP.
   . .63
           10-APR-1998; U06956.
10-APR-1997; US-837312.
   Align seg 1/1 to: V88170
  alignment_block:
US-08-653-294-17 x V88170
  321 BP;
  WO9850547-A2.
   Homo sapiens
  alignment_scores:
   sig_peptide
  mat_peptide
  Sequence
   therapy
```

```
Through the transpose of the property of the present sequence encodes human DTLR3 (laim) 13; Page 104-108; 171pp; English.

Claim 13; Page 104-108; 171pp; English.

The present invention specifically described are: (1) a fusion protein given in the present invention. Also described are: (1) a fusion protein comprising a DTLR protein or peptide; (2) a binding compound, preferably an antibody fragment which specifically binds to a DTLR protein or peptide; (3) a nucleic acid encoding a DTLR protein or peptide; (3) an uncleic acid encoding a DTLR protein or peptide; (4) an expression vector comprising the nucleic acid of (3); and (5) a host cell comprising the vector of (4). The host cell of (3) and (5) a host cell comprising the vector of (4). The bost cell of (3); and (5) a host cell comprising the vector of (4). The bost cell of (3); and (5) a host cell comprising the vector of (4). The bost cell of (3); and (5) a host cell comprising the vector of (4). The host cell of (3); and (5) a host cell comprising the vector of (4). The bost cell of (5) and (5) a host cell comprising the vector of (4). The host cell of (3); and (5) a host cell comprising the vector of (4). The host cell of (5) and (5) a host cell comprising the vector of (4). The host cell of (5) and (5) a host cell comprising the vector of (4). The host cell of (5) and (5) a host cell comprising the vector of (4). The host cell of (5) and (5) a host cell comprising the vector of (4). The host cell of (5) and (5)
   seq_documentation_block:

ID 079140 standard; cDNA; 9487 BP.

AC 079140;

DT 07-SEP-1995 (first entry)

DE Hepatitis C virus; HCV; non-B; HC-G9; treatment; ss. Hepatitis C virus; HCV; non-A non-B; HC-G9; treatment; ss.
  aa:Cys
aa:Ser
aa:Leu
aa:Thr
aa:Pro
   aa:Ala
aa:Arg
aa:Ser
aa:Lys
aa:Tyr
aa:Asp
aa:Val
  aa:Lys
aa:Gln
  aa:Leu
aa:Pro
   aa:Ala
   aa:Pro
   aa:His
   aa:Ser
  aa:Ile
   aa:Ala
   Ratio: 3.600 Gaps: 10 Percent Similarity: 100.000 Percent Identity: 60.000
   7973,
  pos:7956.
pos:7959.
pos:7962.
pos:7965.
pos:7968.
   pos:7971.
pos:7974.
   pos:7986.
pos:7989.
   pos:7995.
   pos:7992
  Align seg 1/1 to: V80665 from: 1 to: 2715
   Dos:7977
  2 ArgleuLeuIleArgArgIleAlaLeuArg 11
  Location/Qualifiers 342. .9377
  /transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
/transl_except.pr/
  /*tag= a
/transl_except= p
/transl_except= p
/transl_except= p
  /transl_except= f
/transl_except= f
/transl_except= f
   seq_name: N_Geneseq_36:Q79140
   alignment_block:
US-08-653-294-17 x V80665
```

```
Align seg 1/1
  T00803;
   =
   interferon gamma claim, and the properties of the control of the control of the control of the control of the control of the control of the control of the control of the control of control of control of the control of co
  08-SEP-1995 (first entry) interferon-gamma binding oligonucleotide 8. Interferon-gamma binding oligonucleotide 8. Interferon gamma; inhlbition; binding; immunomodulation; septic shock; rheumatoid arthritis; HIV infection; ss.
   A hepatitis C virus gene and oligo-nucleotide(s) - used for the treatment of hepatitis C claim 1; Pages 10-15; 41pp; Japanese. 079140 is the hepatitis C virus (HCV) gene HC-G9 cDNA, it encodes the protein described in R67588. Both the cDNA and protein can be used in the treatment of HCV infection Sequence 9487 BP; 1905 A; 2798 C; 2687 G; 2097 T;
   Oligo-nucleotide(s) which bind to interferon-gamma - used for modulating, inhibiting or enhancing the activity or function of
/transl_except= pos:8028. .8030, aa:Gly /transl_except= pos:8031. .8033, aa:Thr /transl_except= pos:8034. .8036, aa:Ser
   Align seg 1/1 to reverse of: Q79140 from: 1 to: 9487
   28
   Length: 11
Gaps: 0
Percent Identity: 63.636
  Gaps: 0
Percent Identity: 58.333
  29 G;
  Length:
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   Beutel BA, Coppola GR;
   16 C;
  alignment_block:
US-08-653-294-17 x Q79140/rev · ..
   seq_documentation_block:
ID Q81920 standard; RNA; 98 BP.
  25 A;
   13-MAY-1993; JP-147133.
(IMMO ) IMMUNO JAPAN KK.
WPT: 95-040318/06.
P-PSDB: R67588.
  36.00
3.600
83.333
  05-JAN-1995.
17-JUN-1994; U06897.
18-JUN-1993; US-079677.
17-MAR-1994; US-210222.
(PHAR-) PHARMAGENICS INC.
   seq_name: N_Geneseq_36:Q81920
  Ratio: 3.182
Percent Similarity: 100.000
   35.00
  alignment_block:
US-08-653-294-17 x Q81920
   13-MAY-1993; 147133
   98 BP;
  WPI; 95-051993/07
   Quality:
Ratio:
  Ouality:
Ratio:
Percent Similarity:
   Bertelsen AH,
  Synthetic.
WO9500529-A.
   alignment_scores:
   alignment_scores:
   22-NOV-1994
```

```
24-APR-1997.

24-APR-1997.

21-OCT-1996; GB-021568.

R JUCCT-1996; GB-021568.

R JUCCT-1997; GB-021568.

R WIT: 97-245121/22.

Pellivering active peptide(s) and antigens in non-pathogenic bacteria per particularly for inducting or regulating protective immune response Disclosure; Page 16; 49pp; English.

P Delivering active peptide(PP) and/or antigen (Ag), where each of a promoter is under the control of a promoter for expression in a non-invasive or non-pathogenic bacterium (e.g. the present lactococcus lactis Pl promoter), can be used to transform such a bacterium. The bacterium, which expresses the PP and/or Ag.

Depending on the nature of the PP and/or Ag, the delivery method used to regulate growth, survival, differentiation, effector function and susceptibility to infection of cells and tissues, boost the immune response to colonise amcosal, or other tissues, modulate the immune response of inflammatory or tumour cells, induce apoptosis in tumour ersponse against a pathogen, regulate infiltration of normal tissues by inflammatory or tumour cells, induce apoptosis in tumour cells or down regulate the immune response in treatment of allergy, autoimmune and other immunity related diseases. The method is survival in human or especially veterinary medicine, with the bacterium formulated as a vaccine. The bacterium can express an Ag, particularly one of low immunogenicity, together with an adjuvant, becamend of a particularly one of the immined of the site of application there should be no systemic and local responses can be improved, and since should be no systemic side effects.

Sould be no systemic side effects.
  09-FEE-1998 (first entry)
Lactococcus lactis P1 promoter.
Non-invasive; non-pathogenic; bacterium; bacteria; P1 promoter;
transformation; expression; delivery; antigen; vaccine; ss.
Lactococcus lactis.
  94
   Length: 12
Gaps: 0
Percent Identity: 50.000
  Align seg 1/1 to reverse of: T38465 from: 1 to: 142
  10 G;
   1 TyrArgLeuLeulleArgArglleAlaLeuArgTyr 12
  73 TATAGATTAATAAAATGTTATCATTAGATTAT 38
   12
  30 AGGCUCGUAUUCGCCGGAUCGUCUUAGAGUAU 62
   2 ArgleuleulleArgArglleAlaLeuArgTyr
       ::
2
to: Q81920 from: 1
  seq_documentation_block:
ID T00803 standard; DNA; 1830 BP.
   seq_documentation_block:
ID T38465 standard; DNA; 142
   27-APR-1996 (first entry)
   35.00
3.500
83.333
   alignment_block:
US-08-653-294-17 x T38465/rev
   seq_name: N_Geneseq_36:T38465
   seq_name: N_Geneseq_36:T00803
   Chloroperoxidase gene
  Quality:
Ratio:
  Percent Similarity:
  WO9714806-A2.
  alignment_scores:
  Sequence
```

```
ន្តម្ភិទ្ឋ
  WPI: 95-358625/46.

WPI: 95-358625/46.

The continuity of the company of the content of the cont
  Use of halo peroxidase enzymes - in antifouling paints and methods for determining the halide concn. of liquids
Example 3; Fig 6; 48pp; English.
A CDNA sequence (T03875) codes for a chloroperoxidase (R82249) of Curvularia inaequalis. The CDNA was obtd. by PCR using primers based on known sequences of the gene and by 5'RACE. The approtetin encoded by the CDNA can be reactivated by addn. of vanadate. The CDNA can be inserted into a vector for expression in procaryotic host cells.
   Chloroperoxidase cDNA.
Chloroperoxidase; haloperoxidase; antifouling paint; preservative;
halide; chloride; ss.
   Wever R;
   Chloroperoxidase; vanadium haloperoxidase; disinfectant;
   Ter Steeg PF;
  Quality: 35.00 Length: 12
Ratio: 3.500 Gaps: 0
Percent Similarity: 83.333 Percent Identity: 50.000
   Van Schijndel JWPM, Vollenbroek EGM,
  31-MAR-1994; EP-200893.
24-JUN-1994; NL-001048.
(SCHE-) STICHTING SCHEIKUNDIG ONDERZOEK IN NEDER.
(TEWE-) STICHTING TECH.
  910 TACAACCAGATCGTACGTCGCATCGCAGTTACGTAC 945
  1 TyrArgLeuLeulleArgArglleAlaLeuArgTyr 12
   Align seg 1/1 to: T00803 from: 1 to: 1830
                                antimicrobial; antiseptic; ss.
Curvularia inaequalis strain CBS102.42.
  (UNIL ) UNILEVER NV.
(UNIL ) UNILEVER PLC.
Barnett P, Hondmann DH, Simons LH,
  Location/Qualifiers
  T03875 standard; cDNA; 2088 BP
   (first entry)
   seq_name: N_Geneseq_36:T03875
  .1229
   /*tag=
   12-OCT-1995.
31-MAR-1995; E01229.
31-MAR-1994; EP-200893.
   Curvularia inaequalis.
   alignment_block:
US-08-653-294-17 x T00803
   12-OCT-1995.
30-MAR-1995; NL0123.
31-MAR-1994; EP-2008
   seg_documentation_block:
   Dekker HL, Van Scl
WPI; 95-358602/46.
P-PSDB; R82249.
   WO9527046-A2.
   WETENSCHAPPEN
   W09527009-A1.
   alignment_scores:
   25-APR-1996
  Wever R;
   ID DOT E PET THE PET T
```

```
Claim 1) Page 1261-1263; 2084pp; English.

A computer readable medium has been developed which has recorded on it

82 nucleotide sequences isolated from the Enterococcus faecalis genome.

82 nucleotide sequences, isolated from the Enterococcus faecalis genome.

83 to X13919 represent these nucleotide sequences which are primary nucleotide sequences, also known as contigs. The computer-based system can identify fragments of the Enterococcus faecalis genome with commercial importance. The products can be used to detect the presence of Enterococcus faecalis in samples. They can also be used for diagnosing Enterococcal infection in an animal and monitoring modulate the growth or pathogenicity of Enterococcus faecalis, or modulate the growth or pathogenicity of Enterococcus faecalis, or another related organism, in vivo or in vitro. In particular the products can be used in vaccines to prevent or attenuate an Enterococcal
   WPI; 99-045171704.

New isolated Enterococcus faecalis polynucleotides and polypeptides - used to develop products for the detection of Enterococcus and for use in vaccines for prevention or attenuation of Enterococcus
   19-MAR-1999 (first entry)
Enterococcus faecalis genome contig SEQ ID NO:268.
Enterococcus faecalis; contig; detection; Enterococcus infection; vaccine; attenuation; computer readable medium; ds.
Enterococcus faecalis.
The recombinant chloroperoxidase is utilised in halide (esp. chloride) analysis, or as an environmentally-friendly antifouling agent in ship paint.

Sequence 2088 BP; 465 A; 622 C; 531 G: 470 T.
  897
   Length: 12
Gaps: 0
Percent Identity: 50.000
  Length: 12
Gaps: 0
Percent Identity: 50.000
  359 G;
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   to: 2088
   to: 2311
  253 C;
   12-NOV-1998.

04-MAY-1998; U08985.

14-NOV-1997; US-066009.

06-MAY-1997; US-044031.

16-MAY-1997; US-046655.

(HUMA) HUMAN GENOME SCI INC.

Barash SC, Dillon PJ, Kunsch CA;
   Align seg 1/1 to: T03875 from: 1
   Align seg 1/1 to: X13205 from: 1
  X13205 standard; DNA; 2311 BP
   793 A;
   35.00
3.500
83.333
   35.00
3.182
91.667
  seq_name: N_Geneseq_36:X13205
   alignment_block:
US-08-653-294-17 x T03875
   alignment_block:
US-08-653-294-17 x x13205
  2311 BP;
  seq_documentation_block:
   Quality:
Ratio:
  Quality:
  Ratio:
  Percent Similarity:
   Percent Similarity:
  alignment_scores:
  alignment_scores:
  infection.
  infection.
  Sequence
```

```
Disclosure; Page 70-72; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant strains were prepared. Resistant gene scaurlk (Q75954) was isolated from 1 library, and resistant gene scaur2k (Q75956) from the other. A DNA fragment of scaurl was used as a probe to isolate a sensitive gene, scaurls (Q75955), from the sensitive strain. A T852A mutation leading to a F158Y conversion gave rise to the sesistance of scaurlk.
Sequence 2340 BP; 583 A; 462 C; 430 G; 865 T;
  Fundal chromosome integration vector contg. aureobasidin resistance gene - which acts as selection marker, useful in genetic engineering of fund selection marker, useful in genetic engineering of fund selection marker, useful in genetic engineering of fund selections. The wild-type aureobasidin sensitivity gene scaurISR (T09350) was obtained, from a genomic library of Saccharomyces cerevisiae using a mutant aureobasidin resistance gene (T09355) as probe. The gene encodes a protein (R88127) sensitive to aureobasidin. Mutagenesis of the gene at codon 240 resulting in a substitution, deletion or insertion at Ala-240 is used to impart aureobasidin resistance, and the mutated DNA may be used as a selectable
   29-MAR-1996 (first entry)
Aureobasidin sensitivity gene scauris.
Aureobasidin resistance; selectable marker; fungus transformation; chromosome integration vector; scauris; ds.
Saccharomyces cerevisiae.
   New genes regulating aureobasidin sensitivity – used to develop prods. for the diagnosis and treatment of diseases such as
   15-JAN 1996.

15-JAN 1995; 304165.

29-JUN 1995; JP-108501.

30-MAR-1995; JP-09595.

30-MAR-1995; JP-095931.

17-MAY-1995; JP-1041391.

17-MAY 1995; JP-1041391.

(TAKI ) TAKRAR SHUZO CO LID.

Kato I, Ogawa J, Okado T, Oshima A, Takesako K;

Yoshioka H;

WPI: 96-070176/08.

P-PSDB; R88127.
   Quality: 35.00 Length: 10
Ratio: 3.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
   from: 1 to: 2340
  2291 ATCTTAGTGAAAAGGTGGTTTTGCGTTAT 2320
  481 C;
  in fungus transformation.
  3 LeuLeulleArgArglleAlaLeuArgTyr 12
  Location/Qualifiers
28-DEC-1993; JP-348893.
(TAKI) TAKARA SHUZO CO LTD.
KALO I, OKAGA T, TAKESAKO K;
WPI; 95-023286/04.
   T09350 standard; DNA; 2340 BP.
   583 A;
  seq_name: N_Geneseq_36:T09350
   Align seg 1/1 to: Q75955
   alignment_block:
US-08-653-294-17 x Q75955
   2340 BP;
   seq_documentation_block:
   P-PSDB; R67690
  marker useful
Sequence 234
  EP-692534-A2
  alignment_scores:
   mycoses
    Disclosure; Page 67-68; 110pp; English.
Saccharomyces cerevisiae DKD5D, which is sensitive to aureobasidin, was mutagenized with EMS and genomic libraries of 2 resistant strains were prepared. Resistant gene scaurIR (Q75954) was isolated from 1 library, and resistant gene scaurIR (Q75956) from the other. A DNA fragment of scaurI was used as a probe to isolate a sensitive gene, scaurIS (Q75955), from the sensitive strain. A T852A mutation leading to a F158Y conversion gave rise to the resistance of scaurIR.
  04-AUG-1995 (first entry)
S. cerevisiae scaurlR gene.
Aureobasidin_resistance; aureobasidin_sensitivity; scaurlR gene; mycosis; antimycotic; fungicide, diagnosis; therapy; ds.
   S. cerevisiae scaurIS gene.
Aureobsasidin-resistance; aureobasidin-sensitivity; scaurIS gene;
mycosis; antimycotic; fungicide; diagnosis; therapy; ds.
Saccharomyces cerevisiae DKD5D.
  New genes regulating aureobasidin sensitivity - used to develop prods. for the diagnosis and treatment of diseases such as
   /*tag= b
/note= "base at position 1544 is unclear in the
  /*tag- a
/note- "bases at positions 765-66 are unclear
in the specification"
  Length: 10
Gaps: 0
Percent Identity: 50.000
   429 G;
  1514 TITAGGATAATCITCAGGAAGATAGCCCTTTITAI 1549
   Align seg 1/1 to: Q75954 from: 1 to: 2340
  461 C;
  2291 ATCTTAGTGAAAGGGTGGTTTTGCGTTAT 2320
   3 LeuLeulleArgArglleAlaLeuArgTyr 12
  Saccharomyces cerevisiae DKD5D.
Key Location/Qualifiers
  24-MAY-1993; JP-142523.
28-DEC-1993; JP-348893.
(TAKI ) TAKARA SHUZO CO LTD.
Kato I, Okada I, Takesako K;
WPI; 95-023286/04.
P-PSDB; R67689.
   specification"
   seq_documentation_block:
ID Q75955 standard; DNA; 2340 BP.
AC Q75955;
   BP
  584 A;
  seq_documentation_block:
ID Q75954 standard; DNA; 2340
AC Q75954;
  04-AUG-1995 (first entry)
  misc_difference 755. .766
  seq_name: N_Geneseq_36:Q75955
   seq_name: N_Geneseq_36:Q75954
  Quality: 35.00
Ratio: 3.500
Percent Similarity: 100.000
   01-DEC-1994.
16-MAY-1994; 063129.
24-MAY-1993; JP-142523.
   US-08-653-294-17 x Q75954
  misc_difference 1544
   16-MAY-1994; 063129
  2340 BP;
  alignment_scores:
   AU9463129-A.
   AU9463129-A.
  alignment_block:
```

Seguence

865 T;

411 G;

ID DT CENTRAL CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRACT CONTRAC

```
Fundal chromosome integration vector contg. aureobasidin resistance gene - which acts as selection marker, useful in genetic engineering of fung of fung.

Disclosure: Page 23-24; 66pp; English.

The aureobasidin resistance gene scaurlR (T09355) was obtd. from a genomic library of Saccharomyces cerevisiae following EMS mutagenesis. Comparison with the wild-type aureobasidin sensitive gene (T00350) showed a T to A mutation at position 852, resulting in a F158Y mutation in the encoded protein (R88132). The gene may be used as a selectable marker component of chromosome integration vectors used for fungus transformation.

S84 A; 505 C; 387 G; 864 T;
   Aureobasidin resistance gene scaurlR.
Aureobasidin resistance; selectable marker; fungus transformation;
chromosome integration vector; Saccharomyces cerevisiae; scaurlR;
   29-JUN-1994; JP-168611.
30-MAR-1995; JP-095955.
30-MAR-1995; JP-095955.
37-MAY-1995; JP-0959831.
37-MAY-1995; JP-141393.
(TAKI ) TAKARA SHUZO CO LID.
KALO I, Ogawa J, Okado T, Oshima A, Takesako K; Voshioka H; G-700176/08.
P-PSDB; R888132.
                             Length: 10
Gaps: 0
Percent Identity: 50.000
   Quality: 35.00 Length: 10
Ratio: 3.500 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 50.000
   to: 2340
   Align seg 1/1 to: T09355 from: 1 to: 2340
   2291 ATCTTAGTGAAAAGGGTGGTTTTGCGTTAT 2320
  2291 ATCTTAGTGAAAAGGGTGGTTTTGCGTTAT 2320
  3 LeuLeuIleArgArgIleAlaLeuArgTyr 12
   3 LeuLeuIleArgArgIleAlaLeuArgTyr 12
   Location/Qualifiers
380. 1585
/*tag= a
   Align seg 1/1 to: T09350 from: 1
   seq_documentation_block:
ID T09355 standard; DNA; 2340 BP
   29-MAR-1996 (first entry)
                             Quality: 35.00
Ratio: 3.500
Percent Similarity: 100.000
  seq_name: N_Geneseq_36:T09355
  seg_name: N_Geneseg_36:X20664
   alignment_block:
US-08-653-294-17 x T09350
   alignment_block:
US-08-653-294-17 x T09355
   17-JAN-1996.
15-JUN-1995; 304165.
  EP-692534-A2
  alignment_scores:
                alignment_scores:
   Synthetic.
```

```
Fraser CM;

WPI; 99-081273/07.

The isolated Treponema pallidum nucleic acids - used to develop are interponema pallidum nucleic acids - used to develop are interponema pallidum infections, particularly syphilis and therapy of T. pallidum infections, particularly syphilis is x20500-21243 represent polynucleotide sequences from the genome of Treponema pallidum. The sequences can be used for detection, and agnosis, characterisation, prevention and therapy for T. pallidum infections, particularly syphilis. They can also be used for detecting diseases related to Borrelia infections in animals, and for the production of blosynthetic products such as enzymes.

Sequence 2529 BP; 589 A; 670 C; 699 G; 567 T;
  detecting
05-MAY-1999 (first entry)
Polynucleotide sequence from the genome of Treponema pallidum.
Treponema pallidum infection; syphilis; Borrelia infection; animal; enzyme production; ds.
Treponema pallidum.
   οţ
   30-APR-1997 (first entry)
Curvularia verruculosa haloperoxidase gene.
Haloperoxidase; halide oxidation; halogenation; antimicrobial; disinfectant; ss.
   Haloperoxidase from Curvularia verruculosa - useful for oxidn. halide, halogenation and, in presence of hydrogen peroxide and thiocymate, as antimicrobial thiocymate, as antimicrobial claim 28; page 33-35; 58pp; English.
   Oxenboll KM
   to: 2529
  /*tag= b
/note= "primer aHaPl binding site"
2293. 2311
/*tag= c
/note= "primer aHaPlA binding site"
  Length: 11
Gaps: 0
Percent Identity: 72.727
  06-FEE-1997.
09-JUL-1996; U1458.
14-JUL-1996; US-001194.
(NOVO ) NOVO NORDISK BIOTECH INC.
(NOVO ) NOVO-NORDISK AS.
BENER RM, Cherry J, Fuglsang C, Halkier T, WPI; 97-132641/12.
  2398 TACAGATTATACGCCCGATCCATTGCGTTACGC 2366
   Align seg 1/1 to reverse of: X20664 from: 1
  Curvularia verruculosa strain CBS 147.63.
Key 477. 2279
/*tag- a
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArg 11
   complement (477. .496)
   seq_documentation_block:
ID T51612 standard; DNA; 2822 BP.
   30-DEC-1998.
23-JUN-1998, U13041.
24-JUN-1997; US-050667.
(HUMA-) HUMAN GENOME SCI INC.
  US-08-653-294-17 x X20664/rev
  35.00
4.375
72.727
   seq_name: N_Geneseq_36:T51612
  Quality:
   Percent Similarity:
   Ratio:
   P-PSDB; W12042
  WO9704102-A1.
   alignment_scores:
  primer_bind
   alignment_block:
   primer_bind
```

```
CC The haloperoxidase gene (T51612) of Curvularia verruculosa CBS.63 CC codes for an enzyme (W12042) that shows optimum activity at about CC deg C and pH 5.5, which retains at least 75% activity after CC incubation for 1 h. at pH 7.0 and 60 deg C in the presence of 0.1% CC H202, and which prefers bromide over chloride as substrate. It was CC solated from a genomic library using a PCR amplifted partial clone (see also T51613-14) as probe. The 2822 bp fragment in a positive CC plaque has been deposited (in pHAP4-1, in E. coli DH10B) as NRRL CC P1519. The gene can be used to express the haloperoxidase in cc transformed host cells for use in halide oxidation, cpd. CC halogenation and (with H202 and thiocyanate) as an antimicrobial. SQ Sequence 2822 BP; 651 A; 808 C; 674 G; 689 T;
```

THIS PAGE BLANK (USPTO)

3.6e+03 3.6e+03 3.6e+03 3.6e+03

82.51 82.51 82.51 82.51

```
Sequence 3, Application US/08466589
Fatent No. 5837489
GENERAL INFORMATION:
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
33.00
33.00
33.00
  seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-466-589-3
   seq_name: /cgn1_6/ptodata/2/ina/5D_COMB.seq:US-08-700-636-3
  Percent Identity: 58.333
   /cgnl_6/ptodata/2/ina/5c_COMB.seq:US-08-530-198-5 + 

cgnl_6/ptodata/2/ina/5c_COMB.seq:US-08-469-880-5 + 

/cgnl_6/ptodata/2/ina/5D_COMB.seq:US-08-728-470-5 + 

/cgnl_6/ptodata/2/ina/5D_COMB.seq:US-08-617-697-5 +
  E: Brown, Martin, Haller & McClaim
1660 Union Street
  <del>ب</del>
   732 TACTCGCTGATCATCCGGCGCGTGTCGTTCTAC 767
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   Length:
  Align seg 1/1 to: US-08-466-589-3 from: 1
  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTSEN VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,589
FILING DATE: June 5, 1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993:
APPLICATION NUMBER: US 08/028,031
FILING DATE: March 8, 1993:
ATTORNEY/AGENT INFORMATION:
NAME: Seldman, Stephanie L
  alignment_block:
US-08-653-294-17 x US-08-466-589-3
   REGISTRATION NUMBER: 33,779 REFERENCE/DOCKET NUMBER: 63
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
  INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1756 base pairs
  37.00
3.700
83.333
   CORRESPONDENCE ADDRESS: ADDRESSE: Brown, Ma
  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
  TYPE: nucleic acid
STRANDEDNESS: both
  39..1553
   STREET: 1660 Un
CITY: San Diego
  ZIP: 92101-2926
  seq_documentation_block
  both
  NAME/KEY: CDS
  Percent Similarity:
  USA
  Quality:
   TOPOLOGY: bo
  LOCATION:
US-08-466-589-3
   alignment_scores
  COUNTRY:
  2822
2822
  3395
  .9e+03
   -MODEL-frame-p2n.model -DEV-x1p
-MODEL-frame-p2n.model -DEV-x1p
-Q-(cgnl_1/USPTO-spool/US08653294/runat_04022000_160701_15794/app_query.fasta.1
-Q=(cgnl_1/USPTO-spool/US08653294/runat_04000_12000
-DB-ISSued_Patents_NA -OFMT-fastap -SUFFIX=rni -GAPOP-12.000
-GAPDXT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-QAPDXT-4.000 -MINMATCH-0.100 -LOOPEXT-0.000
-GAPDXT-4.000 -GAPDEXT-0.000 -YGAPOP-11.000 -YGAPDEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -YAAPOP-10.000 -YGAPDEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS=human40.cdi -LIST-45 -DOCALIGN-200 -THR_SCORE-pct
-MALICN-15 -MODE-LOCAL -OUTFWT-pfs -NORM-ext -MINLEN-0
-MAX.ERN-1000000 -USER-US08653294 -NCPU-6 -ICPU-3 -NO_XLPXY -WAIT
   702.1
   Sequence

| Sequence | Strd Orlg | ZSSCOLE | ESCOLE | DOCUMENTATION | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUED | CONTINUE
  82.51
  About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
   33.00
OM of: US-08-653-294-17 to: Issued_Patents_NA:*
   Database sequences: 207703
Database length: 57918730
Search time (sec): 310.290000
  Database: Issued_Patents_NA:*
  Search information block:
Query: US-08-653-294-17
Query length: 12
   Date: Feb 7, 2000 6:04
   Command line parameters:
  score_list:
```

```
NUMBER OF SEQUENCES:
  GENERAL INFORMATION:
APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Ellis, Steven B.
APPLICANT: Harbold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: Los Angeles
STARET: CA Angeles
STARET: CA Angeles
STARET: USA
STARET: USA
ZIP: 90071
  APPLICANT: Coppola, George R.
APPLICANT: Beutel, Bruce A.
APPLICANT: Bettelsen, Arthur H.
TITLE OF INVENTION: Inhibition of Interferon- with Oligonucleotides
  seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-210-222-8
  MEDIOM TIPE: FIDEPY GISK

COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,636

FILING DATE: 16-JUL-1996

CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031

FILING DATE: 08-MRR-1993

ATTORNEY/AGENT INFORMATION:
NAME: RELEAT STEPHONE: STEPHONE: 619-546-4737

TELECOMMUNICATION INFORMATION:
TELEFHONE: 619-546-4737

TELEFRA: 619-646-6737

   Percent Identity: 58.333
  Align seg 1/1 to: US-08-700-636-3 from: 1 to: 1756
  732 TACTCGCTGATCATCCGGCGCGCTGTCGTTGTTCTAC 767
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
                                       Sequence 3, Application US/08700636
Patent No. 5910582
  seq_documentation_block:
; Sequence 8, Application US/08210222
; Patent No. 5599917
; GENERAL INFORMATION:
   alignment_block:
US-08-653-294-17 x US-08-700-636-3
   Floppy disk
   Quality: 37.00
Ratio: 3.700
Percent Similarity: 83.333
  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
   ) NAME/KEY: CDS
) LOCATION: 39..1553
US-08-700-636-3
   TYPE: nucleic acid
STRANDEDNESS: both
  TOPOLOGY: both
MOLECULE TYPE: CDNA
    seq_documentation_block
   alignment_scores:
```

```
EE: NO. 58663930 NO. 5866393d1sk of No. 5866393th America, Inc.
405 Lexington Avenue, Suite 6400
   GENERAL INFORMATION:
APPLICANT: Fuglsang, Claus
APPLICANT: Halker, Torben
APPLICANT: Genboll, Karen M.
APPLICANT: Berka, Randy M.
APPLICANT: Cherry, Joel
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
TITLE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: NO. 58663930 NO. 586639341 Amer.
   seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-679-405-1
   Percent Identity: 63.636
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
ADDRESSEE: Cecchi, Stewart & Oistein
STREET: 6 Becker Farm Road
CITY: Roseland
STREET: New Jersey
CONTYRY: USA
ZIP: 07068
COMPUTRY: BADABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM
  Align seg 1/1 to: US-08-210-222-8 from: 1
   23550-114
   US/08/210, 222
  seq_documentation_block:
    Sequence 1, Application US/08679405
    Patent No. 5866393
  OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/210
FILING DATE: Unassigned
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: HERTON, Charles J.
REGISTRATION NUMBER: 28,019
  alignment_block:
US-08-653-294-17 x US-08-210-222-8
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
  REFERENCE/DOCKET NUMBER: 2:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
   CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174
COMPUTER READABLE FORM:
   SEQUENCE CHARACTERISTICS LENGTH: 98 BASES
  TELEFAX: 201-994-1744 INFORMATION FOR SEQ ID NO:
   Percent Similarity: 100.000
  STRANDEDNESS:
  alignment_scores:
   US-08-210-222-8
  STREET:
```

```
APPLICANT:
TITLE OF INVENTION: Haloperoxidases from Curvularia
TITLE OF INVENTION: Verruculosa and Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Novo Nordisk of North America, Inc.
STREET: 405 Lexington Avenue, Suite 6400
  seq_name: /cgn1_6/ptodata/2/ina/PCTUS9_COMB.seq:PCT-US96-11458-1
  COMPUTER: NEW IOEK

ZIP: 10174

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLOPPY disk
COMPUTER: PATENTER PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION TOWNER: PCT/US96/11458
FILING DATE: 9-JUL-1996
CLASSIFICATION:
  Gaps: 0
Percent Identity: 50.000
  Align seg 1/1 to: US-08-842-799-1 from: 1 to: 2822
   1377 TACAATCAGATTGTGCGTCGCATCGCAGTGACTTAC 1412
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   CLASSIFICATION DATA:
PULDA PELICATION DATA:
APPLICATION NUMBER: 08/679,405
FILING DATE: JULY 9, 1996
APPLICATION NUMBER: 60/001,194
FILING DATE: JULY 14, 1995
PILOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,534
FILING DATE: February 21, 1996
ATTONNEY/GENT INFORMATION:
NAME: Lambiris, Elas J.
REGISTRATION NUMBER: 33,728
REGISTRATION NUMBER: 33,728
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 867-0123
UMBER: US/08/842,799
16-APR-1997
  seq_documentation_block:
; Sequence 1, Application PC/TUS9611458
; GENERAL INFORMATION:
; APPLICANT:
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,194
  alignment_block:
US-08-653-294-17 x US-08-842-799-1
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
   LENGTH: 2822 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  35.00
3.500
83.333
   CDS
477..2276
          APPLICATION NUMBER:
FILING DATE: 16-APR-
CLASSIFICATION: 435
   New York
   Ratio:
Percent Similarity:
   Quality:
   ; NAME/KEY:
; LOCATION:
US-08-842-799-1
   alignment_scores:
   STATE:
   CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59654180 No. 5965418disk of No. 5965418th America, Inc. STREET: 405 Lexington Avenue, Suite 6400 CITY: New York STATE: New York COUNTRY: U.S.A.
   seq_documentation_block:
    Sequence 1, Application US/08842799
    Patent No. 5965418
    GENERAL INFORMATION:
    APPLICANT: Fuglsang, Claus
    APPLICANT: Halkier, Torben
    APPLICANT: Osenboll, Karen M.
    APPLICANT: Cherry, Joel
    TITLE OF INVENTION: Halpperoxidases from Curvularia
    TITLE OF INVENTION: Halpperoxidases from Curvularia
    TITLE OF SEQUENCES: 21
  seq_name: /cgn1_6/ptodata/2/ina/5D_COMB.seq:US-08-842-799-1
  Length: 12
Gaps: 0
Percent Identity: 50.000
     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
   Align seg 1/1 to: US-08-679-405-1 from: 1 to: 2822
  CURRENCE CONTRACT
CURRENCE CONTRACT
APPLICATION DATA:
APPLICATION NUMBER: US/08/679,405
FILING DATE: July 9, 1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,194
FILING DATE: July 14, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,534
FILING DATE: FEBURATY 21, 1996
ATTORNEY AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTATION NUMBER: 4441.210.
REGISTATION NUMBER: 4441.210.
TELEPHONE: (212) 867-0123
TELEPHONE: (212) 878-955
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2822 base pairs
TELEPACE AND SEG ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2822 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGIE
   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  alignment_block:
us-08-653-294-17 x us-08-679-405-1
   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
  35.00
3.500
83.333
  COMPUTER READABLE FORM:
  ; NAME/KEY: CDS
; LOCATION: 477...2276
US-08-679-405-1
   alignment_scores:
    Quality:
    Ratio:
    Percent Similarity:
```

```
to: 3096
   APPLICANT: Young, Michael W.
APPLICANT: Sehgal, Amita
APPLICANT: Sehgal, Amita
APPLICANT: Vosshall, Leslie B.
APPLICANT: Price, Michael
TITLE OF INVENTION: WICHEAR LOCALIZATION FACTOR ASSOCIATED
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
   from: 1
  seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-2
  Length: 11
Gaps: 0
Percent Identity: 63.636
   Align seg 1/1 to reverse of: PCT-US96-05320A-897
  2526 TICAGAITITAAAAICAAACGIATAGCCITGCGG 2494
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArg 11
  alignment_block:
US-08-653-294-17 x PCT-US96-05320A-897/rev
                           APPLICATION NUMBER: 08/476,102
FILING DATE: June 7, 1995
PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/487,429
FILING DATE: June 7, 1995
ATTORNEY/AGENT INFORMATION:
  ALTORNIA DE LETA K. STEFFE

REGISTRATION NUMBER: 35,688

REFERENCE/DOCKET NUMBER: 1488.

TELECOMMULCATION INFORMATION:
TELEPHONE: (202) 371-2500

INFORMATION FOR SEQ ID NO: 897:
SEQUENCE CHARACTERISTICS:
LENGTH: 3096 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 48-5800
TELEPHONE: 201 48-5800
   Sequence 2, Application US/08619198
Patent No. 5885831
  E: Klauber & Jackson
411 Hackensack Avenue
  Quality: 34.00
Ratio: 3.400
Percent Similarity: 90.909
            PRIOR APPLICATION DATA:
  COMPUTER READABLE FORM MEDIUM TYPE: Floppy
  CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
   linear
  seq_documentation_block:
   GENERAL INFORMATION:
   ; TOPOLOGY: 1
PCT-US96-05320A-897
   alignment_scores:
   STREET:
   APPLICANT: Hamilton O. Smith
APPLICANT: J. Craig Venter
TITLE OF INVENTION: Uncleotide Sequence of the Haemophilus Influenzae Rd Genome,
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Recele-
  seq_name: /cgn1_6/ptodata/2/ina/PCTUS9_COMB.seq:PCT-US96-05320A-897
   STATE: D.C.
COUNTRY: USA
ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
   Gaps: 0
Percent Identity: 50.000
  Align seg 1/1 to: PCT-US96-11458-1 from: 1 to: 2822
  1377 TACAATCAGATTGTGCGTCGCATCGCAGTGACTTAC 1412
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
  Length:
FILING DATE: 14-JUL-1995
PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 08/603,534
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REFERENCE/DOCKET NUMBER: 34,728
REFERENCE/DOCKET NUMBER: 4441.204-WO
TELECOMMUNICATION INFORMATION:
TELEPRAM: (212) 867-0123
TELEPRAM: (212) 878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2022 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
FORMATION STANDENES: SINGLE
  Human Genome Sciences
9410 Key West Avenue
Rockville, MD 20850
United States of America
Johns Hopkins University
720 Rutland Avenue
Baltimore, MD 21205
United States of America
Mark D. Adams
  PCI/US96/05320A
   Sequence 897, Application PC/TUS9605320A GENERAL INFORMATION:
  STATE: D.C.
  alignment_block:
US-08-653-294-17 x PCT-US96-11458-1
   April22, 1996
  MOLECULE TYPE: DNA (genomic)
  35.00
3.500
83.333
  ), NAME/KEY: CDS
; LOCATION: 477..2276
PCT-US96-11458-1
  APPLICATION NUMBER:
  seq_documentation_block:
   linear
  Quality:
Ratio:
Percent Similarity:
   alignment_scores:
   TOPOLOGY:
   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
```

```
TOPOLOGY: linear
MOLECULE TYPE: cDNA
DESCRIPTION: tim cDNA sequence wherein R at position 1335
   seq_name: /cgn1_6/ptodata/2/ina/5A_COMB.seq:US-08-121-713D-59
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTON REY/AGENT INFORMATION:
NAME: COSMAN, RACHARD #5,627
REGISTRATION NUMBER: 36,627
RESPENCE/DOCKET NUMBER: 36,627
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1873-4341
  Align seg 1/1 to reverse of: US-08-619-198-2 from: 1
  Length: 10
Gaps: 0
Percent Identity: 70.000
  APPLICANT: Goodman, Corey S.
APPLICANT: Goodman, Corey S.
APPLICANT: Matthes, David
APPLICANT: Matthes, David
APPLICANT: Bentley, David
APPLICANT: Bentley, David
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
  Drosophila melanogaster
   alignment_block:
US-08-653-294-17 x US-08-619-198-2/rev
  seq_documentation_block:
    Sequence 59, Application US/08121713D
    Patent No. 563956;
    GENERAL INFORMATION:
  INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3369 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
  34.00
3.778
90.000
  ; NAME/KEY: CDS
; LOCATION: 1..3369
US-08-619-198-2
  S
  HYPOTHETICAL: NC
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Dros
   Ratio:
Percent Similarity:
  Quality:
  USA
   ß
   ZIP: 94104
   alignment_scores:
  COUNTRY:
   STATE:
  FEATURE:
```

```
seq_name: /cgn1_6/ptodata/2/1na/5B_COMB.seq:US-08-835-268-59
   Align seg 1/1 to: US-08-121-713D-59 from: 1 to: 3560
  Gaps: 0
Percent Identity: 58.333
   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
FILING DATE:
   APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
ITILE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
  3151 TACACACACATCATATCTAACGTGGCGCTGCGATAT 3186
  ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200 CITY: San Francisco STATE: CA
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   PRICR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13.5EP-193
ATORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELECHONE: (415) 343-4341
TELEFRAX: (415) 343-4341
   ZIP: 94104
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
  alignment_block:
US-08-653-294-17 x US-08-121-713D-59
   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
   34.00
3.778
75.000
  TYPE: nucleic acid
STRANDEDNESS: double
  CDS
1..1953
  linear
   GENERAL INFORMATION:
APPLICANT: GOOGMAN
   CLASSIFICATION:
   Quality:
Ratio:
Percent Similarity:
   TOPOLOGY: 11ne
MOLECULE TYPE: C
FEATURE:
  USA
  ; NAME/KEY:
; LOCATION:
US-08-121-713D-59
  alignment_scores
  COUNTRY:
```

NAME/KEY:

Gaps: 0 Percent Identity: 58.333

3.778

Percent Similarity:

ဖ

```
seq_name: /cgn1_6/ptodata/2/ina/5D_COMB.seq:US-09-060-692-59
  Gaps: 0
Percent Identity: 58.333
  to: 3560
  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
FILING DATE:
   APPLICANT: Goodman, Corey S.
APPLICANT: Goodman, Alex L.
APPLICANT: Matthes, David
APPLICANT: Matthes, David
APPLICANT: Dentley, David R.
APPLICANT: O'CONNOR, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
   ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP STREET: 268 Bush Street, Suite 3200 CITY: San Francisco
   1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
  Align seg 1/1 to: US-08-835-268-59 from: 1
   CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-5EP-1993
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
   REFERENCE/DOCKET NUMBER: B94-002-1
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   eq_documentation_block:
Sequence 59, Application US/09060692
Patent No. 5935865
   alignment_block:
US-08-653-294-17 x US-08-835-268-59
   TELECOMMUNICATION INFORMATION TELEPHONE: (415)343-4341
   TELEFAX: (415) 343-4342
   SEQUENCE CHARACTERISTICS:
LENGTH: 3560 base pairs
  34.00
3.778
75.000
   INFORMATION FOR SEQ ID NO:
   TYPE: nucleic acid
STRANDEDNESS: double
; LOCATION: 1.1953
US-08-835-268-59
  TOPOLOGY: linear MOLECULE TYPE: CDNA
   1..1953
   GENERAL INFORMATION:
APPLICANT: GOODMAI
   USA
  NAME/KEY: CDS
   alignment_scores:
Quality:
  Quality:
Ratio:
Percent Similarity:
  alignment_scores:
   ;
US-09-060-692-59
  COUNTRY:
   STATE:
```

```
seq_name: /cgn1_6/ptodata/2/ina/PCTUS9_COMB.seq:PCT-US94-10151A-59
  seq_documentation_block:
Sequence 59, Application PC/TUS9410151A
Sequence 59, Application
GAPPLICANT:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR HOHBACH TEST ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STRATE: GA
COUNTRY: USA
ZIP: 94111-4187
  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEN PC compatible
COMPUTER: TEN PC compatible
COMPUTER: TEN PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: PCT/US94/10151A
FILING DATE: 13-SEP-1994
CLEASIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COSMON ALCHARD A.
REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
TELECOMMUTCATION INFORMATION:
TELECOMMUTCATION INFORMATION:
TELEFAX: (415) 781-1989
TELEFAX: (415) 781-1989
TELEFAX: (415) 789-3249
TELEFAX: (415) 399-3249
   seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-4
   Percent Identity: 58.333
  3151 TACACACACATCATATCTAACGTGGCGCTGCGATAT 3186
   3151 TACACACAACTCATATCTAACGTGGCGCTGCGATAT 3186
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   to: PCT-US94-10151A-59 from: 1
  Align seg 1/1 to: US-09-060-692-59 from: 1
  alignment_block:
US-08-653-294-17 x PCT-US94-10151A-59
alignment_block:
US-08-653-294-17 x US-09-060-692-59
   Quality: 34.00
Ratio: 3.778
Percent Similarity: 75.000
  TYPE: nucleic acid
STRANDEDNESS: double
  TOPOLOGY: linear MOLECULE TYPE: CDNA
   | NAME/KEY: CDS
| LOCATION: 1..1
| PCT-US94-10151A-59
   alignment_scores:
Quality:
   Align seg 1/1
```

```
seq_documentation_block:
; Sequence 4, Application US/08619198
; Patent No. 5885831
; GENERAL INFORMATION: Michael W.
APPLICANT: Young, Michael W.
APPLICANT: Sehgal, Amita
APPLICANT: Price, Jeffrey L.
; TILLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
; TILLE OF INVENTION: WITH CIRCADIAN RHYTHMS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
  MOLECULE TYPE: CDNA DESCRIPTION: tim CDNA sequence wherein R at position 1335
  seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-8
   COMPUTER: LOOPING TEACHER TOWN:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
ATTONEY/AGENT INFORMATION:
NAME: Jackson ESG., David A.
REGISTRATION NUMBER: 26,742
RECERENCE/POCKET UNMBER: 26,742
RECERENCE/POCKET UNMBER: 26,742
RELEPHONE: 201 487-5800
TELEFAK: 201 343-1684
  from: 1
   Percent Identity: 70.000
   Align seg 1/1 to reverse of: US-08-619-198-4
   1563 AGGCTTCTGGTGCTGCGGCTTGCCCTGCGG 1534
   2 ArgLeuLeuIleArgArgIleAlaLeuArg 11
  ORGANISM: Drosophila melanogaster
   alignment_block:
US-08-653-294-17 x US-08-619-198-4/rev
  STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
   Klauber & Jackson
   TELEX: 13351
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 4170 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
   34.00
3.778
90.000
   seq_documentation_block:
  linear
  alignment_scores:
Quality:
  USA
   Percent Similarity:
   ADDRESSEE:
   ; NAME/KEY:
; LOCATION:
US-08-619-198-4
  COUNTRY:
```

Sequence 8, Application US/08619198 Patent No. 5885831

```
APPLICANT: Vosshall, Lealle B.
APPLICANT: Price, Jeffrey L.
APPLICANT: Price, Jeffrey L.
APPLICANT: Myers, Michael
TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED
TITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rlauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STREET: New Jersey
COUNTRY: USA
ZIP: 07601
  TITLE OF INVENTION: NUCLEAR LOCALIZATION FACTOR ASSOCIATED ITLE OF INVENTION: WITH CIRCADIAN RHYTHMS
  seq_name: /cgn1_6/ptodata/2/ina/5C_COMB.seq:US-08-619-198-1
   from: 1
  Gaps: 0
Percent Identity: 70.000
   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,198
FILING DATE: 20-MAR-1996
CLASSIFICATION: 514
   Align seg 1/1 to reverse of: US-08-619-198-8
   1805 AGGCTTCTGGTGCGGGCTTGCCCTGCGG 1776
   2 ArgleuLeulleArgArglleAlaLeuArg 11
  ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   alignment_block:
US-08-653-294-17 x US-08-619-198-8/rev
  ATTONNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
-REFERENCE/DOCKET NUMBER: 600-:
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAK: 201 343-1684
  APPLICANT: Sehgal, Amita
APPLICANT: Vosshall, Leslie B
  Coung, Michael W.
   LENGTH: 5192 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
  TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   34.00
3.778
90.000
   TOPOLOGY: linear MOLECULE TYPE: CDNA
  GENERAL INFORMATION:
   Percent Similarity:
   Quality:
   alignment_scores;
```

```
ADDRESSEE: Klauber & Jackson

CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack Avenue
CITY: Hackensack
COUNTR: 10.07601

COUNTR: 10.07601

COUNTR: PLOPPY disk
WEDIUM TYEE: PLOPPY disk
COUNTR: STEEN COUNTR: STATE
COUNTR: JACKSON ESS., David A.
RECISTRATION NUMBER: 26.72
REPERRECE/DOCKET NUMBER: 26.72
REPERRECE/DOCKET NUMBER: 26.73
RECISTRATION NUMBER: 26.73
RECISTRATION NUMBER: 26.73
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.74
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMBER: 26.77
RECISTRATION NUMER: 26.77
RECISTRA
```

```
AQ815539 HS_5348_A2_A09_SP6E
AA478141 zu42e09.rl Soares o
  A0851612 724 bp DNA GSS 18-OCT-1999 CpG1352B CpIOWAgDNA1 Cryptosporidium parvum genomic similar to SKB1 homologue (negative regulator of mitosis) (regulator of Shk1, a p21(CdC42/Rac)-activated kinase (PAK)), genomic survey sequence. AQ851612 GI:6063307
   Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seg primer: T3
Class: shotgun.
   /db_xref__txxn:5807"
/dlob_lb="CplOWAgDNA1"
/lab_host="col1 XL2 Blue MRF'"
/note="Vector: pBlueScript II (SK-); Site_1: EcoRV; C.
parvum (IOWA isolate) genomic DNA was hydrodynamically sheared to produce fragments having a tight size distribution between 2-4 kb by Dr. Yvonne Thorstenson of the Stanford DNA Sequencing and Technology Center
   (http://sequence.www.stanford.edu/shear.htm). The randomly sheared gDNN was chromotographed on Sephacryl S-400 to remove any small fragments and DNN eluting in the void volume was subcloned into an EcoR V-digested, alkaline phosphatase-treated pBlueScript II (SR-) vector and transformed into E. coli strain XL2 Blue MRF'. Recombinant clones from the first plating of the library were selected for sequence analysis using T3 and T7
   Cryptosporidium parvum.

Cryptosporidium parvum.

Eukaryota: Alveolata: Apicomplexa: Coccidia: Eimeriida:

Eukaryotasporidiidae: Cryptosporidium.

Cryptosporidiudae: Cryptosporidium.

S Strong, W. B. and Nelson, R.G.

Cryptosporidium parvum GSS Project
Unpublished (1997)
On Sep 10, 1998 this sequence version replaced gi:3553959.

Contact: Nelson, R. G.

Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
  2 others
   to: 724
  11
0
90.909
  Location/Qualifiers
1. .724
/organism="Cryptosporidium parvum"
/strain="LOWA"
   Box 0811, San Francisco, CA 94143-0811, USA
  440
447
448
   Gaps:
Percent Identity:
  244 t
   from: 1
  Length:
376.35
383.03
383.98
  520
   1 TyrArgLeuLeulleArgArglleAlaLeuArg
  þ
   Align seg 1/1 to reverse of: AQ851612
124.17
124.04
124.02
  121
   alignment_block:
US-08-653-294-17 x AQ851612/rev
37.00
37.00
37.00
  93 c
  43.00
4.300
90.909
   primers.
   seq_name: gb_gss6:AQ851612
   seq_documentation_block:
  Francisco
   Ratio:
Percent Similarity:
  Quality:
  264
gb_gss3:B74688
gb_gss5:AQ815539
gb_est15:AA478141
   alignment_scores:
  LOCUS
  source
   ACCESSION
VERSION
KEYWORDS
  ORGANISM
  BASE COUNT
ORIGIN
  TITLE
JOURNAL
COMMENT
  REFERENCE
AUTHORS
  FEATURES
   SOURCE
  AQUELLEL CPG1352B CPIOWAGDNA1 C AL2010 9902121 r1 Appergillus AQU29209 CITB1-E12565K-TR CIT AUG05267 AUG05267 Bombyx mori p A1426843 mm95508.x1 Stratagene AV186651 AV182651 Yuji Kohara u AQU30530 CIT-HSP-230417 Kohara u AQU30530 CIT-HSP-230417 Kohara u AQU30530 CIT-HSP-230417 KOhara u AQU3089371 HE_5471_B2_CO_TTA RPC AGU30734 Homo sapiens genomic C AQU38810 HS_5056_Al_DOS_TY RPCI-1 AC02930 CIT-HSP-2340P9 JR CIT AQU3994 Arabidopsis thaliana 9 AQ16695 HS_3146_Al_B09_MR CIT AQ189484 HS_2061_Al_B09_MR CIT AQ05939 CIT-HSP-2340P9 JR CIT AC05939 CIT-HSP-2340P9 JF CIT AC05059 SWAMCAC12C11SK Brugia AQ108050 SWAMCAC12C11SK Brugia AQ108050 SWAMCAC12C11SK Brugia AQ1060698 CIT-HSP-2346DB JR CIT-F29413 HSPD19267 HM3 Homo sapie F24270 HSPD19267 HM3 Homo sapie F24270 HSPD10415 HM3 Homo sapie F24270 HSPD10415 HM3 Homo sapie F24270 HSPD10415 HM3 Homo sapie AM197413 xm42908 x1 NCI_CGAP_PC AM18257 256693 x1 N
   AA265909 mz72c02.rl Soares mous
AA572328 v188a05.rl Stratagene
A1050480 uc86g01.yl Sugano mous
AW091827 EST285007 tomato mixed
AU031224 AU031224 Rice cDNA frd
  B60584 CIT-HSP-2013F20 TRC CIT-
AQ075747 CIT-HSP-2354G2 TR CIT-
8085646 HS 5555 A2 E12 SP6E FB
B31543 HS-1011-A2-A06-MF.abi CI
   About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
  out_format : pfs
   ESCOIE 38.74 438.74 67.75 67.75 112.71 59.23 191.49 191.49 292.23 191.49 292.24 202.94 202.94
  ZSCOTE
1141.90
11340.92
11340.52
1133.58
1139.58
1139.50
1129.84
1129.66
1129.66
1129.66
  OM of: US-08-653-294-17 to: EST:*
   Search information block:
Query: US-08-653-294-17
Query length: 12
Database: EST:*
Database sequences: 4538634
Database length: 1887831982
Search time (sec): 8553.36000
  443.00
441.00
441.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
440.00
44
  ₹
  Command line parameters:
  4:03
   Strd
   gb_est11:F24270
gb_est16:C26415
gb_est15:AA523786
gb_est19:AA748739
gb_est44:AW197413
   gb_est27:A1426843
gb_est56:AV182651
gb_gs8:A0015503
gb_est39:AW127330
gb_gs8:AM27331
gb_gs8:AQ433893
gb_gs8:AQ433893
  9b-9ss10:3019

9b-9ss10:A02019

9b-9ss9:A016659

9b-9ss9:A0137850

9b-9ss10:A055939

9b-est21:A1678132

9b-est22:A1056050

9b-est22:A1056218

9b-est22:A1056218

9b-9ss6:A0835306

9b-9ss1:A0808CV
  gb_est10: AA182557
gb_est24: AI202172
gb_est33: AV090309
gb_gss8: B0584
gb_gss8: AQ075747
gb_gss6: AQ826246
  gb_gss3:B31543
gb_est11:AA265909
gb_est15:AA572328
gb_est22:AI050480
gb_est28:AW091827
gb_est24:AU031224
  Date: Feb 8, 2000
  gb_est24:AI210579
gb_gss13:AQ429279
gb_est26:AU005267
  gb_gss6:AQ851612
  score_list:
```

```
Shao,S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and Venter, J.C.
Venter, J.C.
Venter, J.C.
Ves of Bac End Sequences from CalTech Libraries for Sequence-Ready
Map Building
Unpublished (1997)
Other_GSSs: CITHLEL-2565KS.TF
Contect: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tes: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
  http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
   /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoR1; Site_2: EcoR1;
CalTech Human BAC Library D"
1 128 c 101 g 122 t
  seg_documentation_block:
LOCUS AUO05267 810 bp mRNA EST 19-JAN-1999
DEFINITION AUO05267 Bombyx mor1 p50(Daizo) Bombyx mor1 cDNA clone ws30474,
   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Pitrysia; Bombycoidea; Botablishment of cDNA database of Bombyx mori Unpublished (1999)
On Jan 19, 1998 this sequence version replaced gi:2150717.
Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Homo.
  Length: 11
Gaps: 0
Percent Identity: 81.818
  Genome Research Group
National Institute of Radiological Sciences
Anagawa 4.9-1, Inage, Chiba 263-8555, Japan
Email: kmita@uexs64.nirs.go.jp
   1. 513
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="25656s"
/clone_lib="CITBI-E1"
  1 TyrArgLeuLeulleArgArglleAlaLeuArg 11
  Location/Qualifiers
  from: 1
  AU005267.1 GI:4162638
  /sex-"male"
Eukaryota; Metazoa;
Eutheria; Primates;
1 (bases 1 to 513)
  domestic silkworm.
  41.00
4.100
90.909
   to: AQ429279
   alignment_block:
US-08-653-294-17 x AQ429279
  seq_name: gb_est26:AU005267
  mRNA sequence.
AU005267
  Bombyx mor1
   Ratio:
Percent Similarity:
  Quality:
   162
   alignment_scores:
   Align seg 1/1
  VERSION
KEYWORDS
SOURCE
ORGANISM
  BASE COUNT
ORIGIN
   source
   TITLE
JOURNAL
COMMENT
   REFERENCE
AUTHORS
  ACCESSION
  REFERENCE
  AUTHORS
   JOURNAL
   FEATURES
  TITLE
   COMMENT
  E checktoria.

I (bases 1 to 377)

Kupfer,D., Gray,J., Hausner,J., Lai,H., Martin,W., Aramayo,R., Prade,R. and Roe,B.
An Aspergillus nidulans EST Database
Unpublished (1988)

On Jan 19, 1998 this sequence version replaced gi:2285706.

Other_ESTs: j9c12all fi
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
We anticipate the future release of the CDNA clones to the Fungal
   /strain="FGSC A26"
/db_xref="taxon:5072"
/db_xref="taxon:5072"
/db_yref="taxon:5072"
/clone="j9012al"
/clone=lib="Appergillus nidulans 24hr asexual
developmental and vegetative cDNA lambda zap library"
/tissue_type="vegetative mycelia, asexual structures"
/note="vector: pBlueScript SK-; Site_1: EcoRI; Site_2:
Ahol; 5' end of cDNA cloned into EcoRI site of pBluescript
3' end of cDNA cloned into Xhol site of pBluescript"
   seq_documentation_block:
LOCUS A1210579 377 bp mRNA EST 19-OCT-1998
DEFINITION j9c12a1.T Aspergillus nidulans 24hr asexual developmental and vegetative cDNA lambda zap library Emericella nidulans cDNA clone j9c12a1 5', mRNA sequence.
   A0429279 513 bp DNA GSS 24-MAR-1999 CITBI-EI-2565K5.TR CITBI-EI Homo sapiens genomic clone 2565K5, genomic survey sequence.
   Emericella nidulans
Eukaryota; Fungi; Ascomycota; Eurotiales; Trichocomaceae;
Emericella.
  to: 377
  Length: 11
Gaps: 0
Percent Identity: 72.727
  /organism="Emericella nidulans"
  from: 1
  1 TyrArgLeuLeulleArgArgIleAlaLeuArg 11
  Align seg 1/1 to reverse of: AI210579
   Location/Qualifiers
1. .377
   103 g
   AQ429279.1 GI:4497045
   AI210579.1 GI:3772521
   alignment_block:
US-08-653-294-17 x AI210579/rev
   Emericella nidulans.
  Ratio: 3.727
Percent Similarity: 100.000
  41.00
                  gb_est24:AI210579
  seq_name: gb_gss13:AQ429279
  seq_documentation_block:
   Homo sapiens
   Quality:
  AQ429279
   74
  human.
   alignment_scores:
  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  LOCUS
DEFINITION
   ORGANISM
  TITLE
JOURNAL
COMMENT
   BASE COUNT
  REFERENCE
AUTHORS
                       sed_name:
  ACCESSION
   VERSION
KEYWORDS
SOURCE
```

FEATURES

Marie Land

1

```
to: AV182651
   ಡ
   Percent Similarity:
  Quality:
Ratio:
Percent Similarity:
   Ratio:
   37
  alignment_scores:
  alignment_scores:
   Align seg 1/1
  BASE COUNT
ORIGIN
  ACCESSION
VERSION
KEYWORDS
SOURCE
   ORGANISM
  TITLE
JOURNAL
COMMENT
  BASE COUNT
ORIGIN
  REFERENCE
   AUTHORS
  FEATURES
  Eutheria; Medazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 21)

S Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R., The WashU-NCI Mouse EST Project 1999

C Onpublished (1999)

On May 7, 1998 this sequence version replaced gi:3119865.

Contact: Marra M/WashU-NCI Mouse EST Project 1999

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1810
   seq_documentation_block:
LOCUS
LOCUS
A1426843 271 bp mRNA EST 09-MAR-1999
DEFINITION mm95b08.x1 Stratagene mouse heart (#937316) Mus musculus cDNA clone
IMAGE:536151 3', mRNA sequence.
   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone was previously sequenced on the 5' end only, this new
data is from the 3' end
High quality sequence stop: 232.

Location/Qualifiers

1. 271

/organism="Mus musculus"
   /tissue_type="heart"
/dev_stage="13 day embryos"
/lab_host="SOLR (kanamychn resistant)"
/lab_host="Organ: heart; Vector: pBluescript SR-; Site_1:
ECORI; Site_2: Xhof; Cloned unidirectionally. Primer:
Oligo dr. 93 pooled NIH/Swiss 13 day embryo hearts.
   /db_xref="itaxon:10090"
/clone="IMAGE:536151"
/clone_lib="Stratagene mouse heart (#937316)"
                                    1. .810
/organism="Bombyx mori"
/strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws30474"
/clone=lib="Bombyx mori p50(Daizo)"
4 a 118 c 215 g 203 t
   to: 810
  Length: 12
Gaps: 0
Percent Identity: 58.333
  from: 1
  1 TyrargLeuLeuIleArgArgIleAlaLeuArgTyr 12
'CREST project by JST'
Location/Qualifiers
   Align seg 1/1 to reverse of: AU005267
   /strain="NIH/Swiss"
   AI426843
AI426843.1 GI:4272769
   /sex="pooled"
  alignment_block:
US-08-653-294-17 x AU005267/rev
  41.00
3.727
91.667
   seq_name: gb_est27:AI426843
   Mus musculus
   house mouse
  Quality:
   Ratio:
   Percent Similarity:
PROJECT
  274
  alignment_scores:
  EST
  BASE COUNT
ORIGIN
   ORGANISM
   TITLE
JOURNAL
  VERSION
KEYWORDS
SOURCE
  REFERENCE
   AUTHORS
                  FEATURES
  FEATURES
   COMMENT
```

```
Kohara,Y., Shin-i,T., Thierry-Mieq,J., Thierry-Mieq,D., Mitsuki,H., Nishigaki,A., Motchashi,T., Zeng,Q., Watanabe,H., Sugimoto,A., Sano,M., Miyata,A., Mitani,Y., Iida,K., Uesugi,H., Sugiyama,Y. and Expressed genes in C.elegans
  seq_documentation_block:
LOCUS AV182651
DEFINITION AV182651 Yuji Kohara unpublished cDNA:Strain N2 hermaphrodite
embryo Caenorhabditis elegans cDNA clone yk640g7 3', mRNA sequence.
ACCESSION AV182651
WERSION AV182651. GI:5562552
   Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 300)
Kohara, Y., Shin-1, T., Thierry-Wior 1 metron
Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTTTTTTTTTTT 3'" adaptor to 66 g = 59 t
  /db_xref="taxon:6239"
/clone="yk640g7"
/clone_lib="vuji Kohara unpublished cDNA:Strain N2
/sex="hermaphrodite"
   Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi:3189500.
Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
  others
  Length: 12
Gaps: 0
Percent Identity: 58.333
  Gaps: 0
Percent Identity: 72.727
   /organism-"Caenorhabditis elegans
  ų
  Length:
   71
  to: 300
   1 TyrArgLeuLeulleArgArglleAlaLeuArg 11
  18 TATCGTCTTGCCCGCCGTGTTGCTGCTCGT 50
  Email: ykohara@lab.nig.ac.jp.
Location/Qualifiers
1. .300
   /dev_stage="embryo" 68 c 54 g
  from: 1
   from: 1
  /strain="N2"
  40.00
4.000
83.333
  4.444
  Align seg 1/1 to: AI426843
  40.00
  alignment_block:
US-08-653-294-17 x AI426843
  alignment_block:
US-08-653-294-17 x AV182651
   seq_name: gb_est36:AV182651
```

Wed Feb

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

```
Medicago.

1 (bases 1 to 310)
Fedorova,M., Pierson,B.L., Samac,D.A., Gantt,J.S., Vance,C.P.,
Gonzales,M.B. and Ellis,L.
ESTS from the infected leaf cDNA library of Medicago truncatula
Unpublished (1999)
On Jul 7, 1999 this sequence version replaced gi:5406207.
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612-625-7219
Fax: 612-649-5058
Email: vance004@marcon.tc.umn.edu
Developmental stage: leaf infected with Colletotrichum: Date:
9/15/99; submitted to the Database of Expressed Sequence Tags
(dbEST) on 10/22/99; More information is available at
'http://chrysie.tamm.edu/medicago'.
Seq primer: T3.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 534)
Mahalas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
  /clone="ILIG"
/clone_lib="DSIL"
/clone_lib="DSIL"
/tlssue_type="Infected leaves"
/note="Vector: pBluescript SK +/-; Site_l: EcoRI; Site_2:
XhoI; leaves infected with Colletotrichum trifolii"
12 c 71 g 73 t
   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
euphyllophytes, Spermatophyta, Magnoliophyta, eudicotyledons, core
eudicots, Rosidae, eurosids I, Fabales, Fabaceae, Papilionoideae;
   AQ883371 534 bp DNA GSS 09-NOV-1999
HS_5471_B2_C05_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=9239 Col=10 Row=F, genomic survey sequence.
AQ883371
  Sequence-tagged connectors: A sequence approach to mapping scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
  to: 310
   Length: 10
Gaps: 0
Percent Identity: 80.000
  /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
  from: 1
   292 CGCTTGATCATCAGAAGGATTTCTCTCAGA 263
  11
   Location/Qualifiers
  Align seg 1/1 to reverse of: AW127330
  2 ArgleuleulleArgArglleAlaLeuArg
   AQ883371.1 GI:6314838
   alignment_block:
US-08-653-294-17 x AW127330/rev
barrel medic.
Medicago truncatula
   Quality: 39.00
Ratio: 3.900
Percent Similarity: 100.000
  seq_name: gb_gss6:AQ883371
   seq_documentation_block:
LOCUS AQ883371
   Homo sapiens
   94
   human.
  alignment_scores:
SOURCE
ORGANISM
  DEFINITION
   ORGANISM
  TITLE
JOURNAL
COMMENT
   BASE COUNT
   REFERENCE
AUTHORS
  JOURNAL
MEDLINE
   ACCESSION
  VERSION
KEYWORDS
SOURCE
  REFERENCE
  AUTHORS
   FEATURES
  TITLE
  ORIGIN
  Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Mammalia; Eukheria; Primates; Catarrhini; Hominidae; Homo.

Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (Dasas 1 to 447)

S Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)

Unpublished (1998)

L Unpublished (1988)

Other_GSS: CIT HSP-2309J17.TF

Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0200
  Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Mil Reverse
Class: BAC ends.
   AQ015503 447 bp DNA GSS 09-JUN-1998 CIT-HSP-2309J17.TR CIT-HSP Homo sapiens genomic clone 2309J17.
  /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
   to: 447
  Length: 11
Gaps: 0
Percent Identity: 72.727
                        1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   Align seg 1/1 to reverse of: AQ015503 from: 1
  132
  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2309117"
/clone_lib="CIT-HSP"
   Socation/Qualifiers
  р
  72
  AQ015503
AQ015503.1 GI:3194239
   alignment_block:
US-08-653-294-17 x AQ015503/rev
  /sex="Male"
  ပ
  HindIII"
   .447
  Ouality: 40.00
Ratio: 3.636
Percent Similarity: 100.000
   seq_name: gb_est39:AW127330
   seq_name: gb_gss8:AQ015503
   seq_documentation_block:
LOCUS AQ015503
  Homo sapiens
   human
   alignment_scores:
```

source

FEATURES

BASE COUNT ORIGIN

and

ACCESSION VERSION KEYWORDS

```
39.00
  US-08-653-294-17 x AQ433893
  seq_name: gb_gss1:AG000734
   seq_documentation_block:
Locus AG000734
  Quality:
   Ratio:
Percent Similarity:
  Quality:
  137
   alignment_scores:
  alignment_scores:
  alignment_block:
  VERSION
KEYWORDS
SOURCE
ORGANISM
  DEFINITION
  AUTHORS
TITLE
JOURNAL
  BASE COUNT
   BASE COUNT
  TITLE
JOURNAL
  ACCESSION
   AUTHORS
  REFERENCE
  REFERENCE
  FEATURES
   FEATURES
   ORIGIN
  ORIGIN
   Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
   401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fmax: (206) 616-3887
Fmax: (206) 616-3887
Fmax: 1060 11 Juan 1 
   /note="Vector: pBACe3.6; Genomic sequence of BAC ends" 98\ c 112 g 171 t 4 others
  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
  Email: jwajlaceeu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
   seq_documentation_block:
LOCUS AQ433893 559 bp DNA GSS 31-MAR-1999
DEFINITION HS_5056_A1_D05_T7 RPCI-11 Human Male BAC Library Homo sapiens
genomic_clone Plate=632 Col=9 Row=G, genomic_survey sequence.
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 559)
  1. .534 // Corganism-"Homo sapiens" // Acadanism-"Homo sapiens" // Ab_xxef="taxon:9606" // Clone="Plate=9239 Col-=10 Row-F" // Clone_lib-"RPCI-11 Human Male BAC Library" // Sex-"male"
  Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
   Length: 12
Gaps: 0
Percent Identity: 66.667
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
  469 TACCGATTGTTATTATGACGTATTGGGCTTCAATAT 504
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
  to: 534
  High quality sequence stop: 534.
Location/Qualifiers
  from: 1
   AQ433893.1 GI:4544228
   39.00
3.545
91.667
  alignment_block:
US-08-653-294-17 x AQ883371
   to: AQ883371
   Seq primer: T7
Class: BAC ends
   seq_name: gb_gss13:AQ433893
   Homo sapiens
  Percent Similarity:
   Ratio:
   AQ433893
  149
   human.
   alignment_scores:
   Align seg 1/1
   source
   ORGANISM
  BASE COUNT
   ACCESSION
  MEDLINE
COMMENT
   VERSION
KEYWORDS
SOURCE
  REFERENCE
   AUTHORS
   JOURNAL
   FEATURES
   TITLE
   COMMENT
  ORIGIN
```

```
(pieter@dejong.med.buffalo.edu). Clones may be purchased from BACBAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 632 row: G column: 9
Seq primer: T7
Class: BAC ends
High quality sequence stop: 559.
Location/Qualifiers
I. 559
//db_xref="haxon:6606"
//db_xref="haxon:6606"
//clone="hplate=632 Col=9 Row=G"
//sex="male"
   Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
E. (Dases 1 to 666)

B. Direct Submission
L. Submitted (31-OCT-1997) to the DDBJ/EMBL/GenBank databases.
Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Saqamihara 228, Japan (E-mail:hattoriehgc.ims.u-tokyo.ac.jp, Tel:0427-78-9551)
Eax:0427-78-9551)
E (Dases 1 to 666)
S Hattori,M., Ishli,K., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
L. Published only in Database (1997) In press
   'note="Vector: pBACe3.6; Genomic sequence of BAC ends"
166 c 91 g 158 t 7 others
   AGUU0734 666 bp DNA GSS 06-FEB-1999
Homo sapiens genomic DNA, 21g region, clone: T171Bm40, genomic
SULYCEY SEQUENCE.
AGOU0734
  others
   Length: 12
Gaps: 0
Percent Identity: 66.667
   0 72
  445 TACCGTCTTCTAAGAAAGAGATAGCGTTACAATAC 480
   ų
  1 TyrArgLeuLeulleArgArglleAlaLeuArgTyr 12
   Length:
Gaps:
   210
   to: 559
   Homo sapiens DNA, clone:T171Bm40. Homo sapiens
   /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
  ρ
   from: 1
   /clone="T171Bm40"
   AG000734.1 GI:2579542
  /map="21q"
  39.00
3.545
91.667
   Align seg 1/1 to: AQ433893
```

us-08-653-294-17.rst

```
1 (bases 1 to 359)
Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P.,
Samson,D., Saurin,W., Weissenbach,J. and Quetier,F.
Unpublished
2 (bases 1 to 359)
                                       seq_documentation_block:

LOCUS
CNS00T90
359 bp DNA
CNS00T90
DEFINITION Arabidopsis thaliana genome survey sequence T7 end of BAC T3N2 of
TAMU library from strain Columbia of Arabidopsis thaliana, genomic
survey sequence.
   Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
euphyllophytes, Spermatophyta, Magnollophyta, eudicotyledons, core
eudicots, Rosidae, eurosids II, Brassicales, Brassicaceae,
   Direct Submission

Direct Submission

Submitted (25-707-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 ENTR cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
   Mahairas, G.G., Waliace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  AQ166595 386 bp DNA GSS 16-OCT-1998 HS_3146_A1_B09_MR CIT Approved Human Genomic Sperm Library D sapiens genomic clone Plate=3146 Col=17 Row=C, genomic survey
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 386)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman,
   Length: 11
Gaps: 0
Percent Identity: 63.636
  Location/Qualifiers
1. 359
/organism="Arabidopsis thaliana"
  116 t
   297 AGAGCCTTGGTGCTTAGCTCTCCGATAC 329
   to: 359
  2 ArgleuleulleArgArglleAlaLeuArgTyr 12
   /strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="TAMU"
/clone="T3N2"
   ρ
   84
   from: 1
  /note="end : T7"
   AQ166595
AQ166595.1 GI:3564790
  AL089394.1 GI:5290534
   38.00
3.800
90.909
   to: CNS00T90
   alignment_block:
US-08-653-294-17 x CNS00T90
  seq_name: gb_gss1:CNS00T90
   seq_name: gb_gss9:AQ166595
  seq_documentation_block:
LOCUS AQ166595
  Homo sapiens
  thale cress.
   Arabidopsis.
   Genoscope
   Quality:
Ratio:
Percent Similarity:
  sednence.
  AL089394
   87
  . gamnc
   alignment_scores:
   Align seg 1/1
   source
   ORGANISM
   DEFINITION
  ORGANISM
  BASE COUNT
  REFERENCE
AUTHORS
TITLE
  ACCESSION
  VERSION
KEYWORDS
SOURCE
  REFERENCE
  ACCESSION
   REFERENCE
  AUTHORS
  JOURNAL
  JOURNAL
  VERSION
KEYWORDS
  AUTHORS
   JOURNAL
  FEATURES
  TITLE
   ORIGIN
  SOURCE
   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 201)
Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K.,
Barry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
Use of human BAC End Sequences for Sequence-Ready Map Building
Unpublished (1998)
  Email: indedensetigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
sesenth Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

      seq_documentation_block:
      201 bp
      DNA
      GSS
      21-APR-1999

      LOCUS
      AQ238101
      201 bp
      DNA
      GSS
      21-APR-1999

      DEFINITION
      RPCIII-73318.TK RPCI-11 Homo sapiens genomic clone RPCI-11-73J18, genomic survey sequence.
      AQ238101
      GI:3570392

      ACCESSION
      AQ238101
      GI:3570392
      GI:3570392

   /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
  Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
   999
  Gaps: 0
Percent Identity: 80.000
  Percent Identity: 58.333
   :
ç
   from: 1
  1 TyrArgLeuLeuIleArgArgIleAlaLeuArgTyr 12
   Length:
   to: 201
   /organism="Homo sapiens"
/db_xref="GDB:7527881"
/db_xref="taxon:9606"
/clone="RPCI-11-73J18"
   /clone_lib="RPCI-11"
   Location/Qualifiers
1. .201
   Align seg 1/1 to reverse of: AG000734
  64 9
   from: 1
   alignment_block:
US-08-653-294-17 x AG000734/rev
   /sex="Male"
  36 c
   Ratio: 3.800
Percent Similarity: 100.000
   38.00
  Align seg 1/1 to: AQ238101
91.667
  Class: BAC ends.
   US-08-653-294-17 x AQ238101
  seq_name: gb_gss10:AQ238101
   Homo sapiens
  Percent Similarity:
   Quality:
  48
   human.
   alignment_scores
   alignment_block
```

ORGANISM

KEYWORDS

SOURCE

REFERENCE AUTHORS TITLE JOURNAL COMMENT

source

FEATURES

BASE COUNT ORIGIN

and

Homo

Karaga A

```
source
   BASE COUNT
ORIGIN
   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 461)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
   seg_documentation_block:

LOCUS AQ137850 461 bp DNA GSS 24-SEP-1998

DEFINITION HS.3058_B2_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=18 Row=F, genomic survey
   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3146 Col=17 Row=C"
/clone=lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
  Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3146 row: C column: 17
Class: BAC ends
   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
Voll Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
  Percent Identity: 54.545
   148 t
   Length:
   Gaps:
   142 CGATTAATGGTGAGAAGTTTGGCTATAAGATAT 174
   to: 386
  2 ArgLeuLeulleArgArglleAlaLeuArgTyr 12
   High quality sequence stop: 386.
Location/Qualifiers
1. .386
  Sequence Tagged Connector
Plate: 3058 row: F column: 18
Class: BAC ende
High quality sequence stop: 461.
Location/Qualifiers
   75 g
  from: 1
  sequence.
AQ137850
AQ137850.1 GI:3528503
   65 C
   38.00
3.800
90.909
  Align seg 1/1 to: AQ166595
  alignment_block:
US-08-653-294-17 x AQ166595
  seq_name: gb_gss9:AQ137850
   Quality:
Ratio:
  Percent Similarity:
   Hood, L.
  human .
  alignment_scores:
   source
   BASE COUNT
ORIGIN
  ORGANISM
    MEDLINE
COMMENT
   ACCESSION
VERSION
KEYWORDS
SOURCE
  REFERENCE
AUTHORS
  JOURNAL
MEDLINE
COMMENT
   FEATURES
   TITLE
   FEATURES
```

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

OM protein - protein search, using sw model

8, 2000, 01:29:40; Search time 122.56 Seconds (without alignments) 2,319 Million cell updates/sec February Run on:

US-08-653-294-18 58 1 YRLAIRRILLRY 12

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

RESULT

188963 seqs, 23686106 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

summaries Post-processing: Minimum Match 0% Listing first 45

A\_Geneseq\_36:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | rip            | 02 8 | Peptide B2702.84-7 | コ   | CTL # | HLA-B2702 84-75-84 | tin | HLA-B2702 CTL modu | HLA-B2702 CTL modu | Peptide B2702.84-7 | Peptide B2702.84-7 | HLA-B2702 84-75T/7 | alpha | Human alpha-2b adr | Human neuronal nic | ď   | lori ORF | cancer a | cancer a             | Protein with Oxeta |     | Homo sapiens don-1 | M. rosa truncated | M. rosa fourth adh |     | tens | type t | e gen | Human MHC 1 alpha | w      | G-protein coupled | χę  | adr    |     | Canine beta-3 adre |
|-----------|----------------|------|--------------------|-----|-------|--------------------|-----|--------------------|--------------------|--------------------|--------------------|--------------------|-------|--------------------|--------------------|-----|----------|----------|----------------------|--------------------|-----|--------------------|-------------------|--------------------|-----|------|--------|-------|-------------------|--------|-------------------|-----|--------|-----|--------------------|
| SUMMARIES | ID             | 542  | 5                  | 79  | 8     | 2                  | 77  | R92909             | 90                 | 2                  | 79                 | 13                 | 7     | 8                  | 15                 | 99  | 36       | 1        | 12                   | 22                 | 22  | 38                 | 33                | 33                 | 37  | 38   | 370    | 724   | 142               | R74034 | 9                 | 99  | R06495 | 7   | W44933             |
|           | DB             | -    | ~                  | Н   | Н     | 7                  | ч   | <b>~</b>           | н                  | Н                  |                    | -                  | -     | Н                  | -                  | -   | ٦        | -        | ٦                    | Ч                  | 근.  | <del>, ,</del>     | ч                 | 7                  | Н   | П    | Н      | ٦     |                   | П      | 7                 | -   | -      | -   | П                  |
|           | Length         | 12   | 12                 | 12  | 20    | 20                 | 20  | 20                 | 20                 | 20                 | 20                 | 20                 | 487   | 487                | 504                | 803 | 804      | 1123     | 1177                 | 216                | 350 | 469                | 546               | 564                | 605 | 647  | 860    | 4473  | 18                | 119    | 362               | 362 | 402    | 405 | 405                |
|           | Query<br>Match |      |                    | 1.4 | 7.2   | 7.2                | 7.7 | 8.6                | 9.6                | 9.0                | 9.                 | 2.5                | 2.5   | 2.5                | 2.5                | £.3 | ۳.       | ۳.       | ۳.<br><del>۱</del> . | 3.4                | 3.4 | 3.4                | 3.4               | 3.4                | 3.4 | 3.4  | 3.4    | 3.4   | ۲.٦               |        | 1.7               |     | 1.7    | 1.7 | ۲.٦                |
| •         | Mai<br>Mai     | 6    | ò                  | ò   | ò     | ف                  | فا  | ភ                  | ഹ്                 | š                  | ഹ്                 | ហ                  | വ്    | ហ                  | ហ                  | ñ   | ഗ്       | 'n       | ń                    | വ                  | 'n  | 'n                 | 'n                | വ്                 | ìń  | വ്   | 'n     | 'n    | 'n                | 'n     | ις                | ίς  | 'n     | ŗγ  | ŗ.                 |
|           | Score          | 53   | 53                 | 53  | 39    | 39                 | 39  | 34                 | 34                 | 34                 | 34                 | 32                 | 32    | 32                 | m                  | ٠   | ij       | ÷        | ä                    | 31                 | 31  | 31                 | 31                | 31                 | 31  | 31   | 31     | 31    | 30                | 30     | 30                | 30  | 30     | 30  | 30                 |
|           | Result<br>No.  | 1    | 7                  | m   | 4     | Ŋ                  | 9   | 7                  | œ                  | Ø                  | 10                 | 11                 | 12    | 13                 | 14                 | 15  | 16       | 17       | 18                   | 19                 | 20  | 21                 | 22                | 23                 | 24  | 25   | 56     | 27    | 28                | 58     | 30                | 31  | 32     | 33  | 34                 |

| 407 1 W53847<br>408 1 R54991<br>428 1 R39264<br>627 1 W44152<br>686 1 R5591<br>20 1 W3779<br>6 1 W47263<br>6 1 W47263<br>6 1 W3778<br>6 1 W3778                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | Human adrenaline b | Human beta-3 adren | Murine somatostati | Human neuronal nic | RING11 antigente p | HLA-B2702 CTL modu | Immunomodulating d | Immunomodulatory p | Immunomodulatory p | Peptide #3 used in | Peptide #2 used in |  |            |  |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--|------------|--|
| 7887900999<br>77777777777777777777777777777                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | W53847             | R54991             | R39264             | W44152             | R25591             | R92911             | W33779             | W47263             | W47262             | W33782             | W33781             |  | ALIGNMENTS |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 7 1                | 8                  | 8                  | 7 1                | 1 9                | 20 1               | 0                  | 9                  | 1 9                | 1 9                | 1 9                |  |            |  |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 51.7               | 51.7               | 51.7               | 51.7               | 51.7               | 50.9               | 50.9               | 50.0               | 50.0               | 50.0               | 50.0               |  |            |  |
| 7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118<br>7.118 | 30                 | 30                 | 30                 | 30                 | 30                 | 29.5               | 29.5               | 29                 | 29                 | 53                 | 29                 |  |            |  |
| 30 51.7<br>30 51.7<br>30 51.7<br>30 51.7<br>29.5 50.0<br>29 50.0<br>29 50.0<br>29 50.0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 35                 | 36                 | 37                 | 38                 | 39                 | 40                 | 41                 | 42                 | 43                 | 44                 | 45                 |  |            |  |

```
WILL'S 9-1940/12/12.

WHILL'S 9-1940/12/12.

WHILL'S 9-1940/12/12.

Inhibit cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp: English.

Example: Page 13: 20pp: English.

Example: Page 14: 20pp: English.

Example: Page 15: 20pa 16: 20pa 
   1.2-NOV-1996 (first entry)
HLA-B2702 84-79-84 palindrome.
HLA-B2702 84-79-84 palindrome.
HLA-B2702 84-79-84 palindrome.
HLA-D74: alphal-helix; human-leucocyte-associated antigen; inhibitor;
T-cell lysate; membrane protein; mammal; heat shock protein; Hsc70; APC;
B cell; calcium influx; cytotoxic I lymphocyte; CLL; differentiation;
  18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
   cytolysis; antigen presenting cell. Synthetic. W09513288-Al.
                          R95429 standard; peptide; 12 AA. R95429;
   Clayberger C, Krensky AM; WPI; 95-194027/25.
```

Gaps ő 91.4%; Score 53; DB 1; Length 12; 91.7%; Pred. No. 0.00042; 1ve 0; Mismatches 1; Indels Query Match
Best Local Similarity 91.7
Matches 11; Conservative

ö

1 YRLAIRRILLRY 12 ŏ g

W33798 standard; peptide; 12 AA. W33798; RESULT W33798 ID W3 AC W3

```
ö
   Example 1: Page 19: 41pp: English.

Peptides W33784-98 and W337789-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa88-79) (laa77-76R); aa76 = E or V; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HAA-B alphal domain (positions)
   19-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
   Gaps
  New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases
Claim 17; Page 35; 41pp; Enlays Specifically claimed immunomodulating This sequence represents a specifically claimed immunomodulating dimer peptide of the invention. A peptide-type compound or variant
19-JUN-1998 (first entry)
Peptide B2702.84-79/79-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
   Immunomodulating dimer peptide #3.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
   New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
   ;
0
  Score 53; DB 1; Length 12;
Pred. No. 0.00042;
0; Mismatches 1; Indels
   24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Bellow R. Clayberger C, Krensky AM;
WPI; 98-086530/08.
  24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
  Beulow R, Clayberger C, Krensky AM;
WPI; 98-086530/08.
  W33799 standard; peptide; 12 AA.
   Query Match 91.4%;
Best Local Similarity 91.7%;
Matches 11; Conservative
  (first entry)
  1 YRLAIRRILLRY 12
  1 YRLAIRRIALRY 12
   22-MAY-1997; U08689.
  22-MAY-1997; U08689.
   Homo sapiens.
WO9744351-A1.
   Homo sapiens.
WO9744351-A1.
  19-JUN-1998
  27-NOV-1997
  27-NOV-1997
   rejection.
   rejection.
   Synthetic
   Synthetic
  Seguence
   alpha-1
  m
   NAME OF THE PROPERTY OF THE PR
```

```
claimed which has immunomodulating activity, including the N-terminal acylated and/or C-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula: A-B, where A, B = (R aaf6-77L) (aa79-84) or (aa84-79) (Laa77-76R); aa76 = E or hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and a represents amino acid; and experient or L; aa83 = G or R; and a represents amino acid; are sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid; sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytocoxic rlymphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CTLS. They can also inhibit the proteins of interest to activate CTLS. They can also inhibit the cused for products of reals in response to anti-CD3. The peptide can be diseases, e.g. diabetes, rheumatoid atthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
   Ĥ
  Example 15; Page 36; 80pp; English.
R83061-R83085, R83090-R83096 and R92207-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of ransplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLS)
   16-MAY-1996 (first entry)
HLA-B2702 CTL modulating peptide (B2702.84-75/75-84).
Cytotoxic T lymphocyte; CTL; major histocompatibility complex; MHC;
Immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
   Gaps
   Gaps
  Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
   ő
   .
6
  91.4%; Score 53; DB 1; Length 12; 91.7%; Pred. No. 0.00042;
  Length 20;
   1; Indels
   Indels
   ;
  Score 39; DB 1;
Pred. No. 0.28;
   0; Mismatches
   Mismatches
  Parham P;
   05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
   R92907 standard; peptide; 20 AA.
   ö
  67.2%;
55.0%;
  50
   Clayberger C, Krensky AM,
WPI; 95-358582/46.
   1 YRLAIR-----RILLRY
  1 YRLAIRLNERRENLRIALRY
   Conservative
   11; Conservative
  1 YRLAIRRILLRY 12
  1 YRLAIRRIALRY 12
   05-APR-1995; U04349
  Query Match
Best Local Similarity
Matches 11; Conserv
   Best Local Similarity
  of the patient
   79-A1.
  Sequence
   Query Match
  Sequence
   Matches
   RESULT
R92907
      88888888888888888888888
   g
  Ġ
  g
```

```
Tigating ductonminute diseases.

It is acquence represents a specifically claimed immunomodulating dimer to peptide of the invention. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acquence represents a specifically claimed which has immunomodulating activity, including the N-terminal acquence and/or C-terminal amidated or esterified forms of up to 60 amount ocids, where he peptide-type compound comprises the formula; A-B, where A, B = (R aa76-77L) (aa79-84) or (aa84-79) (lea77-76R); aa76 = E or N; aa77 = D, S or N; aa79 = R or G; aa80 = I or N; aa81, aa84 = a represents amino acid; The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a class I HLA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic T-lymphocytes (CTL) from undesirably attacking cells in a host or in proteins of interest to activate CTLs. They can also inhibit the proteins of interest to activate CTLs. They can also inhibit the profice of or proteins of interest to activate CTLs. They can also inhibit the close of or class in especial or treating autoimmune diseases, e.g. daabetes, rheumatoid arthritis and lupus erythematosis.
  R92909 standard; peptide; 20 AA.
  1 YRLAIR-----RILLRY 12
  |||||||
| YRLAIRLNERRENLRIALRY 20
   autoimmune diseases
  Query Match 67.2
Best Local Similarity 55.0
Matches 11; Conservative
  of the patient
   Synthetic.
WO9526979-A1.
   12-OCT-1995.
  Sequence
  Sequence
  RESULT
  R92909
 ò
  유
  ò
   With 30-1940/123.

Composes. Comperising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example, Page 12: 29pp; English.

Example, Page 13: 29pp; English.

Example, Page 13: 29pp; English.

CC PS 24-75-84 palindrome. These sequence represents the human-leucocyte-associated antigens. This sequence represents the HA-B7002 84-75-84 palindrome. These sequences can be used to isolate the protein p74 from a T-cell lysate. P74 is a T-cell surface membrane protein protein protein protein protein associated with T-cell activation in manmalian T-cells, and is also immunologically cross reactive with the heat shock protein Hsc70.

CC P74 is found in a limited number of cell types, but is particularly p74 is found in a limited number of cell types, but is particularly cell with an amphoteric detergent, and then passed through an affinity compositions comprising the extracellular fragment of p74 combined with HA-B2702.60-84 (see R95416), induces calcum influx, and inhibits compositions comprising the extracellular fragment of p74 and determining the amount of binding between the candidate compound and p74.

Modulation of CTL activity can be inhibited in a cellular composition containing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount sufficient to compete containing the binding of the p74 ligand.
   ï
   12-NOV-1996 (first entry)
HLA-B2702 84-75-84 palindrome.
HLA-B2702 84-75-84 palindrome.
HLA-D2702 84-75-84 palindrome.
TA-Cell 19sate; membrane protein; mammal; heat shock protein; Hsc70; APC; B Cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
   Gaps
   Immunomodulating dimer péptide #1.
Immunomodulating dimer; immunosuppressant drug; CTL activation;
transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
  New immunomodulating dimer peptide(s) - based on a Class I HLA-B alpha-1 domain, used for preventing rejection of transplants or
   .;
8
   67.2%; Score 39; DB 1; Length 20; 55.0%; Pred. No. 0.28;
   1; Indels
   Mismatches
   10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM;
WPI; 95-194027/25.
  24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
  Beulow R, Clayberger C, Krensky AM; WPI; 98-086530/08.
                                     R95428 standard; peptide; 20 AA.
   W33778 standard; peptide; 20 AA.
   ö
   1 YRLAIR-----RILLRY 12
   1 YRLAIRLNERRENLRIALRY 20
   (first entry)
   Matches 11; Conservative
  27-NOV-1997.
22-MAY-1997; U08689
   Query Match
Best Local Similarity
  Homo sapiens.
WO9744351-Al.
   WÔ9513288-A1.
18-MAY-1995.
   19-JUN-1998
   rejection.
   Synthetic.
  Sequence
S
   ø
RESULT
R95428
   RESULT
   ò
   g
```

.; 8

1; Indels

Length 20;

67.2%; Score 39; DB 1; 55.0%; Pred. No. 0.28;

Pred. No. 0.28; 0; Mismatches

```
ä
   Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92913 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-i domain of the class I MHC HIA-B2702. These sequences can be used to extend the period of acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
                               HLA-B2702 CTL modulating peptide (B2702.84-75/75-84(T)). Cytocoxic T lymphocyte; CTL; major histocompatibility complex; MHC; immunosuppressant; graft versus host disorder; transplantation; therapy; class I MHC; HLA-B2702.
  Gaps
  WPI: 95-358582/46.
Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
  .;
œ
   Length 20;
  2; Indels
   58.6%; Score 34; DB 1;
50.0%; Pred. No. 2.4;
tive 0; Mismatches
   Krensky AM, Parham P;
   05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham F
  1 YRLAIR-----RILLRY 12
16-MAY-1996 (first entry)
   Ouery Match 58.6
Best Local Similarity 50.0
Matches 10; Conservative
   05-APR-1995; U04349.
  20 AA;
```

셤

```
Sequence
  Sequence
 888888888888888888888
   à
  셤
   HLA-B2702 CTL modulating peptide (B2702.84-75(T)/75-84).
Cytotoxic T lymphocyte: CTL; major histocompatibility complex; MHC;
immunosuppressant; graft versus host disorder; transplantation; therapy;
class I MHC; HLA-B2702.
   Example 15; Page 36; 80pp; English.

R83061-R83085, R83090-R83096 and R92907-R92914 represent fragments of class I major histocompatibility complex (MHC) antigens. This sequence is an inverted dimer of residues 75-84 of the alpha-1 domain of the class acceptance by a recipient of a transplant from an MHC unmatched donor. The peptides are administered to a patient in conjunction with a subtherapeutic amount of an immunosuppressant. This is administered to the patient for a limited period of time (compared to the lifetime administration for current treatments). The peptides particularly modulate (or inhibit) the activity of the cytotoxic I lymphocytes (CTLs)
   New immunomodulating dimer peptide(s) - based on a class I HLA-B alpha-1 domain, used for preventing rejection of transplants or treating autoimmune diseases Example 1; Page 19; 41pp; English.

Example 1; Page 19; 41pp; English.

Peptides W33784-98 and W33778-9 were assayed for their immunomodulating activity. A peptide-type compound or variant is claimed which has immunomodulating activity, including the N-terminal acylated and/or
  Gaps
  19-JUN-1998 (first entry)
Peptide B2702.84-75Fy75-84 tested for immunomodulating activity.
Immunomodulating dimer; immunosuppressant drug; CTL activation; transplantation; autoimmune disease; Class I HLA-B alpha-1 domain;
  Extension of acceptance period of transplants from MHC unmatched donor hosts - using Class I B75-84 MHC antigen of the recipient
  .;
æ
   DB 1; Length 20;
  2; Indels
  58.6%; Score 34; DB 1
50.0%; Pred. No. 2.4;
iive 0; Mismatches
  05-APR-1994; US-222851.
(STRD ) UNIV LELAND STANFORD JUNIOR.
Clayberger C, Krensky AM, Parham P;
  27-NOV-1997,
22-MAY-1997,
24-MAY-1996, US-653294,
(STRD ) UNIV LELAND STANFORD JUNIOR.
Beulow R, Clayberger C, Krensky AM;
  R92908 standard; peptide; 20 AA
   W33791 standard; peptide; 20 AA.
1 YRLAIR-----RILLRY 12
   Query Match
Best Local Similarity 50.0
Matches 10; Conservative
   05-APR-1995; U04349.
  Clayberger C, Krel
WPI; 95-358582/46.
   WPI; 98-086530/08
   of the patient.
Sequence 20 P
  Homo sapiens.
WO9744351-A1.
27-NOV-1997.
  16-MAY-1996
   12-OCT-1995
  rejection.
   Synthetic
  W33791;
   6
   RESULT
W33791
  RESULT
```

ò

```
c-terminal amidated or esterified forms of up to 60 amino acids, where the peptide-type compound comprises the formula; A-B, where A, B = (R a876-77) (a479-84) or (a884-79) (Laa77-76R); aa76 = E or V; aa77 = E or N; aa76 = E or V; aa77 = E or N; aa79 = R or G; aa80 = I or N; aa81 = a hydrophobic or small amino acid; aa82 = R or L; aa83 = G or R; and aa represents amino acid. The sequence in the brackets may optionally be absent or truncated at any peptide type bond within the brackets. The compounds comprise amino acid sequences related to a Class I HIA-B alphal domain (positions 79-84). They can be used to inhibit cytotoxic I-lymphocytes (CIL) from condistrably attacking cells in a host or in Vitro. They can also be used in combination with antigenic peptides or proteins of interest to activate CILs. They can also inhibit the proliferation of I cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rheumatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
  Bellow R, Clayberger C, Krensky AM:

NPI: 98-086330/08

NPI: 98-086330/08

NPI: 98-086330/08

New immunomodulating dimer peptide(s) - based on a Class I HLA-B
alpha-1 domain, used for preventing rejection of transplants or
treating autoimmune diseases

Example 1: Page 19: 41pp: English.

Example 1: Page 19: 41pp: English.

Example 1: Page 19: 41pp: English.

Cotivity. A peptide-type compound or variant is claimed which has
activity. A peptide-type compound or variant is claimed which has
cotivity. A peptide-type compound or variant is claimed which has
the peptide-type compound comprises the formula: A-B, where A, B

C -terminal amidated or esterified forms of up to 60 amino acids, where
the peptide-type compound comprises the formula: A-B, where A, B

C -terminal amidated or esterified forms of up to 60 amino acids, where
the peptide-type compound comprises the formula: A-B, where A, B

C -terminal amidated or esterified forms of up to 60 amino acids and an arepresents amino
small amino acid; aa82 - R or L; aa83 - G or R; and as represents amino
acid; account of the brackets may optionally be absent or truncated
at any peptide type bond within the brackets. The compounds comprise
and any peptide type bond within the brackets. The compounds comprise
and an acid sequences related to a Class I HLA-B alphal domain (positions)
  79-84). They can be used to inhibit cytotoxic T-imphocytes (CTL) from undesirably attacking cells in a host or in vitro. They can also be activate CTLs. They can also in the properties or proteins of interest to activate CTLs. They can also inhibit the proliferation of T cells in response to anti-CD3. The peptide can be used for preventing rejection of transplants or for treating autoimmune diseases, e.g. diabetes, rhemmatoid arthritis and lupus erythematosis. The products can also be used for detection and diagnosis.
   Immunomodulating dimer; immunosuppressant drug; CTL activaty. Transplantation; autoimmune disease; Class I HLA-B alpha-1 domain; Synthetic.
   19-JUN-1998 (first entry) Peptide B2702.84-75/75-84T tested for immunomodulating activity.
   .;
æ
   Score 34; DB 1; Length 20;
Pred. No. 2.4;
0; Mismatches 2; Indels
  24-MAY-1996; US-653294.
(STRD ) UNIV LELAND STANFORD JUNIOR.
   W33792 standard; peptide; 20 AA.
   58.6%;
   12
   20
  1 YRLAIR-----RILLRY
   1 YRLATRINERRENLRIALRY
  Query Match
Best Local Similarity 50.0
Matches 10; Conservative
   27-NOV-1997.
22-MAY-1997; UO8689.
24-MAY-1996; US-6532
   Homo sapiens.
WO9744351-A1.
```

ö

Gaps

ö

ô g

```
Assay for alpha-2b adrenergic receptor ligands - using membranes of cells expressing recombinant receptor
Disclosure: Fig 2A-E; 16pp; Bng1ish.
Human alpha-2B adrenergic receptor (Wil804) is a member of the rhodopsin-like signal transducer family. Its amino acid sequence was deduced from a genomic DNA clone (T59499) obtd. from a human spleen DNA library. Vectors have been adapted to allow prodn. of alpha-2B adrenoceptor in bacterial, yeast or mammalian cells; transfected Lik-cells, designated L-NGC-alpha-2B, are deposited as ArCC CRL 10275. Membranes of transfected mammalian cells an novel methods to identify drugs which specifically interact with, and bind to, the alpha-2B adrenergic receptor.
   Disclosure, Fig 2; 15pp; English.
Clone NGC-alpha2beta was isolated from a human spleen genomic
Library by screening with a fragment of the human 5-Hirb receptor
gene. The gene was used to express recombinant receptor protein
which can be used to produce antibodies for inhibition of receptor
   Isolated DNA encoding human adrenergic receptor - for detecting nucleic acids encoding alpha, 2-beta adrenergic receptor, for screening drugs.
   06-MAY-1997 (first entry)
uman alpha-2b adrenergic receptor.
Alpha-2b adrenergic receptor; adrenoceptor; adrenaline;
epinephrine; signal transduction; neurotransmitter; ligand.
  Score 32; DB 1; Length 487;
Pred. No. 1.4e+02;
L; Mismatches 3; Indels
  Score 32; DB 1; Lengtn vc...
Pred. No. 1.4e+02;
   1; Mismatches
   1; Mismatches
   W11804 standard; Protein; 487 AA.
  W44156 standard; Protein; 504 AA.
  55.2%;
  55.2%;
  (SYNA-) SYNAPTIC PHARM CORP.
Hartig PR, Weinshank RL;
WPI; 97-107576/10.
N-PSDB; T59499.
   W44156;
14-MAY-1998 (first entry)
  Ouery Match
Best Local Similarity 63.0.
  Query Match 55.2
Best Local Similarity 63.6
Matches 7; Conservative
       (NEUR-) NEUROGENETIC COR
Weinshank RL, Hartig PR;
WPI; 91-310087/42.
N-PSDB; Q14151.
  30-0CT-1989; 428856.
30-0CT-1989; US-428856.
30-0MAY-1991; US-707604.
22-0CT-1992; US-965040.
   470 FRRAFRRILCR 480
   1 YRLAIRRILLR 11
  1 YRLAIRRILLR 11
  487 AA;
   Homo sapiens.
US5595880-A.
   unction.
  Sequence
   RESULT 14
W44156
  RESULT
W11804
       g
  ò
  õ
   g
  SAF
  Will 3-1940.7(2).

Tomposns. comprising lymphoid surface membrane proteins - which may inhibit cytolytic activity and differentiation of CTLS.

Example: Page 12: 29pp: English.

R95413, and R95415-R9543 represent palindromes and fragments of human-leucocyte-associated antigens. This sequences can be used too the protein associated with T-cell lyaste. P74 is a T-cell surface membrane protein p74 from a T-cell activation in mammalian T-cells, and is also immunologically cross reactive with the heat shock protein CT as as a laso immunologically cross reactive with the heat shock protein theory. P74 is found in a limited number of cell types, but is particularly expressed on B and T cells. P74 can be isolated by lysis of a suitable cell with an amphototaric detergent, and then passed through an affinity column containing a covalently bound HA-B2702 palindromic affinity column containing a covalently bound HA-B2702 palindromic combined with HA-B2702.60-84 (see R95416), induces calcium influx, and inhibits cytotoxic T lymphocyte (CTL) differentiation or cytolysis.

Candidate compounds can be screened for their effect on the cytolytic activity of T-cells, by combining them with the extracellular portion of p74 and determining the amount of binding between the candidate compound can determining the amount of binding between the candidate compound companing T-cells and antigen presenting cells (APCS), by adding to the mix the extracellular portion of p74, in an amount cut in the binding of the p74 ligand.

Sequence 20 AA;
                            ij
  ä
  HIA-B2702 84-75T/75-84T palindrome.

HIA-B2702 84-75T/75-84T palindrome.

HIA-B2702 84-75T/75-84T palindrome.

HIA-B2702 84-75T/75-84T palindrome.

HIA-B2702 84-775-84T palindrome.

HIA-B2703 84-775-84T palindrome.

B cell; calcium influx; cytotoxic T lymphocyte; CTL; differentiation; cytolysis; antigen presenting cell.
                            Gaps
  Gaps
                            .;
æ
  .,
  Human alpha 2 beta adrenergic receptor.
Neurotransmission; adrenaline; epinephrine; NGC-alpha2beta.
  Score 32; DB 1; Length 20;
Pred. No. 5.7; .
); Mismatches 1; Indels
                         5
  Pred. No. 2.4;
); Mismatches
   18-MAY-1995.
10-NOV-1994; U12985.
10-NOV-1993; US-150493.
(STRD ) UNIV LELAND STANFORD JUNIOR.
  R14149 standard; Protein; 487 AA.
  standard; peptide; 20 AA.
                         ö
  1 YRLAIR-----RILLRY 12
   55.2%;
   1 YRLAIRLNERRENLRIALRY 20
    50.0%;
  1 YRLAIR-----RILLR 11
   1 YRLAIRLNETRENLRIALR 19
  12-NOV-1996 (first entry)
   Krensky AM;
   06-JAN-1992 (first entry)
Similarity 50.0
10; Conservative
   Query Match
Best Local Similarity 52.6
Matches 10; Conservative
   30-OCT-1989; 428856.
30-OCT-1989; US-428856.
  Clayberger C, KrewPI; 95-194027/25
  WO9513288-A1.
   Homo sapiens.
US5053337-A.
  01-0CT-1991
  Best Local
  R95430
   RESULT 11
R95430
   RESULT 12
```

ö

Gaps

.. 0

R14149

ò g Length 487;

```
Example 2; Page 72-73; 99pp; English.

Example 2; Page 72-73; 99pp; English.

The present sequence repersents a human neuronal nicotinic acetylcholine receptor (NAChR) subunit. The cells expressing the alpha and/or beta NAChR subunits may be used in a method of screening compounds to identify any which modulate the activity of human neuronal NAChR. Subunit specific antibodiate the activity of human neuronal NAChR. Subunit specific antibodies may be used to monitor the distribution and expression density of various subunits in normal vs diseased brain tissues. Testing of single receptor subunits or specific receptor subunit combinations with a variety of potential agonists or antagonists provides information with respect to the function and activity of the individual subunits and should lead to the identification and design of compounds that are capable of very specific interaction with one or
  more receptor subtypes. The resulting drugs should exhibit fewer unwanted side effects than drugs identified e.g. screening with cells that express a variety of subtypes.
Human neuronal nicotinic acetylcholine receptor alpha-3 subunit.
Human; neuronal nicotinic acetylcholine receptor; alpha-3 subunit;
brain tissue; screening; NAChR; antibody.
   Human neuronal nicotinic acetylcholine receptor subunits and DNA also transformed cells useful for screening cpds. which modulate
  /note= "encoded by TWC"
459..480
/label= TMD4
/note= "transmembrane domain"
327..458
   /label= unspecified
/note= "encoded by AWC"
273. 296
/label= TMD2
/note= "transmembrane domain"
  /note= "transmembrane domain"
   /note= "transmembrane domain"
  (SALK ) SALK INST BIOTECHNOLOGY IND ASSOC
   /label- cytoplasmic_loop
   /label= unspecified
/note= "encoded by AMC"
354
  /label- unspecified
/note- "encoded by WWC"
240. .265
/label- TMD1
  /label= unspecified
/note= "encoded by WWC"
  /note= "encoded by rGY"
302. .326
/label= TMD3
  Location/Qualifiers
  (SIBI-) SIBIA NEUROSCIENCES INC.
Ellott KJ, Ellis SB, Harpold MM;
WPI: 94-303024/37
N-PSDB; V12200.
   . .30
'label= signal
  .458
  08-MAR-1993; US-028031
  Misc_difference 235
   Misc_difference 309
   Misc_difference 347
   Misc_difference
   Misc_difference
  Misc_difference
   Homo sapiens
   Peptide
  Domain
  Domain
   Domain
   Domain
  Region
   é
```

```
Pricobacter pylori nucleic acid sequences and encoded pricobacter pylori nucleic acid sequences and encoded polypeptide(s) - useful in vaccines to treat or prevent H. pylori infection and for diagnosis of H. pylori infection acid the sequence of a H. pylori cell envelope flagellar protein. This is the sequence of a H. pylori cell envelope flagellar protein. The protein may be used in a vaccine to prevent or treat H. pylori life cycle activators or inhibitors. The constant probes derived from it may be used for the identification of the pylori in a sample and the diagnosis of H. pylori infection. Nucleic acid sequences complementary to the DNA act as antisense sequences and can be used to prevent the translation of H. pylori mRNA. Antibodies and saminst the protein can be used in immunoassays to evaluate the abundance against the protein can be used in immunoassays to evaluate the abundance condition of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for significant homology to other known or exported coding regions continued by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. Pylori by PCR by amplification for recombinant polypeptide production, e.g. in E. coli
   ä
   protein.
   Gaps
   24-JUN-1998 (first entry)
H. pylori ORF hp4ell394_3368767_c1_80 cell envelope flagellar prote Fropblasmic, vaccine; prevention; treatment, infection; envelope; identification; binding compound; bacteria; life cycle; activator; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis. Helicobacter pylori.
09-071-1997, UD5213.
   .,
m
  Score 31.5; DB 1; Length 803; Pred. No. 3e+02; 2; Mismatches 2; Indels
   W55668 standard; Protein; 803 AA
   Query Match 54.3
Best Local Similarity 53.3
Matches 8; Conservative
   06-DEC-1996; US-751318.
29-MAR-1996; US-625611.
02-APR-1996; US-758731.
25-OCT-1996; US-738959.
(ASTR) ASTRA AB.
ALM RA, SMILL D;
WPI, 97-503122/46.
   1 YRLAIR---RILLRY 12
232 YSLXIRRLSLFY 243
  Sequence
                       g
```

Search completed: February 8, 2000, 01:29:40 Job time: 1752 sec

301

287 YKQAVRYYKRILLEY

ద

Conservative

Query Match Best Local Similarity Matches 7; Conserv

ö

Gaps

ö

55.2%; Score 32; DB 1; Length 504; 58.3%; Pred. No. 1.5e+02; Live 1; Mismatches 4; Indels

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

sw model using protein search, OM protein 7, 2000, 11:54:28; Search time 117.7 Seconds (without alignments)
4.809 Million cell updates/sec February Run on:

US-08-653-294-18 58 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 YRLAIRRILLRY 12 Scoring table:

142080 seqs, 47169319 residues Searched:

142080 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

1: pir1:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_62:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

|           | Description      | histocompatibility | P-glycoprotein - C | P-glycoprotein - C | p-glycoprotein iso | ribosomal protein | probable oxidoredu | L17 ribosomal prot | hypothetical prote |        | iron-sulfur cluste | conserved hypothet | ш      | ATM1 protein precu |        |        |        |        | RNA    |        | hypothetical prote | F420-nonreducing h | hypothetical prote | Na+/H+ antiporter | <ul> <li>type II restrictio</li> </ul> | glyceraldehyde-3-p | MHC class I histoc | MHC class I histoc | hemo. | a  | DNA |
|-----------|------------------|--------------------|--------------------|--------------------|--------------------|-------------------|--------------------|--------------------|--------------------|--------|--------------------|--------------------|--------|--------------------|--------|--------|--------|--------|--------|--------|--------------------|--------------------|--------------------|-------------------|----------------------------------------|--------------------|--------------------|--------------------|-------|----|-----|
| SUMMARIES | QI               | 299                | 812                | 811                | 812                | 7150              | 986                | 205                | 559                | A47377 | E72382             | G69807             | G70542 | S54211             | T13646 | T00953 | C71618 | RNBY2L | F64429 | S73487 | D72110             | A69422             | T16556             | JC5342            | B71808                                 | 25                 | _                  | A60384             | 37    | S) | 149 |
|           | Length DB        | :                  |                    |                    |                    |                   |                    |                    |                    |        | 152 2              |                    |        |                    |        | •      | •      | 733    |        |        |                    | •                  |                    |                   |                                        |                    |                    |                    |       |    |     |
| æ         | Query<br>Match I | . 0                | Э                  | 63.8               | m                  | 2                 | $^{\circ}$         | 0                  | 0                  | 0      | 58.6               | æ                  | æ      | æ                  | æ      | æ      | æ      | ø      | 9      | ø      | 9                  | 9                  | 9                  | 9                 | 9                                      | 9                  | Ø                  | 9                  | 9     | 9  | 9   |
|           | Score            | 41                 | 37                 | 37                 | 37                 | 36                | 36                 | 35                 | 35                 | 35     | 34                 | 34                 | 34     | 34                 | 34     | 34     | 34     | 34     | 33     | 33     | 33                 | 33                 | 33                 | 33                | 33                                     | 33                 | 33                 | 33                 | 33    | 33 | 33  |
|           | Result<br>No.    | , r-1              | 7                  | m                  | 4                  | 5                 | 9                  | 7                  | 00                 | თ      | 10                 | 11                 | 12     | 13                 | 14     | 15     | 16     | 17     | 18     | 19     | 20                 | 21                 | 22                 | 23                | 24                                     | 25                 | 56                 | 27                 | 28    | 58 | 30  |

## ALIGNMENTS

```
Associated to the substance of the subst
  ö
  Gaps
  ô
  Length 348;
  Indels
  ö
  70.7%; Score 41; DB 2; 63.6%; Pred. No. 1.8;
  4; Mismatches
  Query Match 70.7
Best Local Similarity 63.6
Matches 7; Conservative
  |:|:|:||| RVALRKLLLRY 108
  2 RLAIRRILLRY 12
   8
RESULT
  g
  ò
```

RESULT

Pelycoprotein - Chinese hamster (fragment)
C:Species: Cricetulus griseus (Chinese hamster)
C:Species: Cricetulus griseus (Chinese hamster)
C:Species: Cricetulus griseus (Chinese hamster)
C:Accession: 148120
C:Accession: 148120
R:Ng, W.F.; Sarangi, F.; Zastawny, R.L.; Veinot-Drebot, L.; Ling, V.
Mol. Cell. Biol. 9, 1224-1232, 1989
A.Title: Identification of members of the P-glycoprotein multigene family.
A:Reference number: 148119; MUID:89261726
A:Accession: 148120
A:Accession: 148120
A:Molecule type: DNA
A:Residues: 1-252 <RES>
A:Cross-references: GB:M25792; NID:9576810; PIDN:AAA53440.1; PID:9576813
C:Genetics:
A:Genetics: A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 148120
A:Accession: 14

A; Introns. Fs. 66/3; 135/3; 184/3 C;Superfamily: multidrug resistance protein; ATP-binding cassette homology C;Reywords: ATP: P-loop F;25-221/Domain: ATP-binding cassette homology <ABG2> F;25-221/Domain: ATP-binding motif A (P-loop)

Query Match

Length 252; 63.8%; Score 37; DB 2;

ò g

```
A; Molecule type: DNA
A; Residues: 1-141 CARNA
A; Residues: 1-141 CARNA
A; Residues: 1-141 CARNA
A; Cross-references: GB: ABC01323; GB: ABC01273; NID: g3328931; PIDN: AAC68107.1; PID: g332
A; Cross-references: GB: ABC01323; GB: ABC01273; NID: g3328931; PIDN: AAC68107.1; PID: g332
A; Experimental source: serotype D, strain UW-3/Cx
R; Gu, L.; Wenman, W.M.; Remacha, M.; Meuser, R.; Coffin, J.; Kaul, R.
J. Bacteriol. 177, 2594-2601, 1995
A; Title: Chlamydia trachomatis RNA polymerase alpha subunit: sequence and structural
A; Reference number: 140743; MUID: 95247702
  Aravind, L.; Mitche
  C;Accession: G70882
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, R.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, A;Authors: Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Qua, Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A;Reference number: A70500; MUID:98295987
   A;Residues: 1-309 <COL>
A;Cross-references: GB:AL008967; GB:AL123456; NID:g3261491; PIDN:CAA15591.1; PID:e129
A;Experimental source: strain H37Rv
   ;Gene: Rv2776c
;Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; fer
;9-211/Domain: cytochrome-b5 reductase homology <CBR>
;240-297/Domain: ferredoxin [2Fe-25] homology <FER>
  humans: Chlamydia
   A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
   C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 13-Aug-1999
C;Accession: H71504; 140747
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, I
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: C}
A;Reference number: A71570; MUID:99000809
  C, Species: Mycobacterium tuberculosis
C, Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 29-Sep-1999
   Gaps
   Gaps
   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 20-115,'R',117-141 <GUL>
A;Cross-references: GB:L33834; NID:g620026; PIDN:AAA74990.1; PID:g620030
   ..
  ö
   probable oxidoreductase - Mycobacterium tuberculosis (strain H37RV)
   Length 141;
   Length 309;
   Indels
   Indels
  C,Genetics:
A,Gene: r117
C;Superfamily: Escherichia coll ribosomal protein L17
C;Keywords: protein biosynthesis; ribosome
  DB 2;
6.9;
  Score 36; DB 2;
Pred. No. 15;
1; Mismatches
   Score 36; DB 2
Pred. No. 6.9;
4; Mismatches
   ribosomal protein L17 - Chlamydia trachomatis
  62.1%;
54.5%;
   Query Match 62.1%;
Best Local Similarity 87.5%;
Matches 7; Conservative
  6; Conservative
   2 RLAIRRILLRY 12
   |||: |:::||
64 RLAVGRLMVRY 74
   Query Match
Best Local Similarity
Matches 6; Conserv
  ||:|||||
65 YRIAIRRI 72
  ω
   A; Accession: H71504
  1 YRLAIRRI
   g
   δ
   ò
  Q.
  R;Endicott, J.A.; Sarangi, F.; Ling, V. DNA Seq. 2, 89-101, 1991
A;Title: Complete cDNA sequences encoding the Chinese hamster P-glycoprotein gene family A;Reference number: 148121; MUID:92135896
                              ö
  ö
  ö
   P-glycoprotein - Chinese hamster (fragment)
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 20-Aug-1999
  p-glycoprotein isoform III - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: I48123
   A; Introns: 566/3; 142/3; 191/3
C:Superfamily: multidrug resistance protein; ATP-binding cassette homology
C:Keywords: ATP: P-loop
F;25-228/Domain: ATP-binding cassette homology <ABC2>
F;42-49/Region: nucleotide-binding motif A (P-loop)
  A.Cross-references: GB:M60042; NID:g191168; PIDN:AAA68885.1; PID:g191169
C.Superfamily: multidrug resistance protein; ATP-binding cassette homology
C.Superfamily: multidrug resistance protein; ATP-binding cassette homology
E:412-606/Domain: ATP-binding cassette homology <ABC1>
F:423-436/Region: nucleotide-binding motif A (P-loop)
F:1074-1250/Domain: ATP-binding cassette homology <ABC2>
F:1071-1078/Region: nucleotide-binding motif A (P-loop)
   C; Accession: I48119
R; Ng, W.F.; Sarangi, F.; Zastawny, R.L.; Veinot-Drebot, L.; Ling, V.
Nol. Cell. Biol. 9, 1224-1232, 1989
A; Title: Identification of members of the P-glycoprotein multigene family. A; Reference number: 148119; MUID:89261726
A; Accession: I48119
  Gaps
   Gaps
  A;Molecule type: DNA
A;Residues: 1-259 <RES>
A;Cross-references: GB:M25792; NID:9576810; PIDN:AAA53439.1; PID:9576812
                              ö
   ó
  ö
   DB 2; Length 1281;
  Length 259;
                                 Indels
   Indels
   Indels
   ij
                              1;
   A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-1281 <RES>
   DB 2;
   A;Status: preliminary; translated from GB/EMBL/DDBJ
Pred. No. 7.8;
1; Mismatches
  Mismatches
  Pred. No. 37;
1; Mismatches
   Score 37;
Pred. No. 8
  Score 37;
   63.8%;
80.0%;
   63.8%;
80.0%;
80.08;
Similarity 80.08; Conservative
  Conservative
   Query Match 63.8
Best Local Similarity 80.0
Matches 8; Conservative
  |||||| |:|
|1184 RLAIRRALIR 1193
  |||||| |:|
|155 RLAIRRALIR 164
  ||||||| |:|
162 RLAIRRALIR 171
  Query Match
Best Local Similarity
Matches 8; Conserv
   RLAIRRILLR 11
  2 RLAIRRILLR 11
  2 RLAIRRILLR 11
   A; Accession: 148123
Best Local
   ~
                        Matches
```

q

ò

ö

ö

g

οy

ö

Gaps

; 0

```
Conserved hypothetical protein yfkC - Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Accesion: G69807
R;Kunst, F; Ogasawara, N.; Moszer, I; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C; Bron, S.; Broulllet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fullita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
A;Authors: Foulger, D.; Fritz, C.; Fullita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
A;Authors: Lauber, J.; Lazarevic, W.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Sato, T.; Sato, T.; Sato, T.; Sato, T.; Sato, S.; Satolletch, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Se
   Across references: GB:L07065
C;Genetics:
A;Cross references: GB:L07065
A;Cross references: FlyBase: FBgn0010241
A;Cross references: FlyBase: FBgn0010241
A;Introns: 87/3; 182/2; 832/3; 934/3; 981/2; 1168/3; 1217/3
A;Introns: 87/3; 182/2; 832/3; 934/3; 981/2; 1168/3; 1217/3
A;Introns: 87/3; 182/2; 832/3; 934/3; 981/2; 1168/3; 1217/3
C;Superfamily: unasigned ATP-binding cassette proteins; ATP-binding cassette homology cABCl>
F;418-613/Domain: ATP-binding cassette homology cABCl>
F;1058-1254/Domain: ATP-binding cassette homology cABC2>
F;1075-1082/Region: nucleotide-binding motif A (P-loop)
   R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
   GB:AE000512; NID:g4980893; PID:g4980900; TIGR:TM0396
   Nature 399, 323-329, 1999
A;Tille: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316
A;Accession: E72382
   iron-sulfur cluster-binding protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun_1999 #sequence_revision 11-Jun-1999 #text_change 20-Sep-1999
   60.3%; Score 35; DB 2; Length 1283; 70.0%; Pred. No. 91; 1.1 Indels 1; Indels
   2; Length 152;
  A; Gene: TM0396
C: Superfamily: nrfC protein; ferredoxin 2[4Fe-45] homology
   58.6%; Score 34; DB 66.7%; Pred. No. 18; iive 3; Mismatches
   A;Molecule type: DNA
A;Rosidues: 1-152 ARN>
A;Cross-references: GB:AE001719; GI
A;Experimental source: strain MSB8
   Query Match 60.3
Best Local Similarity 70.0
Matches 7; Conservative
   Conservative
A; Molecule type: DNA
A; Residues: 1-1283 <GER>
   |:|||| |:|
547 RIAIRRALIR 556
   Local Similarity
nes 6; Conserv
   2 RLAIRRILLR 11
   :|:||||:|
3 IAVRRILIR 11
   3 LAIRRILLR 11
   A; Status: preliminary
   C; Accession: E72382
   Query Match
Best Local S:
Matches 6;
   ö
   g
   δ
  ద
  hypothetical protein (insertion sequence ISH27-3) - Halobacterium halobium C;Species: Halobacterium halobium C;Species: Halobacterium halobium C;Species: Halobacterium halobium C;Species: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 30-Jun-1998 C;Accession: S15593 W.Cleic Acids Res. 18, 6921-6925, 1990 A;Pitle: Transposition burst of the ISH27 insertion element family in Halobacterium halo A;Reference number: S15591; MUID:91088266 A;Accession: S15593 A;Accession: S15593 A;Accession: S15593 A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-388 cPFE> A;Molecule type: JA A;Molecule typ
   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-142 <ARN>
A;Residues: 1-142 <ARN>
A;Cross-references: GB:AE001647; GB:AE001363; NID:g4376920; PIDN:AAD18764.1; PID:g437692
A;Experimental source: strain CWL029
C;Genetics:
  Genomics 17, 83-88, 1993
A;Title: Analysis of Mdr50: a Drosophila P-glycoprotein/multidrug resistance gene homolo A;Reference number: A47377; MUID:94010914
A;Accession: A47377
   b
  L.; Grimwood,
   ö
   ö
  multidrug resistance protein Mdr50 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Bate: 19-May-1995 #sequence_revision 19-May-1995 #text_change 10-Jul-1998
C;Accession: A4/377
R;Gerrard, B.; Stewart, C.; Dean, M.
   C;Species: Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: C72053
   Gaps
   Gaps
  R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis. A;Reference number: A72000; MUID:99206606
A;Accession: C72053
   ö
   ö
   Score 35; DB 2; Length 142;
Pred. No. 11;
4; Mismatches 1; Indels
  Length 388

    Chlamydia pneumoniae (strain CWL029)

   A;Gene: rll7
C;Superfamily: Escherichia coli ribosomal protein Ll7
  Score 35; DB 2;
Pred. No. 29;
2; Mismatches
   C:Genetics:
A:Mobile element: insertion sequence ISH27-3
A:Start codon: GTG
   60.3%;
54.5%;
  60.3%;
   Conservative
   6; Conservative
   2 RLAIRRILLRY 12
   |:|| |:::||
64 RIAIGRLMVRY 74
   Query Match
Best Local Similarity
  Best Local Similarity
Matches 6; Conser
  154 YRLAVRRL 161
   A;Status: preliminary
   1 YRLAIRRI 8
  Query Match
   Matches
   δy
   g
   ò
  a
```

ö

Gaps

ö

Indels

ö

```
A; Molecule type: DNA
A; Residues: 1-690 <COND
A; Cross-references: CENBL: Z49212; NID: 9798940; PIDN: CAA89134.1; PID: 9798943; MIPS: YMR3
R; Leighton, J.; Schatz, G
EMBO J. 14, 188-195, 1995
A; Title: An ABC transporter in the mitochondrial inner membrane is required for norma
A; Reference number: S51801; MUID: 95129546
  700953
hypothetical protein F20D22.3 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Preb-1999 #sequence_revision 12-Feb-1999 #text_change 20-Sep-1999
C;Accession: T00953
R;Vysotskaia, V.S.; Osborne, B.I.; Schwartz, J.R.; Toriumi, M.; Kwan, A.; Yu, G.; Oji
  Agenome: nuclear

C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

C; Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog

C; Superfamily: unassigned ATP-binding reassette proteins; ATP-binding cassette homolog

C; Stywords: ATP, mitochondrial inner membrane #status predicted <TM1>
F; 148-164/Domain: transmembrane #status predicted <TM2>
F; 233-249/Domain: transmembrane #status predicted <TM3>
F; 258-274/Domain: transmembrane #status predicted <TM4>
F; 452-648/Domain: ATP-binding cassette homology <ABC>
F; 469-476/Region: nucleotide-binding motif A (P-loop)
  A;Cross-references: EMBL:AL021728; NID:e1355643; PID:e1301392; PIDN:CAA16821.1
C;Genetics:
  C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C;Accession: T13646
R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
A;Bescription: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: Z17694
A;Accession: T1364
A;Actus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-735 <FFR>
  A;Molecule type: DNA
A;Residues: 1-27,'RNHS',28-690 <LEI>
A;Cross-references: EMBL:X82612; NID:9575392; PIDN:CAA57938.1; PID:9575393
C;Genetics:
   hypothetical protein EG:95B7.9 - fruit fly (Drosophila melanogaster)
  ö
   ö
  Length 690;
  Length 735;
  Indels
   Indels
  58.6%; Score 34; DB 2; 75.0%; Pred. No. 82; 1ve 2; Mismatches
   ;;
  Score 34; DB 2
Pred. No. 77;
2; Mismatches
   A;Gene: SGD:ATM1; MDY
A;Cross-references: SGD:S0004916; MIPS:YMR301c
A;Map position: 13R
  A; Introns: 39/3; 93/2; 294/2; 387/2
A; Note: EG:95B7.9
  Query Match 58.6%;
Best Local Similarity 70.0%;
Matches 7; Conservative
  Query Match 58.6
Best Local Similarity 75.0
Matches 6; Conservative
   580 RLAIARVLLK 589
   2 RLAIRRILLR 11
   111:1:11
473 IRRLLIRY 480
  5 IRRILLRY 12
   A; Accession: S51801
   ò
   ò
  g
  셤
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamancto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; Alathors: Yoshikway, H.; Zanametein, E.; Yoshikway, H.; Danchin, A. A.Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A. Reference number: A69580; MUID:98044033
  R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature, 333, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:98295987
  A;Cross-references: GB:295586; GB:AL123456; NID:g3261785; PIDN:CAB09080.1; PID:e317168; C;Genetics:
  A;Status: preliminary, nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Cross-treferences: GB:259108; GB:AL009126; NID:g2633055; PID:e1182784; PID:g2633118 A;Experimental source: strain 168
  ö
  ö
  A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-349 <COL>
  C.Species: Saccharomyces cerevisiae
C.Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C.Accession: 554.211, 533971; $51801
S.K.Kispal, G.; Lill, R.; Neupert, N.
submitted to the EMBL Data Library, November 1994
   C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Jul-1999
  A:Molecule type: DNA
A:Residues: 1-690 <KIS>
A:Cross-treferences: EMBL:X81715; NID:g793876; PIDN:CAA57359.1; PID:g793877
A:Connor, R.; Churcher, C.M.
submitted to the EMBL Data Library, April 1995
   Gaps
   ö
  ö
  ATM1 protein precursor - yeast (Saccharomyces cerevisiae)
N;Alternate names: MDY protein; protein YM9952.03c; protein YMR301c
   probable bioB protein - Mycobacterium tuberculosis (strain H37RV)
  Length 280;
  Length 349;
   Score 34; DB 2;
Pred. No. 32;
  Score 34; DB 2;
Pred. No. 40;
  3; Mismatches
  Mismatches
   58.6%;
  58.6%;
  C; Superfamily: biotin synthetase
  Query Match
Best Local Similarity 66.7
Matches 6; Conservative
   Query Match
Best Local Similarity 50.0
Matches 6; Conservative
   A; Reference number: S54211
A; Accession: S54211
  :|||: | :||:
280 FRLALPRIMLRF 291
  1 YRLAIRRILLRY 12
   252 LAVRRVLVR 260
   3 LAIRRILLR 11
  ò
   g
   g
  ò
```

ö

Gaps

ö

Gaps

Trans Translation Contraction

1、1、黄粉香力 1

```
K.; Feng, J.; Kim, C.; Kurtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.;
submitted to the EMBL Data Library, May 1998
A.Pescription: Arabidopsis thaliana chromosome 1 BAC F20D22 complete sequence.
A.Reference number: 214214
A.Accession: T00953
A.Status: preliminary: translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-814 <VYS>
A.Cross-references: EMBL.AC002411; NID:g2570223; PID:g3142290; GSPDB:GN0059; ATSP:F20D22
A.Cross-references: EMBL.AC002411; NID:g2570223; PID:g3142290; GSPDB:GN0059; ATSP:F20D22
A.Gene: A.FSP:F20D22.3
A.Map position: 1
A.Introns: 64/1; 144/1; 239/3; 304/1; 386/1; 415/2; 473/3; 516/3; 554/3; 594/2; 624/3; 6
   ö
  Gaps
  ö
   Ouery Match 58.6%; Score 34; DB 2; Length 814; Best Local Similarity 60.0%; Pred. No. 91; Matches 6; Conservative 2; Mismatches 2; Indels
   3 LAIRRILLRY 12
| :|{:|| |
263 LVVRRLLLNY 272
   qq
  ò
```

Search completed: February 7, 2000, 11:54:29 Job time: 24339 sec

THIS PAGE BLANK (USPTO)

```
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
```

- protein search, using sw model OM protein

; Search time 63.71 Seconds
(without alignments)
5.625 Million cell updates/sec 8, 2000, 00:59:56 February Run on:

US-08-653-294-18 58 Title:

1 YRLAIRRILLRY 12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

82229 segs, 29864866 residues Searched:

82229 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

SwissProt\_38:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|           | Description | ;     |            |      | _          |            | _          |            | P04050 saccharomyc |            | P75111 mycoplasma | Q59309 clostridium | P16215 pan troglod | P30511 homo sapien | P45082 haemophilus | P44407 haemophilus | P76585 escherichia |           |            |            |            |            | _          |            |          |                | mycobacte  |            |            |            | _<br>E     | 0         | 긆          | 4         |            | 2          |
|-----------|-------------|-------|------------|------|------------|------------|------------|------------|--------------------|------------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|-----------|------------|------------|------------|------------|------------|------------|----------|----------------|------------|------------|------------|------------|------------|-----------|------------|-----------|------------|------------|
| SUMMARIES | Ę           | -     | HLAF_MACMU |      | RL17_CHLTR | CRTI_CERNC | BIOB_MYCTU | ATM1_YEAST | RPB1_YEAST         | RPOH_METJA | RNPA_MYCPN        | G3P_CLOPA          | 1C28_PANTR         | HLAF_HUMAN         | CYDD_HAEIN         | MSBA_HAEIN         | YPHG_ECOLI         | V187_BPT3 | YCD4_YEAST | TER4_ECOLI | TER8_PASPI | YHS5_CAEEL | A2AB_CAVPO | A2AB_HUMAN | A2AB_RAT | A2AB_MOUSE     | Y221_MYCTU | BGL2_BACSU | PGKD_TRYBB | YETI_SCHPO | RNPA_MYCGE | DP1_MOUSE | RPO6_VACCV | RPO6_VARV | NH10_YEAST | BCRA_BACLI |
|           | a c         | 3 ; , |            |      |            |            |            |            |                    |            |                   | Н                  | Н                  | Н                  | Н                  | Н                  | Н                  | -         | Н          | Н          |            | Н          | -          |            | -        | <del>, ,</del> | Н          | -          | Н          | ~          | Н          | Н         | 1          | Н         | Н.         | -1         |
|           | L'ength     |       | 348        | 1281 | 122        | 621        | 349        | .069       | 1733               | 78         | 118               | 334                | 346                | 362                | 286                | 587                | 1124               | 83        | 212        | 217        | 218        | 411        | 448        | 450        | 453      | 455            | 469        | 477        | 508        | 693        | 128        | 185       | 185        | 185       | 203        | 306        |
| d         | Query       |       | 0          | m    | 2          | 3          | 8          | œ          | æ                  | 9          | 9                 | 9                  | 9                  | 9                  | 9                  | 9                  | 56.9               | S         | S          | S          | S          | S          | S          | S          | S        | S              | S          | S          | S          | S)         | 53.4       | 53.4      | S          | m         | 53.4       | 53.4       |
|           | Stone       |       | 41         | 37   | 36         | 36         | 34         | 34         | 34                 | 33         | 33                | 33                 | 33                 | 33                 | 33                 | 33                 | 33                 | 32        | 32         | 32         | 32         | 32         | 32         | 32         | 32       | 32             | 32         | 32         | 32         | 32         | 31         | 31        | 31         | 31        | 31         | 31         |
|           | Result      | ; ;   | н,         | 7    | က          | 4          | ហ          | 9          | 7                  | ω          | თ                 | 10                 | 11                 | 12                 | 13                 | 14                 | 15                 | 16        | 17         | 18         | 19         | 20         | 21         | 22         | 23       | 24             | 25         | 56         | 27         | 28         | 29         | 30        | 31         | 32        | 33         | 34         |

Score 41; DB 1; Length 348;

70.7%;

Query Match

| P31132 escherichia 004630 herpes simp P52449 herpes simp P24653 orgyia pseu 008370 pseudomonas 009842 schizosacch P22638 anabaena sp P2729 escherichia 027707 nosema locu P74856 salmonella P45306 haemophilus |
|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| OPPB_ECOLI<br>VGLM_HSV6U<br>VGLM_HSV6Z<br>YIOL_NPVOP<br>HEMA_PSESY<br>YAEL_SCHPO<br>HERA_ANASP<br>MSBA_COLI<br>SYI_NOSLO<br>SSAV_SALTY<br>PRC_HAEIN                                                            |
| нанананана                                                                                                                                                                                                     |
| 3300<br>3300<br>3300<br>3300<br>3300<br>3300<br>3300<br>330                                                                                                                                                    |
| . 4444444444                                                                                                                                                                                                   |
|                                                                                                                                                                                                                |
| 33333333333333333333333333333333333333                                                                                                                                                                         |
| ₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩                                                                                                                                                                          |

## ALIGNMENTS

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  EMBL; 221819; CAL...

JR EMBL; 221819; CAL...

DR PIR; S29990; S29990;

DR HSSP; P03989; 118A.

DR PRAM; PF00129; MHC; 1.

DR PFAM; PF00129; MHC, 1.

DR PFAM; PF00129; MHC, 1.

DR PFAM; PF00129; MHC, 1.

TT SIGNAL

2. 348 HIA CHAIN F.

FT CHAIN 22 348 HIA CHAIN F.

FT CHAIN 22 113 EXTRACELLULAR ALPHA-1.

FT NOMAIN 22 113 EXTRACELLULAR ALPHA-2.

CONNECTING PEPTIDE.
   01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
115-JUL-1999 (Rel. 38, Last annotation update)
HIA CLEASI I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F PRECURSOR (HLA F ANTIGEN) (LEUKOCYTE ANTIGEN F).
  OTTING N., BONTROP R.E.; "Characterization of the rhesus macaque (Macaca mulatta) equivalent of HLA-F.";
  Immunogenetics 38:141-145(1993).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE INVOLWE SYSTEM.
-!- SUBDINIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
  Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae;
  CYTOPLASMIC TAIL.
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
; 3A375142 CRC32;
                             348 AA
                             PRT;
   39300 MW;
                           STANDARD;
   22
114
206
308
332
124
109
348 AA;
   SEQUENCE FROM N.A. MEDLINE; 93246295.
                          HLAF_MACMU P33617;
   DOMAIN
DISULFID
DISULFID
CARBOHYD
SEQUENCE
  Macaca.
KESULT 1
HLAF_MACMU
```

Wed Feb

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                ö
   DNA Seq. 2:89-101(1991).

-!- FUNCTION: ENERGY-DEPENDENT EFFLUX PUMP RESPONSIBLE FOR DECREASED DEUCTION: ENERGY-DEPENDENT EFFLUX PUMP CELLS.

-:- SUBCELLULAR LOCATION IN MUTITEGRAL MEMBRAPE PROPEIN.

-!- SUBCELLANEOUS: PGP ISOPORMS DIFFER IN THEIR DRUG TRANSPORT CAPABILITIES: PGP1 AND PGP2 CAN MEDIATE MDR, WHILE PGP3 APPARENTLY
   SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MDR SUBFAMILY.
                Gaps
   MEDLINE; 92135896.
ENDICOTT J.A., SARANGI F., LING V.;
"Complete CDNA sequences encoding the Chinese hamster P-glycoprotein
  Cricetulus griseus (Chinese hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Cricetulus.
   PFAM; PF00005; ABC_tran; 2.
PFAM; PF00664; ABC_membrane; 2.
ATP-binding; Glycoprotein; Transmembrane; Transport; Duplication;
                ö
   Score 37; DB 1; Length 1281; Pred. No. 14;
                Indels
  CYTOPLASMIC (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
  CYTOPLASMIC (POTENTIAL)
  CYTOPLASMIC (POTENTIAL)
   01-NOV-1991 (Rel. 20, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MULTIDRUG RESISTANCE PROTEIN 3 (P-GLYCOPROTEIN 3).
                ö
   9FE9DF5C CRC32;
Pred. No. 0.52;
1; Mismatches
  (POTENTIAL)
   1281 AA
   POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
  PS00211; ABC_TRANSPORTER; 1.
  01-NOV-1991 (Rel. 20, Created)
   EMBL; M60042; AAA68885.1; -.
   63.68;
   140866
                Conservative
   STANDARD;
  429 43
1071 107
1281 AA;
   |:|:||:||||
98 RVALRKLLLRY 108
  2 RLAIRRILLRY 12
Best Local Similarity
Matches 7; Conserv
   P13569; 1NBD
  SEQUENCE FROM N.A.
  Multigene family
   PGY3 OR PGP3
  gene family
  MDR3_CRIGR
P23174;
   NP_BIND
SEQUENCE
  TRANSMEM
TRANSMEM
TRANSMEM
  FRANSMEM
   FRANSMEM
  FRANSMEM
   TRANSMEM
   FRANSMEM
  FRANSMEM
  PRANSMEM
  FRANSMEM
  FRANSMEN
  NP_BIND
  MDR3_CRIGR
  DOMAI
  RESULT
  Ω
```

63.8%; 80.0%;

Query Match Best'Local Similarity

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
ö
  ö
 Gaps
  Gaps
  GULJ., WENMAN W.M., REMACHA M., MEUSER R.U., COFFIN J.M., KAUL R.; "Chlamydia trachomatis RNA polymerase alpha subunit: sequence and structural analysis.";
J. Bacteriol. 177:2594-2601(1995).
J. Bacteriol. 177:2594-2601(1995).
  Cercospora nicotianae.
Eukaryota: Fungi; Ascomycota; Euascomycetes; Loculoascomycetes;
Pleosporales; Leptosphaeriaceae; mitosporic Leptosphaeriaceae;
;
0
  ö
  "Isolation, sequence, and characterization of the Cercospora nicotianae phytoene dehydrogenase gene."; Appl. Environ. Microbiol. 60:2766-2771(1994).
   Length 122;
   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE)
Indels
   1; Indels
1;
   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia
   122 AA; 13969 MW; B8C43F7D CRC32;
   Score 36; DB 1;
Pred. No. 1.7;
  Last sequence update)
Last annotation update)
  621 AA.
   122 AA
  Pred. No. 1.7;
4; Mismatches
 Mismatches
  PROSITE; PS01167; RIBOSOMAL_L17; 1.
PFAM; PF01196; Ribosomal_L17; 1.
  PRT;
 ï
  Created)
   EMBL; L33834; AAA74990.1; -. PROSITE; PS01167; RIBOSOMAL L
   62.1%;
54.5%;
  SEQUENCE FROM N.A.
STRAIN-434/BU / SEROVAR L2;
MEDLINE; 95247702.
   50S RIBOSOMAL PROTEIN L17.
   STRAIN-ATCC 18366;
MEDLINE; 94368091.
EHRENSHAFT M., DAUB M.E.;
Conservative
   Conservative
  STANDARD;
  Chlamydia trachomatis.
  |||||| |:|
1184 RLAIRRALIR 1193
   45 RLAVGRLMVRY 55
  2 RLAIRRILLRY 12
                          2 RLAIRRILLR 11
  Query Match
Best Local Similarity
   Ribosomal protein.
SEQUENCE 122 AA;
   SEQUENCE FROM N.A.
  CRTI_CERNC
P48537;
  ;
9
   Cercospora.
.;
0
   CRII_CERNC
  Matches
Matches
                            õ
   ò
   g
```

```
EMBL; X82612; CAA57938.1; -.
  MEDLINE; 98089018.
  SEQUENCE FROM N.A
  homeostasis.
  ATM1_YEAST
P40416;
  SEQUENCE
  ATM1_YEAST
 ŏ
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   ö
  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
  STRAIN-H37RY
MEDLINE: 98295987.
MEDLINE: 98295987.
GOLE S.T., BROSCH R., GAS S., BARRY C.E. III, TEKAIA F.,
GONDON S.V., EIGLMEIER K., GAS S., BARRY C.E. III, TEKAIA F.,
BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
BADCOCK K., BASHAM D., BROWN D., CHILLINGWORTH T., CONNOR R.,
BADCOCK K., BASHAM D., ELTWELL T., GENTLES S., HAMLIN N., HOLROYD S.,
HONNISH T., JAGELS K., KROGH A., MCLENN J., MOULE S., MURPHY L.,
OLIVER S., SEEGER K., SKELTON S., SQUARES S., SQARES J.,
TAYLOR K., WHITHERDAD S., BARRELL B.G.,
"Deciphering the biology of Mycobacterium tuberculosis from the
complete genome sequence.";
 THE
   SIMILARITY: TO BACTERIAL PHYTOENE DEHYDROGENASES AND TO BACTERIAL METHOXYNEUROSPORENE DEHYDROGENASE (CRID).
  Gaps
   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
FUNCTION: THIS ENZYME CONVERTS PHYTOENE INTO ZETA-CAROTENE VIA INTERMEDIARY OF PHYTOFLUENE BY THE SYMMETRICAL INTRODUCTION OF
   EMBL; U03903; AAB86988.1; -.
PROSITE; PS00982; PHYTOENE_DH; 1.
Carotenoid biosynthesis; Oxidoreductase; FAD; Flavoprotein; NAD;
  ô
                         DOUBLE BONDS AT THE C-11 AND C-11' POSITIONS OF PHYTOENE.
  Score 36; DB 1; Length 621;
Pred. No. 10;
  Indels
  FAD (ADP PART) (POTENTIAL).
   15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
BIOB OR RV1589 OR MICY336.15C.
   CDA97504 CRC32;
   349 AA.
  3; Mismatches
                                      COFACTOR: FAD (PROBABLE).
PATHWAY: CAROTENOID BIOSYNTHESIS.
   69529 MW;
  62.1%;
54.5%;
  Mycobacterium tuberculosis.
   complete genome sequence.
Nature 393:537-544(1998).
  Conservative
   STANDARD;
   STRAIN-PASTEUR;
YU S., JACOBS W.R. JR.;
   140 YELSVREVLLR 150
   621 AA;
   1 YRLAIRRILLR 11
  Ouery Match
Best Local Similarity
Matches 6; Conserv
  SEQUENCE FROM N.A.
   FROM N.A.
  Transmembrane.
   BIOB_MYCTU
006601;
  NP_BIND
TRANSMEM
   SEQUENCE
  SEQUENCE
   BIOB_MYCTU
ŏ
   qq
```

```
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb.sib.ch/announce/or send an email to license@isb-sib.ch).
   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
   ö
  STRAIN-S288C / AB972;
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
CONNOR R., CHURCHER C.M., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
SUDMILTEG (APR-1995) to the EWEL/Genbank/DDBJ databases.
-!- FUNCTION: PROBABLE TRANSPORTER FOR A YET UNKNOWN SUBSTRATE.
REQUIRED FOR MITOCHONDRIAL IRON HOREOSTASIS.
-!- SUBUNIT: HOMODIMER OR HETREODIMER (POTENTIAL).
-!- SUBUNIT: HOMODIMER OR HETREODIMER (POTENTIAL).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
   SEQUENCE FROM N.A.
STRAIN=JK9-12D ALPHA;
MEDLINE; 95129546.
LEIGHTON J., SCHATZ G.;
"An ABC transporter in the mitochondrial inner membrane is required for normal growth of yeast.";
EMBO J. 14:188-195(1995).
   -!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Hemiascomycetes; Saccharomycetales;
Saccharomycetaceae; Saccharomyces.
   ö
  KISPAL G., CSERE P., GUIARD B., LILL R.; "The ABC transporter Atmlp is required for mitochondrial iron
   Score 34; DB 1; Length 349;
Pred. No. 14;
Mismatches 2; Indels
  EMBL; AF041819; AAB969b2.1; -
Biotin biosynthesis; Iron-sulfur; Transferase.
METAL 85 85 IRON-SULFUR (POTENTIAL).
METAL 89 IRON-SULFUR (POTENTIAL).
   31B0B9DA CRC32
   01-FEB-1996 (Rel. 33, Last sequence update)
115-UTL-1999 (Rel. 38, Last annotation update)
11TCHONDRIAL TRANSPORTER ATMI PRECURSOR.
ATMI OR MDY OR YMR301C OR YM9952.03C.
   690 AA
   (ABC TRANSPORTERS). MDR SUBFAMILY.
  PRT;
   01-FEB-1995 (Rel. 31, Created)
   37550 MW;
   58.6%;
  FEBS Lett. 418:346-350(1997).
   EMBL; 295586; CAB09080.1; -. EMBL; AF041819; AAB96962.1; -
   Conservative
   STANDARD;
  :|||: | :||:
280 FRLALPRIMLRF 291
   1 YRLAIRRILLRY 12
   349 AA;
   Query Match
Best Local Similarity
Matches 6; Conserv
  SEQUENCE FROM N.A.
   INNER MEMBRANE
```

```
PROSITE;
  g
  ID ACCOOC ON THE SERVICE OF THE SERV
  ò
   ö
   FEMS Microbiol. Lett. 130:221-230(1995).
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALXZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
  Transmembrane; Transport; Mitochondrion; Inner membrane;
   Gaps
   RPBI_YEAST STANDARD; PRT; 1733 AA.
P04050; Q12364; Q92315;
P04050; Q12364; Q92315;
D1-NOV-1986 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNN-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (B220).
RPB1 OR RPD21 OR RPB220 OR SUAB OR YDL140C OR D2150.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
  CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE
   STRAIN-A364A;
MEDLINE; 85282617.
ALLISON L.A., MOYLE M., SHALES M., INGLES C.J.;
Extensive homology among the largest subunits of eukaryotic and prokaryotic RNA polymerases.";
Cell 42:599-610(1985).
  STRAIN-S288C;
MEDILINE; 95377607.
CRONAN J.E. JR., WALLACE J.C.;
"The gene encoding the biotin-apoprotein ligase of Saccharomyces
   RNA(N).
SUBUNIT: RNA POLYMERASE II CONSISTS OF 12 DIFFERENT SUBUNITS.
   ó
  MITOCHONDRION (POTENTIAL).
MITOCHONDRIAL TRANSPORTER ATMI.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
  WOELFL S., HANEMAN V., SALUZ H.P.;
"Analysis of a 26,756 bp segment from the left arm of yeast
  DB 1; Length 690;
29;
   1; Indels
   REF. 1)
   ATP (POTENTIAL).
S -> SRNHS (IN RE
2E8AEC70 CRC32;
  Pred. No. 29;
; Mismatches
  Score 34;
Pred. No. :
                            SGD: LO000140; ATM1.
PROSITE: PS00014; ER_TARGET; 1.
PROSITE: PS00211; ABC_TRANSPORTER; 1.
PFAM; PF000005; ABC_Ltran; 1.
PFAM; PF000664; ABC_membrane; 1.
ATP-binding; Transmembrane; Transport
  Saccharomycetaceae; Saccharomyces.
   SEQUENCE OF 1669-1733 FROM N.A.
   77522 MW;
  58.6%;
                    EMBL; Z49212; CAA89134.1; -.
CAA57359.1;
  Ouery Match
Best Local Similarity 70.۰۰
نمر 7; Conservative
   chromosome IV.";
Yeast 12:1549-1554(1996).
   SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
MEDLINE; 97127826.
   27
690 AA;
  ||||| |:||:
580 RLAIARVLLK 589
   RLAIRRILLR 11
   SEQUENCE FROM N.A.
  Transit peptide
TRANSIT
   NP_BIND
CONFLICT
SEQUENCE
   TRANSMEM
   TRANSMEM
   FRANSMEM
  TRANSMEM
  FRANSMEM
  TRANSMEM
   RPB1_YEAST
ò
  g
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
   ö
  PROMISE STANDARY PROBLES : NAME PROBLES : NAME PROBLES : NAME PROBLES : NAME PROBLES : NAME PROBLES : NAME PROBLES : NAME PROBLES : NAME PROBLES : NAME : NA
                                      -:- SUBCELLULAR LOCATION: NUCLEAR.
-:- PTM: THE TANDEM T RESIDUES REPEATS CAN BE HIGHLY PHOSPHORYLATED.
THE PHOSPHORYLATION ACTIVATES POL2.
-:- MISCELLANGOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN BURARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE II FOR 5S AND TRIM GENES.
-:- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
  STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

STRAIN-JAL-1 / DSM 2661 / ATCC 43067;

BULT C.J., WHITE O., OLSEN G.J., ZHOU L., FLEISCHMANN R.D.,

SUTTON G.G., BLAKE J.A., FITZGERALD L.M., CLAYTON R.A., GOCAYNE J.D.,

KERLAVAGE A.R., DOUGHBERTY B.A., TOMB J.D., REFORT C.I.,

OVERBEEK R., KIRKNESS E.F., WEINSTOCK K.G., MERRICK J.M., GLODEK A.,

SCOTT J.L., GEOGHAGEN N.S.M., WEIDMAN J.E., FUHRMANN J.L., NGUYEN D.,

UTTERBACK T.R., KELLEY J.M., PETERSON J.D., SADOW P.W., HANNA M.C.,

COTTON M.D., ROBERTS K.M., HURST M.A., WOBSE C.R., VENTER J.C.,

"COMPLETE GENOME SEQUENCE Of the methanogenic archaeon, Methanococcus
  Gaps
   ;
0
SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE II.
  Length 1733;
  Archaea; Euryarchaeota; Methanococcales; Methanococcaceae; Methanococcus.
   3; Indels
   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
DNA-DIRECTED RNA POLYMERASE SUBUNIT H (EC 2.7.7.6).
  Score 34; DB 1;
Pred. No. 79;
1; Mismatches
   78 AA.
   POL_II_REPEAT; 22
  EMBL; X03128; CAA26904.1; -.
EMBL; X96876; CAA65619.1; -.
EMBL; Z418B; CAA98713.1; -.
EMBL; UZ7182; AAC49058.1; -.
PIR; A00692; RNBYZL.
   58.68;
   jannaschii.";
Science 273:1058-1073(1996).
  Query Match 58.6
Best Local Similarity 63.6
Matches 7; Conservative
  Methanococcus jannaschii.
   STANDARD;
  ||| ||:| |
1025 RLATRRVLQEY 1035
   2 RLAIRRILLRY 12
  RPOH OR MJ1039
  RESULT
RPOH_METJA
REOH_METJA
~~~443;
```

```
Query Match 56.9
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE OF 1-26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:||: | |:|
53 YKLAVERNLIR 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. OSTER I., ASSOBHEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 98291870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   G3P_CLOPA
Q59309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /CP 18).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G3P_CLOPA
  ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHODOS SON STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT STANTANT S
                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE OF RNA, REMOVING
5'-EXTRA-NUCLEOTIDE FROM TRNA PRECURSOR.
18CELLANEOUS: RNASE P CONSISTS OF A RNA MOIETY (M1, RNPB) AND THE
PROFIEIN COMPONENT. BOTH ARE NEESESSARY FOR FULL ENTMATIC ACTIVITY.
HOWEVER, IT IS THE RNA THAT CARRIES THE CATALYTIC SITE (BY
                                                                                                          "RNA polymerase subunit H features a beta-ribbon motif within a novel fold that is present in archaea and eukaryotes.";
J. Mol. Biol. 287:753-760(1999).
-:- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Transcription; DNA-directed RNA polymerase; 3D-structure.
SEQUENCE 78 AA; 9001 MW; 9F10C0F3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
                                                                                                                                                                                                                                                   CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                           -!- SIMILARITY: TO OTHER ARCHAEBACTERIAL RPOH AND TO THE C-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
RIBONUCLEASE P PROTEIN COMPONENT (EC 3.1.26.5) (PROTEIN C5) (RNASE
                                                                                                                                                                                                    OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSIRATES.
                                                               HODACH M., ELORANTA J.J., KOSTOUROU V., WEINZIERL R.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.5S RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HIMMELREICH R., HILBERT H., PLAGENS H., PIRKL E., LI B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.9%; Score 33; DB 1; Length 78; 66.7%; Pred. No. 4.2; 1: Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.";
Nucleic Acids Res. 24:4420-4449(1996).
-i- FUNCTION: RIBONUCLEASE P GENERATES MATURE TRNA CLEAVING THEIR 5' ENDS. IT CAN CLEAVE ALSO THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE RNPA FAMILY.
                                                                                                                                                                                                                                                                                                                   OF EUKARYOTIC SUBUNIT ABC27 (RPB5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01110; RNA_POL_H_23KD; 1.
PFAM: PF01191; RNA_POI_H; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U67546; AAB99042.1; -. PDB; 1HMJ; U5-APR-99.
TIGR; MJ1039; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=ATCC 29342 / M129;
MEDLINE; 97105885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 66.7
tes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| |:||:
70 YRLVIKRII 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 YRLAIRRIL 9
[2]
STRUCTURE BY NMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                      THIRU A., HOI
MATTHEWS S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNPA_MYCPN
P75111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 6
                                                                  THIRU A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNPA_MYCPN
  ò
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLENGRRUD R., SKUELDAL L.;

"TWO-dimensional gel electrophoresis separation and N-terminal
"TWO-dimensional gel electrophoresis separation and N-terminal
sequence analysis of proteins from Clostridium pasteurianum W5.";
Electrophoresis 19:802-806 (1998).
-!- CATALYTIC ACTIVITY: D-GLYCERALDEHYDE 3-PHOSPHATE + ORTHOPHOSPHATE
+ NAD(+) = 1,3-DIPHOSPHATEGLYCERALE + NADH.
-!- PATHWAY: FIRST STEP IN THE SECOND PHASE OF GLYCOLYSIS.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SUBLILARITY: BELONGS TO THE GLYCERALDEHYDE 3-PHOSPHATE
--- DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING CATALYSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12) (GAPDH) (CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium pasteurianum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSTER T., ASSOBHEI O., SCHERRER S., BRANLANT G., BRANLANT C.; Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 33; DB 1; Length 118;
Pred. No. 6.6;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                       EMBL; AE000017; AAB95809.1; -.
PROSITE; PS00648; RIBONUCLEASE_P; 1.
FYM; PF00825; Ribonuclease_P; 1.
Hydrolase; Nuclease; trnA processing.
SEQUENCE 118 AA; 14003 WW; 5DB7B1B1 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00071; GAPDH; 1.
PFAM; PF00044; gpdh; 1.
Glycolysis; Oxidoreductase; NAD.
BINDING 150 150 GLY
ACT_SITE 177 177 ACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X72219; CAA51020.1; -. HSSP; P00362; 2GD1.
```

¥.

362

STANDARD;

```
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-JUL-1999 (Rel. 38, Last amoutation update)
HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN F PRECURSOR (HLA F
                                      |:|:| :| ||
RVALRNLLRRY 106
                 RLAIRRILLRY 12
                                                                                                                              HLAF_HUMAN
ID HLAF_HUMAN
AC P30511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                    96
                                                    셤
                                                                                                                                                                   à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMEM Outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CH28 ALPHA CHAIN.
STRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                             Gaps
                                                                                                                                                                                                                                                                                                               01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
CHLA CLASS I HISTOCOMPATIBILITY ANTIGEN, CH28 ALPHA CHAIN PRECURSOR.
Pan troglodytes (Chimpanzee)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 335:268-271(1988).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMMUNE SYSTEM.
-!- SUBBNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 88319000.
LAWLOR D.A., WARD F.E., ENNIS P.D., JACKSON A.P., PARHAM P.;
"HLA-A and B polymorphisms predate the divergence of humans and
                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Mammalia;
Catarrhini; Hominidae; Pan.
                                                        Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 346;
                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAWLOR D.A., WARREN E., WARD F.E., PARHAM P.; "Comparison of class I MHC alleles in humans and apes."; Immunol. Rev. 113:147-185(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONNECTING PEPTIDE
                                                      DB 1;
21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
9061EAF0 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78B65140 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 346 AA
                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33;
Pred. No. 2
                                                      Score 33;
Pred. No.
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY
BY
BY
36078 MW;
                                                                                                                                                                                                                                                                                                01-APR-1990 (Rel. 14, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39084 MW;
                                                      56.9%;
87.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M30685; AAA87973.1; -. HSSP; P03989; 1HSA. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                   Query Match
Best Local Similarity 87...
7; Conservative
                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHC I; Transmembrane;
SIGNAL 1 21
CHAIN 22 346
                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Eutheria; Primates;
334 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 90201944.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                   14 RLALRRIL 21
                                                                                                                              2 RLAIRRIL 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chimpanzees.
                                                                                                                                                                                                                                                             1C28_PANTR
P16215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISULFID
CARBOHYD
SEQUENCE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                      RESULT 11
1C28_PANTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
So
                                                                                                                                  ò
                                                                                                                                                                   셤
                                                                                                                                                                                                                                                               DDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDDT-TDDD-TDDD-TDDD-TDDD-TDDD-TDDD-TDDD-TDDD-TDD-TDD-TDD-TDDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD-TDD
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifited and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                             SEQUENCE FROM N.A.
MEDLINE; 90111605.
GERAGHTY D.E., WEI X., ORR H.T., KOLLER B.H.;
"Human leukocyte antigen F (HLA-F). An expressed HLA gene composed of a class I coding sequence linked to a novel transcribed repetitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                                                                                                                                                                                                                           ;
0
                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALPHA CHAIN F.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
; E9B29521 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC TAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A60384; A60384.

PIR; JL0147; JL0147.

MIN; 143110. -.

PROSITE: PS00290; IG_MHC; 1.

PRAM; PF0047; ig_1.

PFAM; PF00129; MHC_I; 1.

MHC I; Transmembrane; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1
Pred. No. 23;
3; Mismatches
ANTIGEN) (LEUKOCYTE ANTIGEN F) (CDA12).
HLA-F OR HLAF OR HLA-5.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X17093; CAA34947.1; -.
                                                                                                                                                                                                              J. Exp. Med. 171:1-18(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 56.9
Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21
362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        362
185
280
                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                        MICROGLOBULIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
112
204
206
3306
122
122
107
362 AA;
```

ö

Gaps

ö

Indels

ed. No. 21; Mismatches

587 AA.

491 RLAIARALLR 500

g

õ 셤

```
MEDLINE; 94341577.

CLIFTON S.W., MCCARTHY D., ROE B.A.;

CLIFTON S.W., MCCARTHY D., ROE B.A.;

"Sequence of the rec-2 locus of Haemophilus influenzae: homologies to come-ORF3 of Bacillus subtilis and msbA of Escherichia coll.";

Gene 146:95-100(1994).

-i- FUNCTION: PROBABLY INVOLVED IN THE SECRETION OF LIPID A (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KERLAVAGE A.R., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLAVAGE A.R., BULT C.J., TOMB J.-F., DOGGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-I., GLODEK A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., SOUGYEN D.T., SAUDEK D.M., BRANDON R.C., GINE L.D., FRITCHMAN J.L., FUHRWANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                            Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                            01-NOV-1995 (Rel. 32, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) PROBABLE TRANSPORT ATP-BINDING PROTEIN MSBA.
                                                                                                             PRT;
                                                                                                                                                                (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64912 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32691; AAC21738.1; -. EMBL; L20805; AAC13734.1; -. TIGR; H10060; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-458 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 269:496-512(1995).
                                                                                                                                                                                                                                                                                    MSBA OR MSH-1 OR HI0060.
                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        influenzae Rd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BC200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VENTER J.C.;
                                                                                                                                                                    01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                         Haemophilus
                                                                                                          MSBA_HAEIN
P44407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
PFAM;
                                                   RESULT 14
MSBA_HAEIN
                                                                                                                   SOLITINE SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION OF SELECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FLEISCHMANN R.D., ADAMS M.D., WHITE O., CLAYTON R.A., KIRKNESS E.F., KERLEAYAGE M., BULT C.J., TOMB J.F., DOGGHERTY B.A., MERRICK J.M., MCKENNEY K., SUTTON G., FITZHUGH W., FIELDS C.A., GOCAYNE J.D., SCOTT J.D., SHIRLEY R., LIU L.-1., GLODER A., KELLEY J.M., WEIDMAN J.F., PHILLIPS C.A., SPRIGGS T., HEDBLOM E., COTTON M.D., UTTERBACK T.R., HANNA M.C., NGUYEN D.T., SAUDEK D.M., BRANDON R.C., FINE L.D., FRIFCHMAN J.L., FUHRWANN J.L., GEOGHAGEN N.S.M., GNEHM C.L., MCDONALD L.A., SMALL K.V., FRASER C.M., SMITH H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SCIENCE 209:496'512(1995).
-!- FUNCTION: SOMEHOW INVOLVED IN THE CYTOCHROME D BRANCH OF AEROBIC RESPIRATION. SEEMS TO BE A COMPONENT OF A TRANSPORT SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROBABLE:
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
(ABC TRANSPORTERS). MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Whole-genome random sequencing and assembly of Haemophilus influenzae \operatorname{Rd}_{-};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 33; DB 1; Length 586; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL).
80EB2DE1 CRC32;
                                                                                                                                                                                                                                                   01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
CYDD OR HI1157.
                                                                                                                                                                                                     586 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Transport; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00211; ABC_TRANSPORTER; 1.
PFAM; PF00005; ABC_tran; 1.
PFAM; PF00664; ABC_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U32795; AAC22812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       Haemophilus influenzae.
                                                      96 RVALRNLLRRY 106
2 RLAIRRILLRY 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           383
586 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLAIRRILLR 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=RD / KW20;
MEDLINE; 95350630.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VENTER J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; HI1157
PROSITE; PS0
                                                                                                                                                                                                  CYDD_HAEIN
P45082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                    HAEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ~
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
(POTENTIAL).
-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS). MSBA SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33; DB 1; Length 587;
Pred. No. 38;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
POTENTIAL.
ATP (POTENTIAL).
FC711A0B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATP-binding; Transport; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                IE; PS00211; ABC_TRANSPORTER; 1. PF00005; ABC_tran; 1. PF00664; ABC_membrane; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.9%;
80.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
```

δ

2 RLAIRRILLR 11

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN+RIZ 'MG1655;
MEDLINE: 97426617.
BLATTNER F.R., PLUNKETT G. III, BLOCH C.A., PERNA N.T., BURLAND V.,
RILEY M., COLLADO-VIDES J., GLASNER F.D., RODE C.K., MAYHEW G.F.,
GREGOR J., DAVIS N.W., KIRKPATRICK H.A., GOEDEN M.A., ROSE D.J.,
MAU B., SHAO Y.;
                                                                                                                                                                                                                                                      Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                         976585;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 127.3 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 87.5%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE000341; AAC75602.1; -.
ECCGENE: EG13468; yphG.
Hypothetical protein.
SEQUENCE 1124 AA; 127284 WW; 0A06B4C6 CRC32;
                                                                                                                          PRT; 1124 AA.
                                                                                                                          STANDARD;
               |||| | |||
493 REAIARALLR 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 YRLAIRRI 8
                                                                                                                                                                                                                                                                                             Sscherichia.
                                                                                                                          YPHG_ECOLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ò
δý
                                qq
```

Search completed: February 8, 2000, 00:59:57 Job time: 3786 sec

|||||| | | 412 YRLAIREI 419

a